

Multibreed Genomic-Polygenic Evaluation: Beef Cattle in Florida and Dairy Cattle in Thailand

M. A. Elzo
University of Florida

Today's Presentation

Animal evaluation models:

- Polygenic
- Genomic
- Genomic-Polygenic

Beef Cattle at UF and Dairy Cattle in Thailand:

- Population Structure
- Animal Evaluations
- Research and Development Results

Multibreed Animal Evaluation Models

Data
Pedigree, Phenotypes, Genotypes

Polygenic: Phenotypes and Pedigree
Genomic: Phenotypes and Genotypes
Genomic-Polygenic: Phenotypes, Pedigree, and Genotypes
Unified Genomic-Polygenic (UGA; Misztal, Legarra, Aguilar)

Polygenic Model Multibreed

Postweaning Gain
=
contemporary group (year-pen)
+ age of dam + sex of calf + age calf
+ Angus fraction calf + heterozygosity calf
+ additive animal polygenic
+ residual

Genomic Model Multibreed

Postweaning Gain
=
contemporary group (year-pen)
+ age of dam + sex of calf + age calf
+ Angus fraction calf + heterozygosity calf
+ additive SNP genomic
+ residual

Genomic-Polygenic Model Multibreed

Postweaning Gain
=
contemporary group (year-pen)
+ age of dam + sex of calf + age calf
+ Angus fraction calf + heterozygosity calf
+ additive animal polygenic
+ additive SNP genomic
+ residual

Polygenic Predictions Multibreed

$$\text{Prediction} = \text{Breed Solution} + \text{Polygenic Prediction}$$

$$\text{EBV}_{\text{animal}} = \text{Animal Angus Fraction} \times \text{Solution (Angus}^\circ - \text{Brahman}^\circ) + \text{Polygenic}_{\text{animal}}$$

Genomic Predictions Multibreed

$$\text{Prediction} = \text{Breed Solution} + \text{Genomic Prediction}$$

$$\text{EBV}_{\text{animal}} = \text{Animal Angus Fraction} \times \text{Solution (Angus}^\circ - \text{Brahman}^\circ) + \text{Sum } [(\# \text{ "Alleles 2" at locus } i) \times (\widehat{\text{SNP}}_i)], i = 1 \text{ to NSNP}$$

Genomic-Polygenic Predictions Multibreed

$$\text{Prediction} = \text{Breed Solution} + \text{Genomic Prediction} + \text{Polygenic Prediction}$$

$$\text{EBV}_{\text{animal}} = \text{Animal Angus Fraction} \times \text{Solution (Angus}^\circ - \text{Brahman}^\circ) + \text{Sum } [(\# \text{ "Alleles 2" at locus } i) \times (\widehat{\text{SNP}}_i)], i = 1 \text{ to NSNP} + \text{Polygenic}_{\text{animal}}$$

Unified Genomic-Polygenic Predictions Multibreed

$$\text{Prediction} = \text{Breed Solution} + \text{Genomic-Polygenic Prediction}$$

$$\text{EBV}_{\text{animal}} = \text{Animal Angus Fraction} \times \text{Solution (Angus}^\circ - \text{Brahman}^\circ) + \text{Genomic - Polygenic}_{\text{animal}}$$

Beef Cattle: UF Multibreed Angus-Brahman Population

Initiated in 1988 at the Pine Acres Unit, Citra; Moved to the BRU in 1995.

Diallel mating design: Sires of 6 breed groups mated to dams of the same 6 breed groups

Breed groups:

BG1 = Angus	= (1.0 to 0.80) Angus (0.0 to 0.20) Brahman
BG2 = ¾ A ¼ B	= (0.79 to 0.60) Angus (0.21 to 0.40) Brahman
BG3 = Brangus	= (0.625) Angus (0.375) Brahman
BG4 = ½ A ½ B	= (0.59 to 0.40) Angus (0.41 to 0.60) Brahman
BG5 = ¼ A ¾ B	= (0.39 to 0.20) Angus (0.61 to 0.80) Brahman
BG6 = Brahman	= (0.19 to 0.0) Angus (0.81 to 1.00) Brahman

Mating (random): 3 to 5 sires & 40 dams per breed group per year

Connectedness across years: One or more sires per breed group used for 2 years

Multibreed Angus-Brahman heifers of various breed compositions



Heifer 3040168: 3_16A 16B; Sire: 4_8A 24B; Dam: 2_24A 8B



Dam 3020119: 5_6A 26B; Sire: 4_10A 22B; Dam: 5_1A 31B



Calf 3070021: 2_22A 10B; Sire: 1_32A 0B; Dam: 3_13A 19B



[3k] Genomic-Polygenic, Genomic, and Polygenic Models

Genomic-polygenic evaluation of Angus-Brahman multibreed cattle using the **Illumina 3K chip** for postweaning feed efficiency and growth [2012] and for postweaning ultrasound carcass and weight traits [2013]

