Hay Burners versus Hay Converters (a.k.a. Feed Efficiency)

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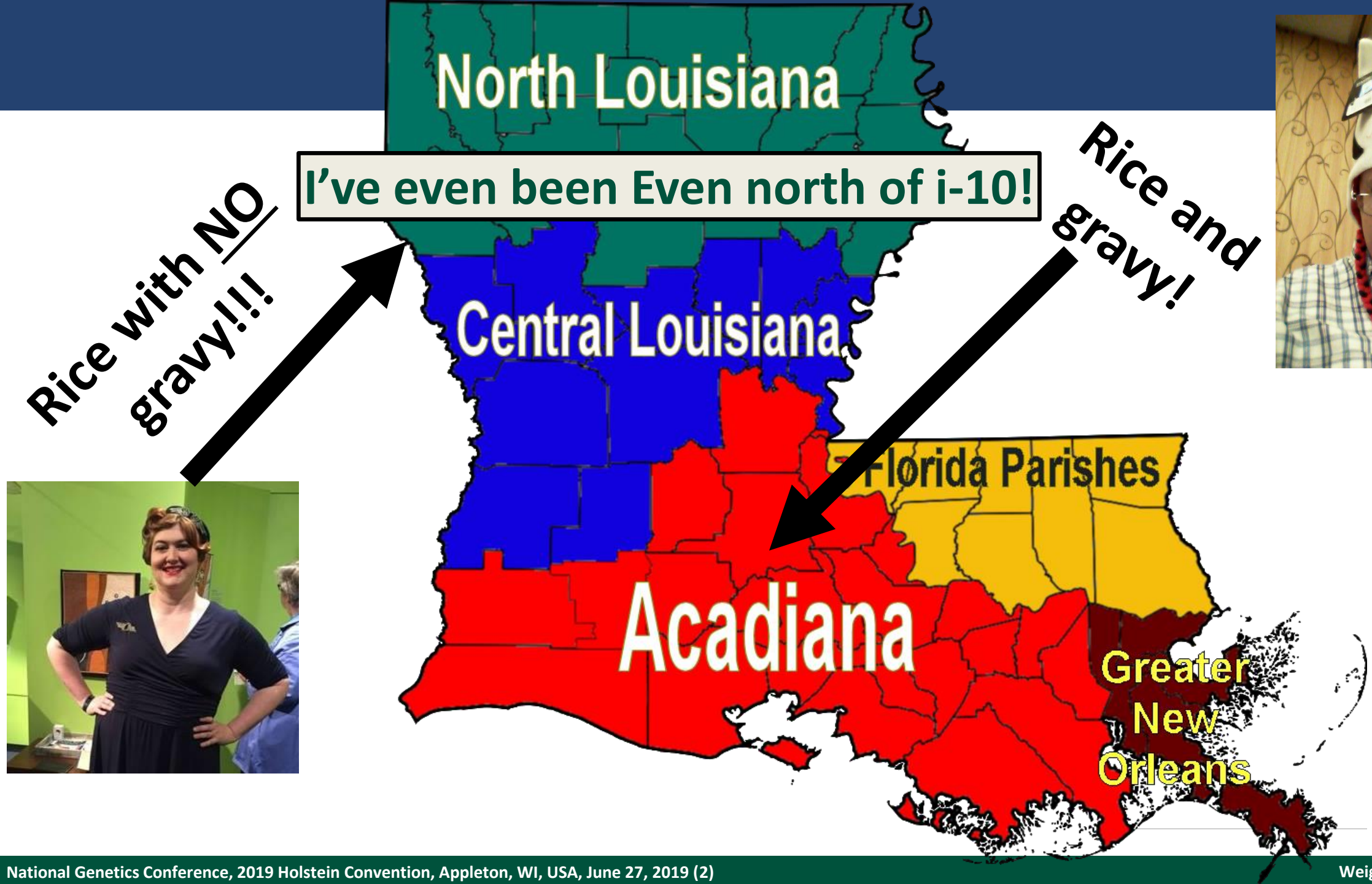
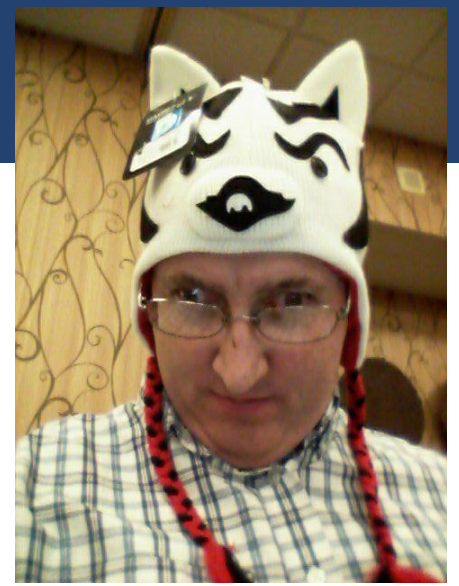

North Louisiana
I've even been Even north of i-10!
Rice with NO gravy!!!
Rice and gravy!
Central Louisiana
Florida Parishes
Acadiana
Greater New Orleans



Topics for discussion

- What is feed efficiency?
- What do we need to develop genomic evaluations?
- How do we include it in selection indices?

