

Genomic evaluation in cattle: Experiences from UF and KU

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UF Beef Genomics Project

KU Dairy Genomics Project

UF Beef Genomics Project

Objectives

Population, Mating System, Data

Results

Objectives

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

Ranking of animals for feed efficiency, growth, ultrasound,
carcass, and meat palatability traits using genomic-polygenic,
genomic, and polygenic models

Trends in calf predicted values with the 3 models for all traits as
Brahman fraction increased from 0% to 100%

Here: RFI, DFI, FCR and PWG

Mating System: Diallel

2012: 22 Sires

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

2012: 322 Dams

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

Matings 2012



| BGDdam | 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 |



Data and Traits (2006 – 2010)

Phenotypic Data
Growth, Feed Intake (UFFEF)

Genomic Data
Genotypes (Illumina3K chip)

Traits
RFI, DFI, FCR and PWG

UF Feed Efficiency Facility

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





Tissue Sampling and Genotyping

| |
|---|
| Sires Semen (4 straws) or Blood (10cc) |
| Dams and Calves Blood (10cc) |
| Genotyping GeneSeek (Illumina3K; 2,900 markers) |

Number of calves by breed group of sire x breed group of dam combination (2006-2010)

| 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 | 48 | 18 | 18 | 7 | 7 | 17 | 105 |
| ¼ A ¼ B | 24 | 21 | 33 | 26 | 14 | 16 | 134 |
| Brangus | 4 | 10 | 60 | 9 | 10 | 7 | 100 |
| ½ A ½ B | 30 | 27 | 21 | 26 | 22 | 20 | 146 |
| ¾ A ¾ B | 13 | 17 | 12 | 9 | 11 | 4 | 66 |
| Brahman | 1 | 2 | 1 | 0 | 0 | 68 | 72 |
| All | 118 | 87 | 145 | 77 | 64 | 132 | 623 |

Genotypes: 2006-2010

Phenotypes & Genotypes: 2006-2010

Genomic-Polygenic Model

RFI, FCR, DFI, PWG

=
 year-pen + age of dam
 + sex of calf + age calf
 + BF calf + Het calf
 + additive animal polygenic
 + additive SNP genomic
 + residual

GS3: VCE (Variance Components)
 GS3: BLUP (Genomic-Polygenic Predictions)

Genomic Model

RFI, FCR, DFI, PWG

=
 year-pen + age of dam
 + sex of calf + age calf
 + BF calf + Het calf
 + additive SNP genomic
 + residual

GS3: VCE (Variance Components)
 GS3: BLUP (Genomic Predictions)

Polygenic Model

RFI, FCR, DFI, PWG

=
 year-pen + age of dam
 + sex of calf + age calf
 + BF calf + Het calf
 + additive animal polygenic
 + residual

GS3: VCE (Variance Components)
 GS3: BLUP (Polygenic Predictions)

Genomic-Polygenic Predictions

$$\text{Prediction} = \text{Breed Solution} + \text{Sum SNP predictions} + \text{Polygenic prediction}$$

$$\text{EBV}_{\text{animal}} = \text{Prob (Alleles Brahman)} * (\text{Brahman}^\circ - \text{Angus}^\circ) + \text{Sum } [(\# \text{ "Alleles 2" at locus } i) * (\widehat{\text{SNP}}_i)], i = 1 \text{ to } 2,899 + \hat{a}_{\text{animal}}$$

Genomic Predictions

$$\text{Prediction} = \text{Breed Solution} + \text{Sum SNP predictions}$$

$$\text{EBV}_{\text{animal}} = \text{Prob (Alleles Brahman)} * (\text{Brahman}^\circ - \text{Angus}^\circ) + \text{Sum } [(\# \text{ "Alleles 2" at locus } i) * (\widehat{\text{SNP}}_i)], i = 1 \text{ to } 2,899$$

Polygenic Predictions

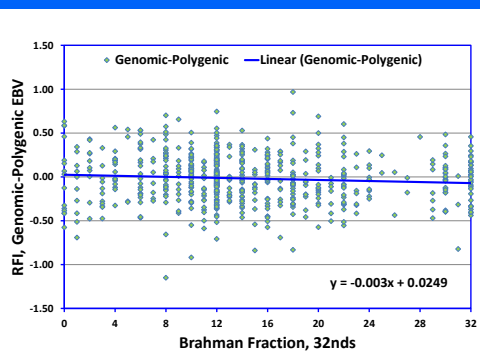
$$\text{Prediction} = \text{Breed Solution} + \text{Polygenic prediction}$$

$$\text{EBV}_{\text{animal}} = \text{Prob (Alleles Brahman)} * (\text{Brahman}^\circ - \text{Angus}^\circ) + \hat{a}_{\text{animal}}$$