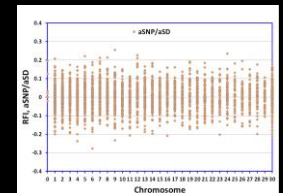
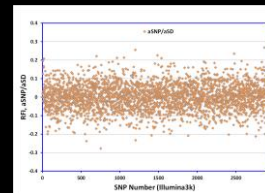
Animals: 620 multibreed calves born from 2006 to 2010

3 models: Genomic-Polygenic, Genomic, Polygenic; Program: GS3

4 traits: Residual feed intake, Daily feed intake, Feed conversion ratio, Postweaning gain

Fraction of additive genetic variance explained by 2,899 Illumina 3k SNP markers

Compare EPD rankings across models



Additive Genetic and Genomic Variation for RFI, DFI, FCR and PWG (nSNP = 2,899)

Trait	Total GenVar	PhenVar	Heritability	GenomVar / Total GenVar
RFI, (kg/d) ²	0.35	1.76	0.20	0.15
DFI, (kg/d) ²	0.73	2.34	0.31	0.11
FCR, (kfd/kgd) ²	1.37	6.51	0.21	0.25
PWG, kg ²	87.2	240.8	0.36	0.15

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

Additive Genetic and Genomic Variation for UREA, UBF, UPIMF and UW (nSNP = 2,899)

Trait	Total GenVar	PhenVar	Heritability	GenomVar / Total GenVar
UREA, cm ⁴	22.2	56.3	0.39	0.09
UBF, cm ²	0.006	0.022	0.25	0.38
UPIMF, % ²	0.31	0.59	0.53	0.06
UW, kg ²	668.9	1227.3	0.54	0.08

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

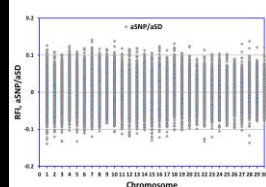
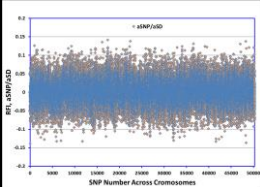
[50k] Genomic-Polygenic, Genomic, and Polygenic Models

Genomic-polygenic evaluation of multibreed Angus-Brahman cattle using actual and imputed Illumina50k SNP genotypes for postweaning feed efficiency and growth [2014] and for postweaning ultrasound carcass and weight traits [2015]

Animals: 807 multibreed calves born from 2006 to 2010

3 models: Genomic-Polygenic, Genomic, Polygenic; Program: GS3

4 traits: Residual feed intake, Daily feed intake, Feed conversion ratio, Postweaning gain
Fraction of additive genetic variance explained by 46,909 Illumina 50k SNP markers
Compare EPD rankings across models



Additive Genetic and Genomic Variation for RFI, DFI, FCR and PWG (nSNP = 46,909)

Trait	Total GenVar	PhenVar	Heritability	GenomVar / Total GenVar
RFI, (kg/d) ²	(0.35) 0.55	(1.76) 1.79	(0.20) 0.30	(0.15) 0.48
DFI, (kg/d) ²	(0.73) 0.85	(2.34) 2.28	(0.31) 0.37	(0.11) 0.36
FCR, (kfd/kgd) ²	(1.37) 1.68	(6.51) 6.62	(0.21) 0.25	(0.25) 0.50
PWG, kg ²	(87.2) 80.8	(240.8) 245.6	(0.36) 0.33	(0.15) 0.28

	Trait			
Correlation	RFI	DFI	FCR	PWG
GP Model, G Model	(0.65) 0.93	(0.62) 0.91	(0.66) 0.89	(0.74) 0.89
GP Model, P Model	(0.98) 0.94	(0.99) 0.97	(0.95) 0.93	(0.99) 0.98
G Model, P Model	(0.52) 0.77	(0.51) 0.80	(0.42) 0.69	(0.65) 0.81

Additive Genetic and Genomic Variation for UREA, UBF, UPIMF and UW (nSNP = 46,909)

Trait	Total GenVar	PhenVar	Heritability	GenomVar / Total GenVar
UREA, cm ⁴	(22.2) 21.9	(56.3) 55.8	(0.39) 0.39	(0.09) 0.17
UBF, cm ²	(0.006) 0.007	(0.022) 0.023	(0.25) 0.31	(0.38) 0.32
UPIMF, % ²	(0.31) 0.32	(0.59) 0.59	(0.53) 0.55	(0.06) 0.25
UW, kg ²	(668.9) 778.2	(1227.3) 1198.8	(0.54) 0.43	(0.08) 0.19

	Trait			
Correlation	UREA	UBF	UPIMF	UW
GP Model, G Model	(0.65) 0.86	(0.79) 0.87	(0.64) 0.94	(0.70) 0.81
GP Model, P Model	(0.99) 0.95	(0.89) 0.93	(0.99) 0.95	(0.99) 0.96
G Model, P Model	(0.58) 0.71	(0.51) 0.66	(0.60) 0.81	(0.65) 0.71