Feed efficiency in dairy cattle

- Units of product output per unit of product input
  - Outputs: milk + meat products consumed by humans
  - Inputs: lifetime feed consumed + energy, fertilizer, . . .
- Biological efficiency vs. economic efficiency
  - Individual cow level vs. whole farm level
- Energy efficiency vs. protein efficiency
  - Both important, but protein usually isn't limiting

→ Our focus is biological efficiency of energy utilization in mid lactation, relative to herdmates fed the same diet

VandeHaar et al., 2016

Selection for feed efficiency – why now?

Before Genomics

- Measurement for 1 cow = $500
- Young bulls per year = 1,500
- Daughters per bull = 100
- Cows per year = 150,000
- Annual cost = $75 million

$50,000 per bull

After Genomics

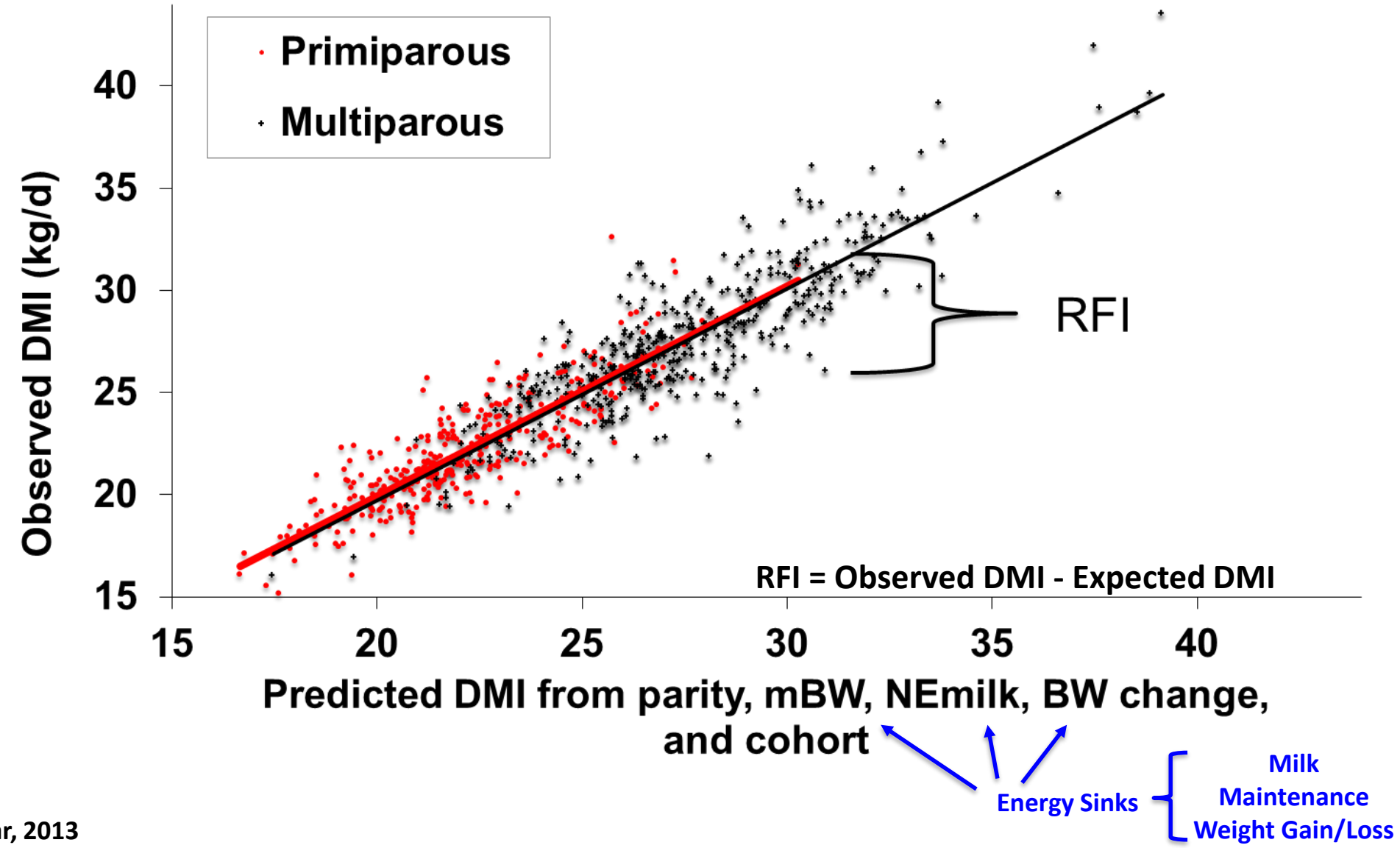
- Measurement for 1 cow = $500
- Cost per genomic test = $40
- No. reference cows = 25,000
- Young bulls per year = 5,000
- One-time cost = $13.5 million
- Annual update cost = $200,000

$310 per bull

Why is it so expensive to measure?