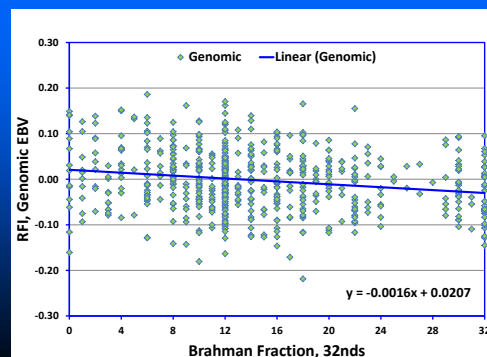
Additive Genetic and Genomic Variation for RFI, DFI, FCR and PWG

| Trait | Parameter | AGVar | PhenVar | Heritability | AGOVari/AGVar |
|-------|--------------|-------|---------|--------------|---------------|
| RFI | Mean | 0.37 | 1.73 | 0.21 | 0.14 |
| | (kg/d) SD | 0.15 | 0.11 | 0.08 | 0.11 |
| DFI | Mean | 0.80 | 2.42 | 0.33 | 0.10 |
| | (kg/d) SD | 0.24 | 0.15 | 0.09 | 0.08 |
| FCR | Mean | 1.32 | 6.50 | 0.20 | 0.26 |
| | (kfd/kgd) SD | 0.56 | 0.40 | 0.08 | 0.17 |
| PWG | Mean | 89.74 | 240.97 | 0.37 | 0.16 |
| | (kg) SD | 25.85 | 15.09 | 0.10 | 0.11 |

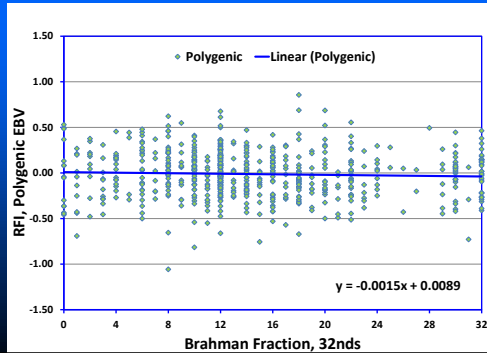
Genomic-Polygenic EBV for RFI



Genomic EBV for RFI



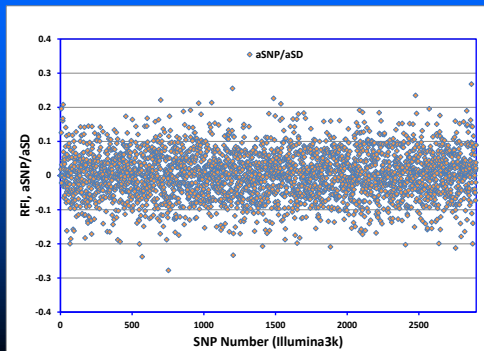
Polygenic EBV for RFI



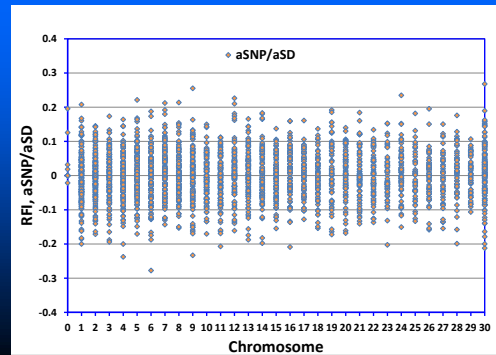
Rank correlations of animals evaluated for RFI, DFI, FCR, and PWG using genomic-polygenic, genomic, and polygenic models

| 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 |

Predicted SNP Values for RFI Ordered by Location Across Chromosomes



Predicted SNP Values for RFI Ordered by Chromosome



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 |

KU Dairy Genomics Project

Project Information

Objectives

Population, Mating System, Data

Current Activities

Project Information

2012 - 2015

Funding

National Science and Technology Development Agency (NSTDA)
Kasetsart University (KU)
Dairy Farming Promotion Organization (DPO)

Participating Organizations

Kasetsart University (KU)
University of Florida (UF)
Dairy Farming Promotion Organization (DPO)
Muaklek Dairy Cooperative Limited (MLDC)

Objectives

Develop a Genetic Evaluation System that Utilizes Phenotypic, Genotypic, and Pedigree Information

Create a Reference Dairy Population for Genomic Evaluation

Construct a Tissue Sample and DNA Repository

Establish a Database System
(Phenotypes, Genotypes, Pedigree, Economic)

Train Graduate Students



Population with Phenotypes and/or Genotypes

Multibreed (Holstein-Other Breeds)

(Other Breeds: Brahman, Brown Swiss, Jersey, Red Dane, Red Sindhi, Sahiwal, Shorthorn, and Thai Native)