[50k] Unified Genomic-Polygenic and Polygenic Models

Genetic parameters and predictions for direct and maternal growth traits in multibreed Angus-Brahman cattle using genomic-polygenic and polygenic models [2015]

Animals: 5,264 multibreed calves born from 1987 to 2013

Animals with actual & imputed 46,768 Illumina 50k genotypes: 1,232

5 traits: Birth Wt Dir & Mat, Weaning Wt Dir & Mat, Postweaning Gain Direct

4 models: 3 Unified Genomic-Polygenic and 1 Polygenic; Program: BLUPF90 FamProg

GP Model 1: All available phenotypes, pedigree, and genotypes (complete model)

GP Model 2: Pedigree relationships among non-genotyped animals; genomic relationships among genotyped animals. Ignore pedigree relationships between genotyped and non-genotyped animals.

(e.g., genotyped animals come from a different unrelated population)

GP Model 3: No pedigree relationships; genomic relationships for genotyped animals.

(e.g., commercial beef producers)

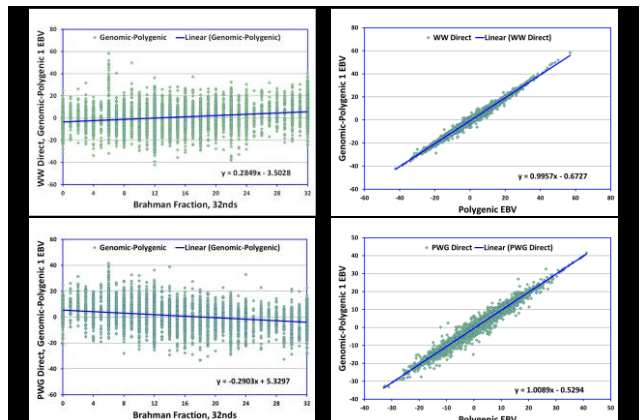
Polygenic Model: All available phenotype and pedigree information.

Variance components and genetic parameters across models

EBV Correlations across models

EBV Trends from Angus to Brahman

Trait pair	Heritabilities and Genetic Correlations			
	PM	GPM1	GPM2	GPM3
BWD, BWD	0.58	0.53	0.62	0.32
BWD, WWD	0.64	0.61	0.67	0.44
BWD, PWGD	0.01	0.04	-0.05	-0.23
BWD, BWM	-0.43	-0.37	-0.47	-0.12
BWD, WWM	-0.16	-0.10	-0.20	0.20
WWD, WWD	0.35	0.36	0.35	0.26
WWD, PWGD	0.50	0.52	0.20	0.28
WWD, BWM	-0.03	0.01	-0.05	0.33
WWD, WWM	0.06	0.05	-0.11	-0.02
PWGD, PWGD	0.33	0.34	0.30	0.22
PWGD, BWM	0.40	0.41	0.20	-0.05
PWGD, WWM	0.21	0.26	0.39	0.08
BWM, BWM	0.26	0.24	0.25	0.40
BWM, WWM	0.37	0.34	0.36	0.15
WWM, WWM	0.21	0.22	0.22	0.13



Correlations between EBV							
Trait	Top	GPM1, GPM2	GPM1, GPM3	GPM1, PM	GPM2, GPM3	GPM2, PM	GPM3, PM
BWD	5%	0.61	0.40	0.90	0.73	0.66	0.47
	10%	0.69	0.54	0.93	0.75	0.74	0.59
	25%	0.78	0.58	0.96	0.64	0.82	0.59
	100%	0.93	0.78	0.99	0.87	0.94	0.80
WWD	5%	0.72	0.49	0.95	0.47	0.76	0.51
	10%	0.72	0.48	0.96	0.54	0.74	0.49
	25%	0.77	0.57	0.96	0.64	0.79	0.59
	100%	0.94	0.85	0.99	0.87	0.94	0.85
PWGD	5%	0.46	0.35	0.88	0.68	0.47	0.36
	10%	0.55	0.36	0.90	0.67	0.55	0.40
	25%	0.58	0.38	0.91	0.59	0.56	0.41
	100%	0.82	0.56	0.98	0.67	0.81	0.56
BWM	5%	0.45	0.04ns	0.83	-0.08ns	0.46	-0.04ns
	10%	0.38	0.03ns	0.86	-0.11*	0.45	-0.04ns
	25%	0.50	0.06*	0.90	-0.13	0.53	-0.04ns
	100%	0.85	-0.08	0.98	-0.19	0.84	-0.12
WWM	5%	0.38	0.11ns	0.88	-0.04ns	0.28	0.06ns
	10%	0.40	0.15	0.89	-0.01ns	0.34	0.10*
	25%	0.53	0.13	0.92	-0.01ns	0.47	0.06*
	100%	0.83	0.26	0.98	0.15	0.82	0.23