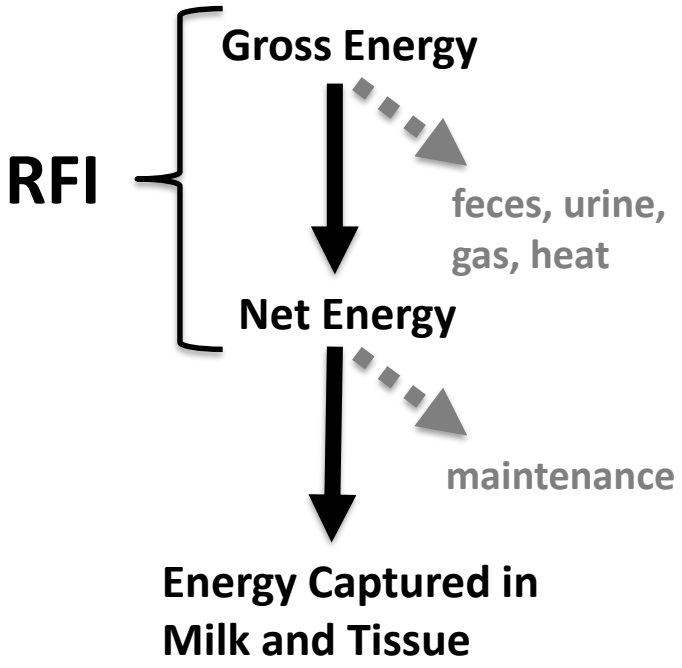
Source: Isa Beefmasters.

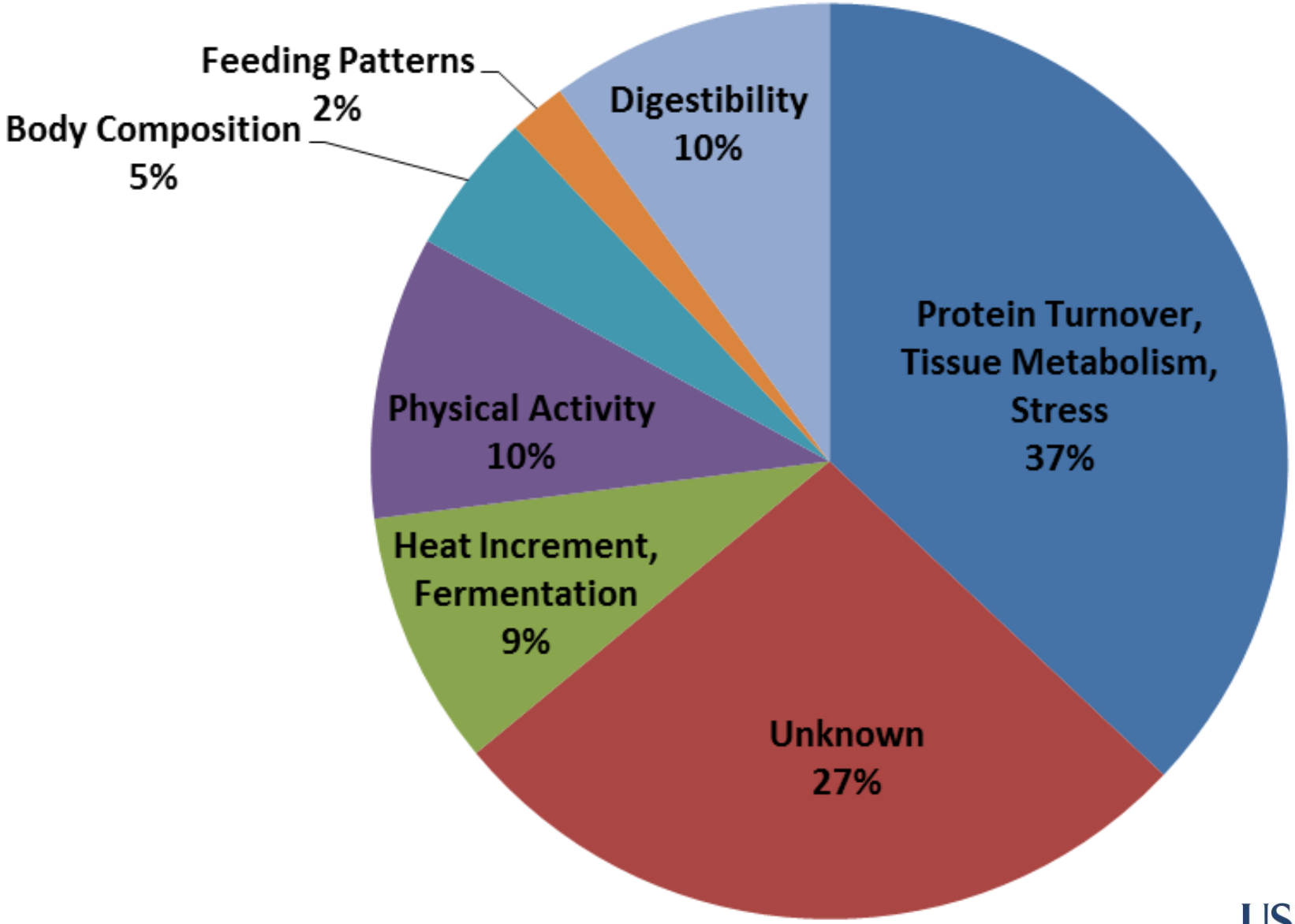
Residual feed intake (RFI)