3,500 Animals

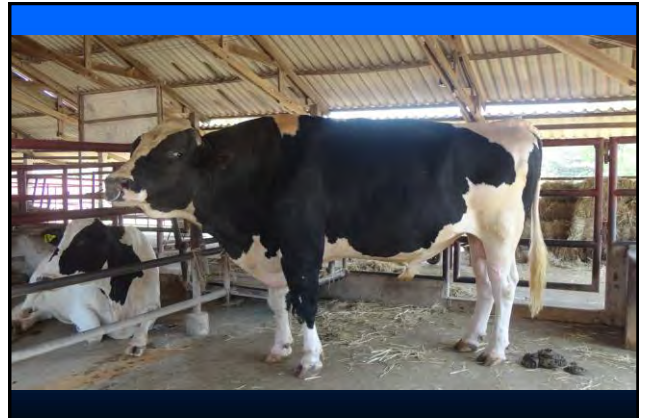
250 Sires (Genotypes)
3,250 Cows (Phenotypes, Genotypes)

240 Farms

70 % in Central Region (168 Farms)
14 % in Northeastern Region (34 Farms)
16 % in Southern Region (36 Farms)

Number of Sires and Dams DPO Population 2012

| Breed group | Sires | Dams |
|----------------------|------------|--------------|
| (0.8 - 1.0) Holstein | 119 | 1,815 |
| (0.6 - 0.8) Holstein | 22 | 530 |
| (0.4 - 0.6) Holstein | 10 | 126 |
| (0.2 - 0.4) Holstein | 0 | 14 |
| (0.0 - 0.2) Holstein | 8 | 15 |
| Total | 150 | 2,500 |





Data and Traits

Phenotypic Data

Milk Yield, Fat %, Protein %, Total Solids %, SNF %
 Initial Yield, Peak Yield, Days to Peak, Persistency
 Lactation Length, Somatic Cell Count
 Body Conformation Traits (e.g., Hip height, udder height)

Genotypic Data

Illumina BovineSNP50: Sires, Dams Highly Represented
 IlluminaLD (7K): Remaining Cows
 IlluminaHD (770K; Funding Permitting): Some Sires & Dams

Tissue Sampling and Genotyping

Sires
Semen (4 straws) or Blood (10cc)

Dams
Blood (10cc)

Genotyping
GeneSeek
Illumina BovineSNP50 (54,609 markers)
IlluminaLD (6,909 markers)
IlluminaHD (777,962 markers)

Tissue Sampling Goals

| Animals | 2012 | 2013 | 2014 | Total |
|---------|-------|-------|------|-------|
| Sires | 150 | 50 | 50 | 250 |
| Cows | 1,500 | 1,000 | 750 | 3,250 |
| Total | 1,650 | 1,050 | 800 | 3,500 |

Tissue Sampling Goals for 2012

| Animals | Semen | Blood | Total | Current |
|---------|-------|-------|-------|---------|
| Sires | 130 | 20 | 150 | 150 |
| Cows | | 1,500 | 1,500 | 987 |
| Total | 130 | 1,520 | 1,650 | 1,137 |

Initial Analyses

Imputation from 7K to 50K (Findhap v2)

Estimation of Variance & Covariance Components
Genomic-Polygenic Models (GS3)

Prediction of Genomic and Polygenic Effects
Genomic-Polygenic Models (GS3)
Genomic Models (GS3)
Polygenic Models (GS3)

Genomic Predictions

Training Population
Cows with first lactation until 2011 (Initial Analysis)
Cows with first lactation until 2013 (Final Analysis)

Validation Population
Cows with first lactation in 2012 (Initial Analysis)
Cows with first lactation in 2014 (Final Analysis)

Genomic-Polygenic Model

Milk Yield
=
Herd-Year-Season + Calving Age
+ "Other Breed" Fraction of Cow
+ Additive Animal Polygenic
+ Additive SNP Genomic
+ Residual

GS3: VCE (Variance Components)
GS3: BLUP (Genomic-Polygenic Predictions)

Genomic-Polygenic Predictions

$$\text{Prediction} = \text{OBreed Solution} + \text{Sum SNP predictions} + \text{Polygenic prediction}$$

$$\text{EBV}_{\text{animal}} = \text{Prob (Alleles OBreed)} * (\text{OBreed}^* - \text{Holstein}^*) + \text{Sum } [(\# \text{ "Alleles 2" at locus } i) * (\widehat{\text{SNP}}_i)], i = 1 \text{ to } 42,000 + \hat{a}_{\text{animal}}$$

Current Work

Tissue Sampling is on schedule
Repository at KU is being created
Phenotypic and Pedigree Database is being expanded

Training of Graduate Students (2 PhD, 2 MS)

Genotyping Schedule: 1 stage or 2 stages
If 2 stages => Initial genomic analyses in 2013-2014
If 1 stage => Initial genomic analyses in 2014-2015

People

Skorn Koonawootrittriron (KU)
Mauricio Elzo (UF)
Thanathip Suwanasopee (KU)
Danai Jattawa (KU)
Bodin Wongprom (KU)
Pimchanok Yodklaew (KU)
Tawee Laodim (KU)

Tummanoon Thongprapai (DPO)
Chockchai Chaimongkol (DPO)