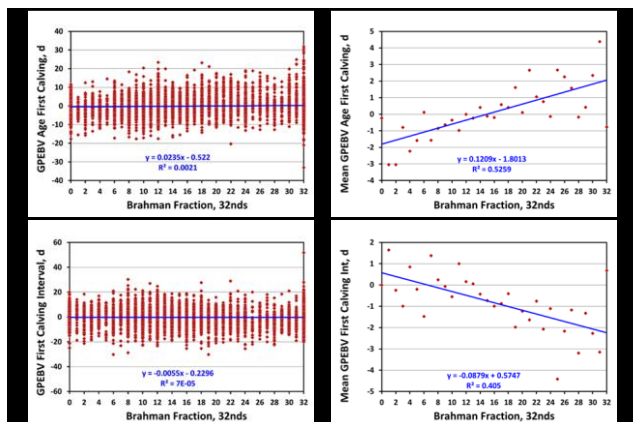
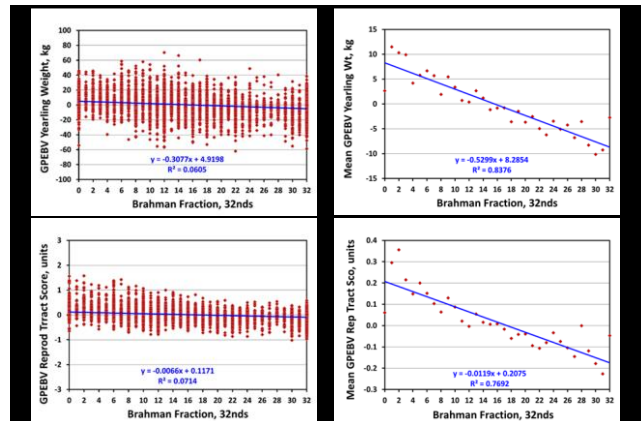
[150k] Unified Genomic-Polygenic and Polygenic Models

Growth and reproduction genomic-polygenic and polygenic parameters and prediction trends as Brahman fraction increases in an Angus-Brahman multibreed population [2016]

Animals: 1,758 multibreed calves born from 2006 to 2015
 Animals with actual & imputed 113,459 GeneSeek GGPHD150k genotypes: 1,547
 4 traits: Yearling Wt, Reproductive tract score, Age at first calving, First calving interval
 2 models: Unified Genomic-Polygenic and Polygenic; Program: BLUPF90 FamProg

Variance components and genetic parameters
 EBV Trends from Angus to Brahman for individual animals and for breed groups

Trait pair	Heritabilities and Genetic Correlations	
	GPM	PM
YW, YW; kg ²	0.47	0.45
YW, RTS; kg*u	0.53	0.60
YW, AFC; kg*d	0.05	-0.02
YW, FCI; kg*d	0.04	-0.01
RTS, RTS; u*u	0.31	0.30
RTS, AFC; u*d	-0.22	-0.55
RTS, FCI; u*d	-0.16	-0.05
AFC, AFC; d ²	0.14	0.12
AFC, FCI; d ²	-0.67	-0.67
FCI, FCI; d ²	0.31	0.29



[250k] Unified Genomic-Polygenic and Polygenic Models

Genomic-polygenic and polygenic predictions for nine ultrasound and carcass traits in Angus-Brahman multibreed cattle using three sets of genotypes [2017]

Animals: 1,981 multibreed calves born from 2006 to 2015
 Animals with 127,016 GeneSeek GGPHD250k genotypes: 782
 9 traits: 4 ultrasound traits and 5 carcass traits
 4 Ultrasound traits: yearling weight, ribeye area, backfat, percent intramuscular fat
 5 Carcass traits: slaughter age, hot carcass wt, ribeye area, backfat, marbling score
 4 models: 3 Unified Genomic-Polygenic and 1 Polygenic; Program: BLUPF90 FamProg