VandeHaar, 2013

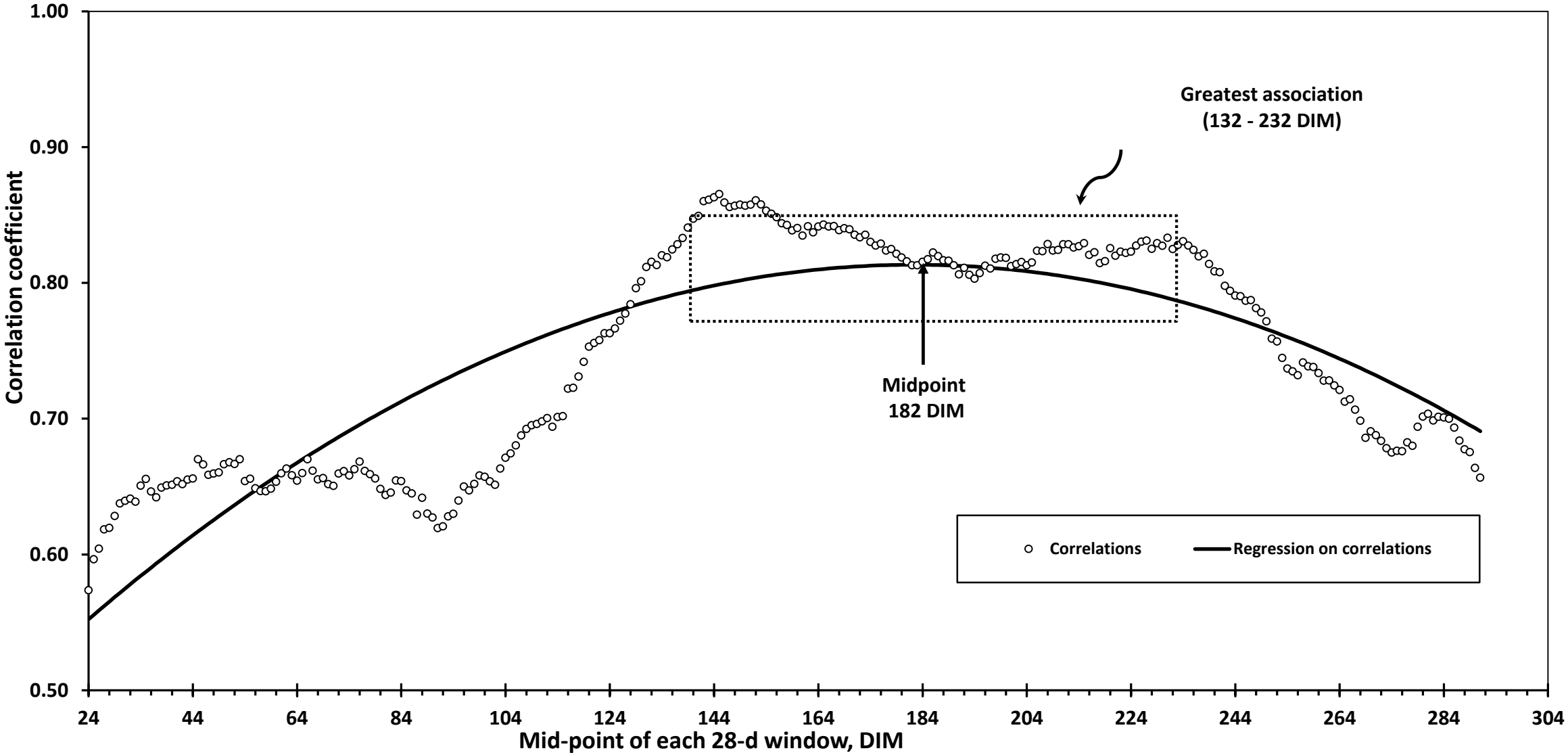
Biology of residual feed intake (RFI)





Herd & Arthur, 2014

When is the best time to measure RFI?