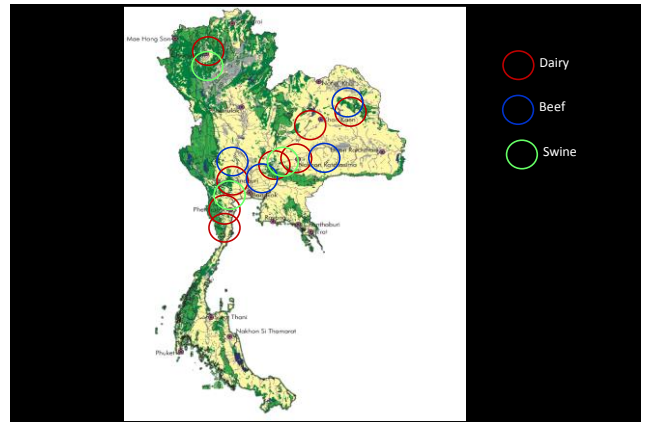
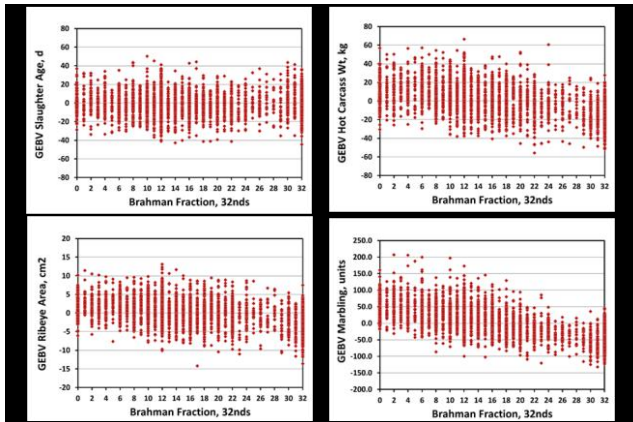
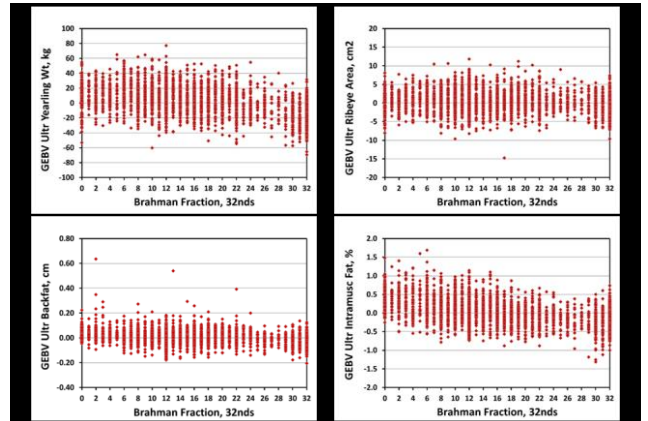
GP Complete Model: All available phenotypes, pedigree, and SNP
 GP Reduced Model 1: All available phenotypes, pedigree, and top 5% SNP (nSNP = 24,761)
 GP Reduced Model 2: All available phenotypes, pedigree, and 5% SNP evenly spread across the genome
 Polygenic Model: All available phenotype and pedigree information

Variance components and genetic parameters (GP Model 1 and Polygenic)
 EBV, accuracies, and rankings across models (GP, GP reduced 1 & 2, and polygenic)

Heritabilities and Genetic Correlations for yearling ultrasound and carcass traits		
Heritabilities and Genetic Correlations		
Trait pair	CPM	PM
UW,UW,kg ²	0.54	0.51
UW,UREA,kg ² cm ²	0.65	0.69
UW,UPM,kg ² cm ²	-0.14	-0.14
UW,SLA,kg ² g	-0.20	-0.26
UW,HCV,kg ² kg	0.67	0.63
UW,REA,kg ² cm ²	0.42	0.36
UW,FAT,kg ² cm	0.11	0.35
UREA,UPM,cm ² %	0.36	0.34
UREA,SLA,cm ² %	-0.30	-0.24
UREA,REA,cm ² %	-0.24	-0.24
UREA,SLA,cm ² cm ²	0.42	0.37
UREA,SLA,cm ² cm ²	0.67	0.58
UREA,REA,cm ² units	-0.12	-0.10
UPM,UPM,cm ² %	0.12	0.11
UPM,UPM,cm ² %	0.25	0.26
UPM,SLA,cm ² %	-0.31	-0.30
UPM,HCV,cm ² %	-0.27	-0.28
UPM,FAT,cm ² cm	0.81	0.69
UPM,REA,cm ² units	0.15	0.16
UPM,REA,kg ² %	0.36	0.30
UPM,SLA,kg ² %	-0.16	-0.16
UPM,SLA,kg ² %	-0.10	-0.11
UPM,SLA,kg ² %	-0.28	-0.16
UPM,REA,kg ² units	0.60	0.56
REA,REA,kg ² %	0.59	0.61
SLA,HCV,d ² kg	0.28	0.29
SLA,REA,d ² cm ²	0.13	0.13
HCV,HCV,kg ²	0.58	0.57
HCV,REA,kg ² cm ²	0.57	0.70
HCV,FAT,kg ² cm	0.12	0.23
REA,REA,cm ² units	0.48	0.45
REA,FAT,cm ² cm	-0.04	0.10
REA,UPM,cm ² units	-0.27	-0.23
FAT,FAT,cm ²	0.42	0.30
FAT,REA,cm ² units	0.19	0.25
REA,REA,kg ² units	0.56	0.51

Mean differences between GPEBV1, GPEBV1, and PEBV relative to GPEBV					
Trait	Animals	N	GPEBV1	GPEBV2	PEBV
UW	Sires	292	-0.09	0.05	-0.14
	Dams	1,238	0.04	0.06	-0.43
	All	3,633	-0.03	0.05	-0.24
UREA	Sires	292	0.00	0.00	-0.06
	Dams	1,238	0.00	0.00	-0.06
	All	3,633	0.01	0.00	-0.08
UPM	Sires	292	0.00	0.00	0.00
	Dams	1,238	0.00	0.00	0.00
	All	3,633	0.01	0.00	-0.07
SLA	Sires	292	-0.06	0.02	-0.69
	Dams	1,238	0.15	0.04	-0.96
	All	3,633	0.00	0.02	-1.37
HCV	Sires	292	-0.07	0.02	-1.18
	Dams	1,238	0.10	0.04	-0.89
	All	3,633	-0.09	0.02	-1.48
REA	Sires	292	-0.01	0.00	-0.24
	Dams	1,238	0.03	0.01	-0.21
	All	3,633	0.00	0.00	-0.31
FAT	Sires	292	0.00	0.00	0.00
	Dams	1,238	0.00	0.00	0.00
	All	3,633	0.00	0.00	0.00
MAR	Sires	292	-0.07	-0.05	1.42
	Dams	1,238	-0.03	0.05	1.42
	All	3,633	-0.22	0.00	0.98

Mean differences between Accuracies of GPEBV1, GPEBV1, and PEBV relative to GPEBV					
Trait	Animals	N	GPEBV1	GPEBV2	PEBV
UW	Sires	292	0.00	0.00	-0.14
	Dams	1,238	-0.02	0.01	-0.43
	All	3,633	-0.01	0.04	-0.24
UREA	Sires	292	0.02	0.02	-0.06
	Dams	1,238	-0.03	0.03	-0.06
	All	3,633	-0.01	0.03	-0.20
UPM	Sires	292	0.00	0.00	0.00
	Dams	1,238	-0.05	0.03	0.00
	All	3,633	-0.02	0.04	0.00
SLA	Sires	292	0.10	0.03	-0.68
	Dams	1,238	-0.03	0.03	-0.96
	All	3,633	0.00	0.05	-1.18
HCV	Sires	292	0.00	0.05	-0.89
	Dams	1,238	-0.03	0.02	-0.89
	All	3,633	0.00	0.05	-1.48
REA	Sires	292	0.04	0.04	-0.24
	Dams	1,238	-0.05	0.03	-0.21
	All	3,633	-0.03	0.04	-0.31
FAT	Sires	292	0.00	0.00	0.00
	Dams	1,238	-0.06	0.03	0.00
	All	3,633	-0.03	0.06	0.00
MAR	Sires	292	0.07	0.05	2.68
	Dams	1,238	-0.04	0.03	1.42
	All	3,633	-0.01	0.06	1.42
Misc	Sires	292	0.05	0.04	3.08
	Dams	1,238	-0.04	0.02	-0.12
	All	3,633	-0.02	0.05	0.07



Dairy Cattle: Thai Multibreed Population

Mating program: Upgrading Thai Native and cattle from 6 other breeds to Holstein

Original breeds: Brahman, Jersey, Brown Swiss, Red Dane, Red Sindhi, Sahiwal and Thai Native

Current breed composition: 94% sires and 73% dams are at least 75% Holstein

Climate: Tropical (high temperature and humidity most of the year)

Typical Management: Cows kept in open barns, fed roughage, concentrate, and free access to a mineral supplement.

Genetic Evaluation System: Multibreed Polygenic (2003 – 2015) and Multibreed Genomic (2016 - present)



Dairy Cattle: Genetic Evaluation and Parameter Estimation Multiple Traits: Milk yield, Fat yield, Fat Percentage

Multibreed Sire-Maternal Grand sire Models with additive and nonadditive group and random genetic effects (unequal variances and covariances across breed groups; MREMLEM)
[Skorn Koonawootrittriron, 2002]

$$\begin{aligned} \text{Additive} \quad u_a &= g_a + a_a, \quad g_a = f_{BT} * Sol(BT - BI) \text{ or } g_a = f_H * Sol(H - O) \\ \text{Nonadditive} \quad u_n &= \sum_{i=1}^2 \sum_{j=1}^2 (p_{ij}) * (g_{nij} + a_{nij}), \text{ where } i, j = BT \text{ and } BI \text{ or } H \text{ and } O \\ \text{Total} \quad u_t &= u_a + u_n \end{aligned}$$

Multibreed Animal Models with additive and nonadditive group and random additive genetic effects (equal variances and covariances across breed groups; ASREML)
[Skorn Koonawootrittriron, 2002]

$$\begin{aligned} \text{Additive} \quad u_a &= g_a + a_a, \quad g_a = f_{BT} * Sol(BT - BI) \text{ or } g_a = f_H * Sol(H - O) \\ \text{Heterosis} \quad u_n &= \sum_{i=1}^2 \sum_{j=1}^2 (p_{ij}) * (g_{nij}), \text{ where } i, j = BT \text{ and } BI \text{ or } H \text{ and } O \\ &\text{Deviated from the average of the base groups (BT and BI or H and O).} \end{aligned}$$

This model became the Multibreed Animal Model used from 2003 to 2015 in the DPO population

Dairy Cattle: Survey Information Factors Influencing Productivity & Revenues at Farm Level