Connor et al., 2019

When is the best time to measure RFI?

DIM at start	Test duration (d)					
	28	42	56	70	84	98
10	0.57	0.63	0.67	0.69	0.71	0.73
24	0.65	0.70	0.71	0.72	0.74	0.78
38	0.67	0.68	0.69	0.72	0.76	0.79
52	0.67	0.68	0.71	0.75	0.79	0.84
66	0.65	0.68	0.73	0.77	0.83	0.87
80	0.63	0.70	0.76	0.82	0.87	0.90
94	0.69	0.76	0.82	0.87	0.89	0.92
108	0.76	0.82	0.87	0.89	0.91	0.93
122	0.82	0.87	0.88	0.90	0.92	0.93
136	0.86	0.86	0.89	0.90	0.91	0.92
150	0.84	0.87	0.89	0.90	0.91	0.91
164	0.82	0.85	0.87	0.89	0.90	0.90
178	0.81	0.84	0.86	0.88	0.88	0.88
192	0.82	0.85	0.86	0.87	0.87	0.87
206	0.83	0.85	0.85	0.85	0.86	0.86
220	0.83	0.83	0.82	0.83	0.83	
234	0.78	0.77	0.78	0.79		
248	0.73	0.74	0.75			
262	0.68	0.71				
276	0.66					

Correlation coefficient
< 0.70
0.70 - 0.74
0.75 - 0.79
0.80 - 0.84
0.85 - 0.89
0.90 - 0.92
> 0.92

Connor et al., 2019

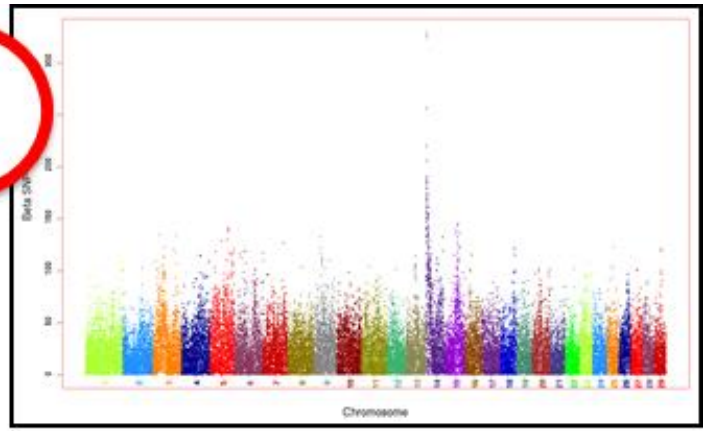
Key steps in genomic selection

1




Build a Reference Population

2



Estimate SNP Effects

3

10120001120222

Test Some Calves

4

Holstein High-ranking cows with genomic information

* = ID was changed after the second test following entry into the herd
@ = Dam was predominantly owner-sampler type-of-test
% = Indicates a crossbred cow

Name	Sire	Birth mo-yr	Last lactation: Herd code	Last lactation: Mo-yr	Last lactation: Term code	Last lactation: DIM	Index: Rel	Index: NM$	No. rec	Std: Milk lb	Std: Fat %	Std: Fat lb
	64700377	07-10	00000000	0-00		0	58	+998	0	00000	0	0
SHR PL SHAKIRA-ET	60597003	06-09	00000000	0-00		0	66	+989	0	00000	0	0
WS FREDDIE CAMEO	60996956	06-10	00000000	0-00		0	65	+976	0	00000	0	0
TOLLENAARS FREDDIE 6588	60996956	06-10	00000000	0-00		0	60	+953	0	00000	0	0
BRN-AKERS PLANET LUISE76-ET	60597003	10-09	00000000	0-00		0	65	+926	0	00000	0	0
AMMON PEACHY SUPER 7068-ET	67065919	07-10	00000000	0-00		0	66	+924	0	00000	0	0
SRP DOBCY 2012787-ET	139005002	09-10	00000000	0-00		0	59	+921	0	00000	0	0
COYNE-FARMS MASS JILL-ET	63026939	11-09	00000000	0-00		0	63	+914	0	00000	0	0
S-S-I ROBUST DESIGN 7229-ET	64966739	12-10	00000000	0-00		0	63	+912	0	00000	0	0
WI-COMP-TRI ORBERV SAINT-ET	65917481	10-10	00000000	0-00		0	63	+907	0	00000	0	0
FARNEAR FREEDOM ADMIN-ET	60996956	10-10	00000000	0-00		0	59	+898	0	00000	0	0

Make Selection Decisions

AFRI feed efficiency project partners

	records*	cows*
– Michigan State University (East Lansing, MI)	315	273
– Iowa State University (Ames, IA)	1,006	953
– University of Florida (Gainesville, FL)	582	491
– University of Wisconsin-Madison (Madison, WI)	1,056	916
– U.S. Dairy Forage Research Center (Madison, WI)	622	474
– USDA-AGIL (Beltsville, MD)	834	534
– Virginia Tech University (Blacksburg, VA)	93	93
– Purina Animal Nutrition Center (Grays Summit, MO)	184	151
– Miner Agricultural Research Center (Chazy, NY)	58	58