Record keeping, genetic selection, educational experience and farm management effects on average milk yield per cow, milk fat percentage, bacterial score and bulk tank somatic cell count of dairy farms in the Central region of Thailand
[Jeff Rhone, 4 papers, Muak Lek Dairy Producer Cooperative, 2007-2008]

Effect of experience, education, record keeping, labor and decision making on monthly milk yield and revenue of dairy farms supported by a private organization in Central Thailand
[Supawadee Yeamkong, 3 papers, Midland Dairy Limited Partnership, 2010-2012]

Winter => Higher milk yields than summer and rainy seasons
Small and large farms => Higher milk yields per cow and lower bacterial score than medium farms
Longer experience, higher educational level, hired labor, recorded data, EBV or phenotypes used for selection => Higher milk yield and revenue per farm and per cow
Muak Lek farms => Higher milk yields than Non-Muak Lek farms
Muak Lek and Midland Dairy Limited Partnership farms => Similar milk production and revenue
Dairy organizations => Support dairy farms according to their individual characteristics
Sharing experiences and information among dairy organizations => Improve productivity and revenues

These studies utilized information produced by the dairy extension program initiated in 2004 and helped target factors affecting farm productivity and revenues

Dairy Cattle: National Genomic Evaluation Project (KU-UF, NSTDA-DPO)

Goal

To improve the sustainability and competitiveness of dairy farmers in Thailand by increasing the rate of genetic progress and the accuracy of genetic selection in dairy cattle through the development of a genomic-polygenic evaluation system that includes a DNA repository, a reference genomic dairy population, and genomic-polygenic models and procedures tailored to Thai tropical environmental conditions.

Research and Development Objectives → Accomplished

Training Objectives → In Progress

National Genomic Evaluation Project

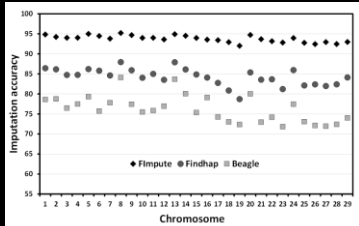
Outcomes by Objective:

- 1) DNA repository of tissue samples from parents and progeny (blood, semen).
[89 sires and 2572 cows; North, Northeastern, Western, Central, and Southern regions]
- 2) To develop a reference genomic dairy population using high- and low-density genotyping chips.
[GeneSeek GGPLD9k (n = 1412), GGPLD20k (n = 570), GGPLD26k (n = 540), and GGPHD80k (n = 139)]
- 3) To develop a database system that integrates pedigree, genotypic, and phenotypic information into a unified system that maximizes its utilization for dairy genetic improvement and scientific research in Thailand.
[Implemented in 2014; North, Northeastern, Western, Central, and Southern regions]
- 4) Genomic-polygenic prediction models that use phenotypes, pedigree, and genotypes.
[Imputation Procedures; Subclass Animal, Random Regression, Spline Models; Papers: 3 published; 2 submitted]
- 5) Association between genomic SNP and economically important traits.
[Linkage Disequilibrium; Genome-Wide Association; GGPLD9k; SNP in all chips; Papers: 1 published; 1 submitted]
- 6) To develop a genomic-polygenic evaluation system that combines phenotypes, pedigree, and genotypes to maximize the accuracy of predictions and rates of genetic change.
[Multiple-Trait Genomic-Polygenic; Implemented in 2016; DPO National Genomic Evaluation]
- 7) To produce graduate students with a strong background in genomic-polygenic evaluation models and procedures and capable of conducting national genomic-polygenic dairy cattle evaluations.
[5 PhD: 2 Graduated, 3 In Progress; 2 MS]

Imputation & Genomic Prediction: Low to Medium Density Chips

Imputation Accuracy from Low to Moderate Density Single Nucleotide Polymorphism Chips in a Thai Multibreed Dairy Cattle Population. [Danai Jattawa, 2016]

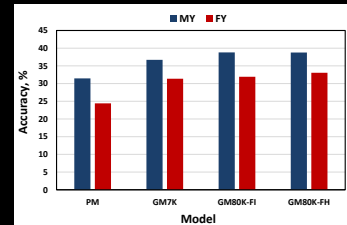
1244 animals (84 sires, 1160 cows); 145 farms; First lactations from 2003 to 2011
Imputation from 7652 SNP (GGPLD9k) to 17779 SNP (GGPLD20k, GGPLD26k, GGPHD80k)
Overall Imputation Accuracies => FImpute (94%), Findhap (85%), Beagle (77%)



Subclass Animal Models: Genomic-Polygenic & Polygenic

Comparison of genetic evaluations for milk yield and fat yield using a polygenic model and three genomic-polygenic models with different sets of SNP genotypes in Thai multibreed dairy cattle [Danai Jattawa, 2015]

8361 first-lactation cows (1210 sires, 6992 dams); 810 farms; First lactations from 1989 to 2014
5 regions: North, Northeastern, Western, Central, and Southern
4 models: Polygenic, GenomPol7k, GenomPol80kFImpute, GenomPol80kFindhap
2 traits: Milk yield and Fat yield
Rank Correlations: Highest => GM80K-FI & GM80K-FH; Lowest => PM & GM7K



Mean prediction accuracies from Genomic-Polygenic and Polygenic models

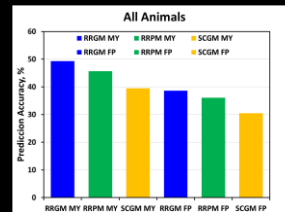
Type of animal	n	GPM		PM		Accuracy Increase
		MY	FP	MY	FP	
All animals	17,363	38.4	27.5	33.1	23.6	4.5
Non-genotyped animals	14,702	36.7	26.4	31.1	22.5	4.8
Genotyped animals	2,661	46.2	32.5	42.6	29.1	3.5
Genotyped cows	2,572	34.5	26.2	26.9	18.9	7.5
Genotyped sires	89	64.5	43.8	59.9	43.2	2.6
Genotyped proven sires	58	69.5	47.1	67.2	49.0	0.2
Genotyped young sires	31	42.3	26.5	27.5	12.5	14.4

Tropical Animal Genetic Unit

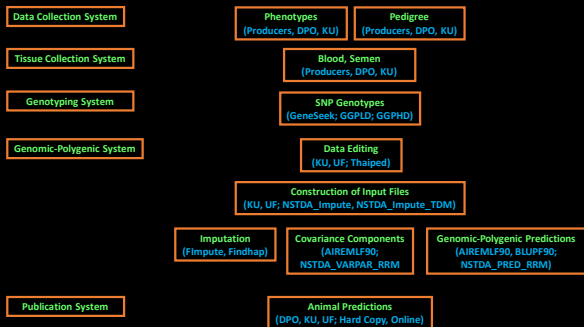
Random Regression Animal Models: Genomic-Polygenic & Polygenic

Genomic-polygenic and polygenic evaluations for milk yield and fat percentage using random regression models with Legendre polynomials in a Thai multibreed dairy population [Danai Jattawa, 2016]

7206 first-lactation cows (933 sires, 6415 dams); 761 farms; First lactations from 1997 to 2014
5 regions: North, Northeastern, Western, Central, and Southern
3 models: RR Pol (RRPM), RR GenomPol (RRGM), Subclass GenomPol (SCGM)
2 traits: Milk yield and Fat percentage
Rank Correlations: Highest => RRRM & RRRM; Lowest => RRRM & SCGM



Current: Thai Dairy Genomic-Polygenic Evaluation



People in Florida

Personnel at UF beef research units
Florida Cattlemen

University of Florida

Don Wakeman Dwain Johnson Carlos Manrique
Jerry Wasdin Owen Rae William Odenya
Paul Dixon Raluca Mateescu Skorn Koonawootrittriron
Danny Driver KC Jeong Carlos Martinez
Michelle Driver Cliff Lamb Danai Jattawa

Colorado State University
Milton Thomas

University of Georgia
Ignacy Misztal
Shogo Isuruta

Texas A&M University
David Riley

People in Thailand

Kasetsart University	Dairy Farming Promotion Organization of Thailand	
National Science and Technology Development Agency	National Research Council of Thailand	
Royal Golden Jubilee Ph.D. Program of the Thailand Research Fund		
Kasetsart University Research and Development Institute		

Dairy, Beef, and Swine Producers	Pon Yang Kharm Beef Cooperative Ltd.	Thai Serve Co. Ltd.
Loongchao Brahman Co. Ltd.	Buriram Beef Producer Network	Smile Beef Co. Ltd.
Muak Lek Dairy Cooperative Ltd.	Midland Dairy Limited Partnership	
Sampran Farm Co. Ltd.	Four T Co. Ltd.	

Skorn Koonawootrittriron	Thanathip Suwanasopee	Thawee Laodim (MS, PhD)
Dalai Jattawa (MS, PhD)	Udomsak Noppibool (PhD)	Mattaneeeya Sarakul (MS, PhD)
Bodin Wongpom (PhD)	Tawirat Konkrua (PhD)	Teerapong Jaichsukkit (PhD)
Pimchanok Yodklaew (MS)	Thirarat Sae-Tiao (MS)	Chatchai Chansomboon (PhD)
Namtip Jirattakarpan (MS)	Chayanid Niyom (MS)	Gebreglabher Gebreyohannes (PhD)
Chauwalit Pluemjai (MS)	Jirayut Kemsawat (MS)	Thuwapol Kongnoi (MS)
Supawadee Yeamkong (PhD)	Jeffrey Rhone (PhD, UF)	Ameena Seangjun (MS)
Somsak Prampree (MS)	Taradon Punsanit (MS)	Praew Thiengimol (MS)
Praniti Pholsing (MS)	Thanathip Lasa-ard (MS)	
Tummanoon Thongrapai (DPO)	Chockchai Chaimongkol (DPO)	Poj Ritsawai (DPO)