Agriculture and Food Research Initiative Competitive Grant no. 2011-68004-30340 from the USDA National Institute of Food and Agriculture

*used in VanRaden et al., 2018 and Li et al., 2019

Genomic predictions for RFI

- **Animals:**
  - **3,947 cows from 9 research herds**
  - **4,823 lactation records**
- **Phenotypes:**
  - **Residual feed intake (RFI), in kg/d, computed from:**
    - **Dry matter intake (DMI), in kg/d**
    - **Metabolic body weight (MBW), in $kg^{0.75}$, and body weight change**
    - **Net energy in milk (Milk NE), in Mcal/d**
  - **Measured on 42 consecutive days between 50 to 200 DIM**
- **Genotypes:**
  - **Low/medium/high density imputed to 278,524K**

Li et al., 2019

National genomic evaluation for RFI

- Feed intakes from research cows already adjusted for phenotypic correlations with milk net energy, metabolic body weight (BW), and weight change to get RFI

- Genetic evaluation model:
  RFI = breeding value + permanent environment + herd × sire + management group + age-parity + b_1(inbreeding) + b_2($GPTA_{\text{milk net energy}}$) + b_3($GPTA_{\text{BW composite}}$)

- Remove remaining genetic correlations and include 60 million nongenotyped Holsteins

- Genomic model:
  Predict 1.4 million genotyped Holsteins

Genomic predictions for RFI

- **Cows with RFI Data (N=3,947)**
  - Standard deviation of RFI breeding values: 0.33 lb/day
  - Average theoretical (observed) reliability: 0.31 (0.26)
- **Young Heifers (N=4,029)**
  - Standard deviation of RFI breeding values: 0.21 lb/day
  - Average theoretical (observed) reliability: 0.15 (0.10)
- **Young Bulls (N=5,252)**
  - Standard deviation of RFI breeding values: 0.22 lb/day
  - Average theoretical (observed) reliability: 0.18 (0.11)

Li et al., 2019

Variance estimates for RFI (and SCS)

Parameter	RFI	SCS
Heritability (%)	14	16
Repeatability (%)	24	35
Phenotypic correlation with yield	0.00	–0.10
Genetic correlation with yield	0.00	–0.03

SCS provided a 2nd trait with similar properties, which allowed genomic predictions from research cows to be compared with national SCS predictions

Feed data vs. other trait data

- Top 100 progeny-tested Holstein bulls for NM$
  - Average 739 milk daughters, <0.1 RFI daughters
  - GREL averages 94% milk, 89% NM$, 16% RFI
- Top 100 young Holstein bulls for NM$
  - GREL averages 75% milk, 71% NM$, 12% RFI
  - REL_{PA} averages 35% milk, 33% NM$, 3% RFI

Computed vs. actual GREL for SCS

- Expected genomic reliability (GREL) was 19% for both RFI and SCS
- SCS GPTA was correlated by only 0.39 for national vs. research-cow reference data
- Observed GREL of SCS was $(0.39)^2 \times 72\% = 11\%$
- RFI GREL was discounted to agree with Var(PTA) for RFI and observed GREL of SCS

Economic progress

- Higher reliability for other traits than for RFI because of more records
  - RELNM$ averages 75% for young and 91% for proven bulls
  - RELRFI averages ~12% for young and 16% for proven bulls
- Progress for lifetime profit may be only 1.01 times or 1% faster than current NM$ progress, but the extra gain is worth $4.5 million per year to the U.S. dairy industry

Economic value of RFI

Statistic	Milk production (3.5% F, 3.0% P)	Dry matter intake	Residual feed intake
Lactation mean (lb/lactation)	25,000	16,600	0
Lactation SD (lb/lactation)	2,900	2,750	1,130
Price/lb	$0.17	$0.12	$0.12
Mean income or cost/lactation	$4,250	–$1,992	0
Lifetime value/lb (2.8 lactations)	$0.253	–$0.336	–$0.336
Relative value (% of NM$)	36%		–16%

- Economic values for milk and BW continue to subtract correlated feed consumption
- Subtraction of expected feed intake from milk yield is the “net” in NM$

Lifetime net merit including RFI

- 20% Fat Yield
- –16% Residual Feed Intake
- 15% Protein Yield
- 11% Productive Life
- 6% Cow Livability
- 6% Udder Composite
- 6% Daughter Pregnancy Rate
- –6% Somatic Cell Score
- –5% Body Weight Composite
- 4% Calving Ability
- 2% Feet & Legs Composite
- 1% Cow Conception Rate
- 1% Heifer Conception Rate
- – 1% Milk Yield

VanRaden et al., 2018

How is this different from feed efficiency in TPI®?

- **An indirect indirect predictor of feed efficiency is included in TPI®**

  (Dollar Value of milk produced) – (Feed costs of extra milk) – (Extra maintenance costs)

- **Milk and components yields are used along with body weight composite**

  FE = (– 0.0187 x Milk) + (1.28 x Fat) + (1.95 x Protein) – (12.4 x BWC)

- **Feed efficiency receives 8% of the weight in TPI®**

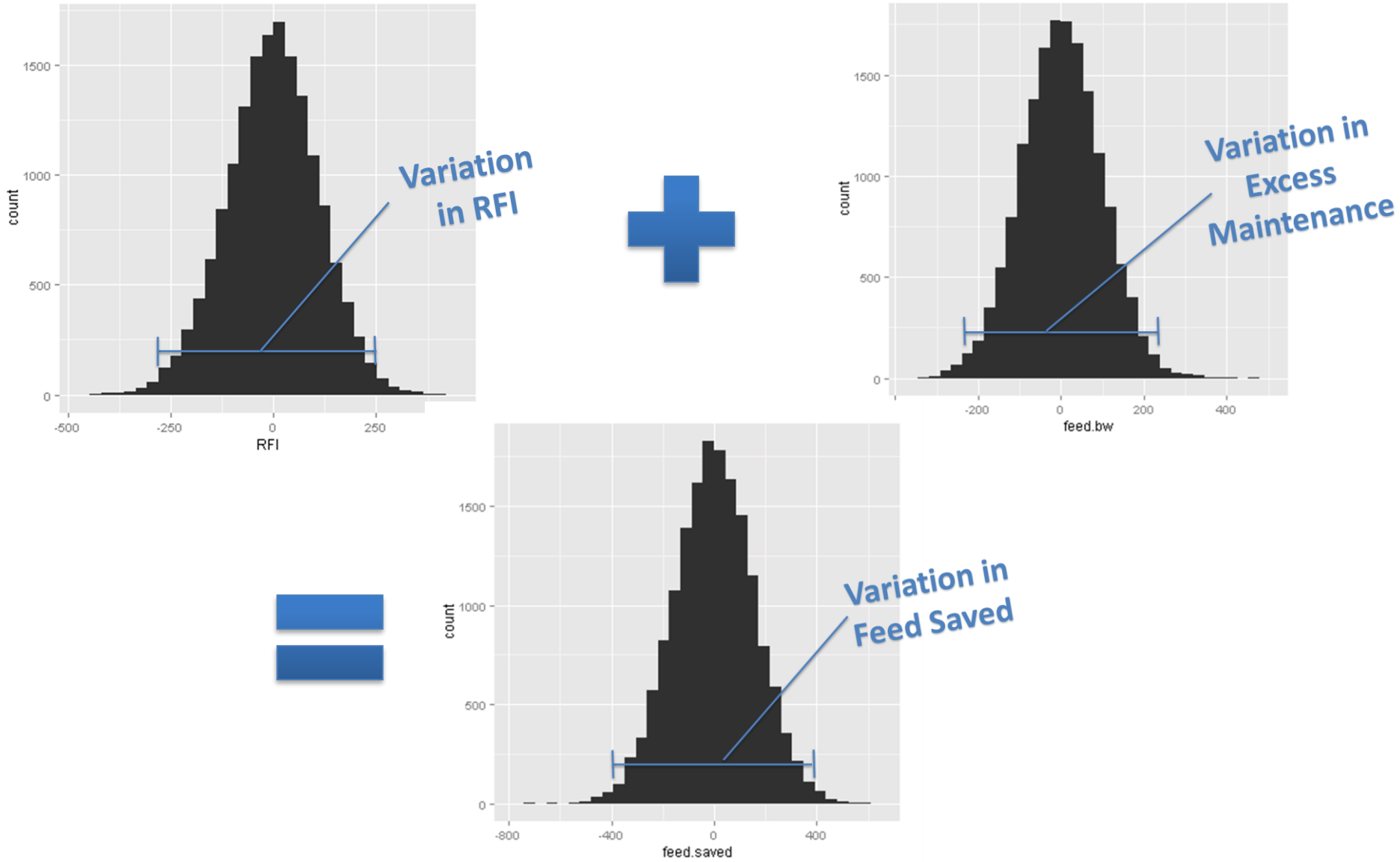
Holstein Association, 2017

Alternatives to publishing RFI

- Feed Saved
  - Index of RFI and excess maintenance costs
  - Feed Saved per Lactation (pounds of dry matter)
    - - (305 days x RFI per day) - (1.67 x 40 x Body Weight Comp.)
  - Lifetime Feed Saved (dollars)
    - - $0.12 x 2.8 lactations x Feed Saved per Lactation
  - Example bull with RFI = -0.6 and BWC = -2.5
    - - (305 x -0.6) - (1.67 x 40 x -2.5)) = 350 pounds per lactation
    - -$0.12 x 2.8 x 350 = $118 lifetime value of feed saved

Pryce et al., 2015; VanRaden et al., 2018

RFI, excess maintenance, and feed saved



Yao et al., 2016

CDCB-FFAR feed efficiency partners

	new phenotypes/year
– Michigan State University (East Lansing, MI)	80
– Iowa State University (Ames, IA)	216
– University of Florida (Gainesville, FL)	150
– University of Wisconsin-Madison (Madison, WI)	320
– USDA-AGIL (Beltsville, MD)	50

Project Aims:

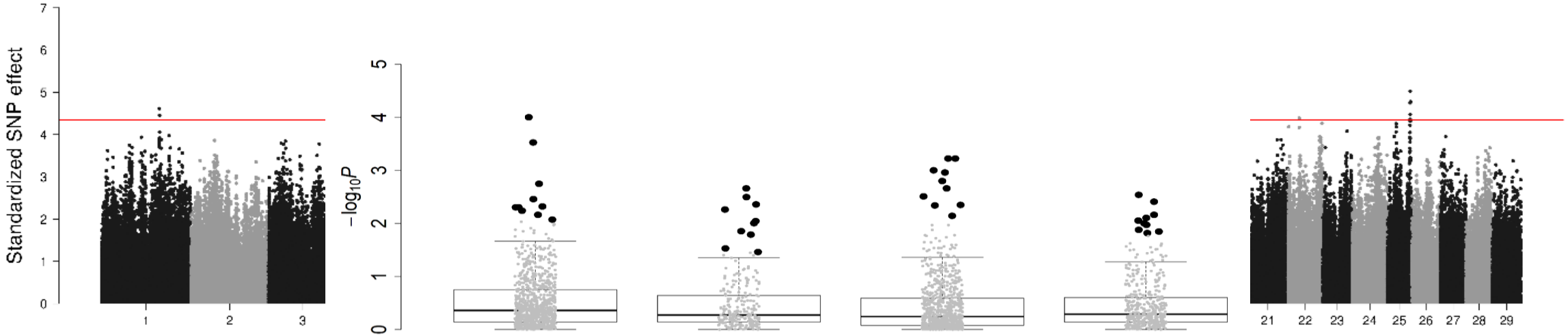
1) increase reliability of genomic predictions for RFI

2) implement plan for updating RFI reference population

3) develop sensor-based index to predict dry matter intake

4) study associations between RFI and methane emissions

Several genomic regions are associated with RFI



GO

Gluconeogenesis
Calcium-dependent protein binding
Skeletal muscle cell differentiation
Mitochondrial electron transport, NADH to ubiquinone
Clathrin-coated vesicle
Homophilic cell adhesion via plasma membrane adhesion molecules
Epithelial cell differentiation
Photoreceptor outer segment membrane
G-protein coupled receptor binding
Positive regulation of fibroblast proliferation

KEGG

Glycosaminoglycan biosynthesis - keratan sulfate
Ubiquinone and other terpenoid-quinone biosynthesis
Valine, leucine and isoleucine biosynthesis
D-Glutamine and D-glutamate metabolism
Terpenoid backbone biosynthesis
Phenylalanine, tyrosine and tryptophan biosynthesis
Linoleic acid metabolism
Porphyrin and chlorophyll metabolism
Carbohydrate digestion and absorption
Alpha-Linolenic acid metabolism

Reactome

Keratan sulfate biosynthesis
SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription
Digestion and absorption
Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer
Keratan sulfate/keratin metabolism
Signaling by TGF-beta Receptor Complex
Signaling by TGF-beta family members
Downregulation of SMAD2/3:SMAD4 transcriptional activity
Signaling by Activin
Toll-Like Receptors Cascades

MeSH

Neurospora crassa
Animals, Inbred Strains
Protein Conformation
Cell Size
Bacteria
Escherichia coli
Carbohydrate Metabolism
Biomechanical Phenomena
Ruminants
Sperm Motility

Future research

- How is feed efficiency related to methane production?
- Can the rumen microbiome be manipulated to improve cow efficiency and enhance sustainability?
- What correlated traits can we use to improve genomic predictions of feed efficiency?

Take-home messages

- Our USDA-AFRI grant ended in 2017
- We have dry matter intake, secreted milk energy, and body weight data for >5,000 Holstein cows
- RFI is the contemporary deviation in dry matter intake after accounting for known energy sinks
- RFI is independent of milk yield and body size
- Significant genetic variation exists in RFI

Take-home messages

- Genomic predictions for RFI can be computed from our Holstein reference population
- RFI will comprise about 16% of Lifetime Net Merit
- Reliabilities will be low, typically only 15 to 20%
- Feed Saved (RFI + body size penalty) is an option
- Collecting more feed intake phenotypes is critical!
- The CDCB-FFAR project will provide > 800 cows per year plus info about sensors and biomarkers

Acknowledgments

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Questions?

Mooving Forward.

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