Including feed intake data from U.S. Holsteins in genomic prediction

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Feed intake topics

- Residual feed intake (RFI) as a new trait
- Data included, models, and parameters
- Reliability of predictions
- Economic value of feed saved
- Reporting of feed intake evaluations

Feed intake data

Research herd	Cows	Records	Researchers
Univ. of Wisconsin and US Dairy Forage Res. Ctr.	1,390	1,678	Weigel, Armentano
Iowa State Univ.	953	1,006	Spurlock
ARS, USDA (Beltsville, MD)	534	834	Connor
Univ. of Florida	491	582	Staples
Michigan State Univ.	273	315	VandeHaar, Tempelman
Purina Anim. Nutr. Ctr. (MO)	151	184	Davidson
Virginia Tech	93	93	Hanigan
Miner Agric. Res. Inst. (NY)	58	58	Dann
All	3,965	4,823	$5 million AFRI grant

Genotypes of research cows

- Chip densities (number of markers) used
  - 502 high density (777K)
  - 1341 GHD or GH2 (77K or 140K)
  - 1251 50K or ZMD (50K)
  - 411 low density (7K to 20K)
- Imputed to 60,671 subset used officially

National RFI genomic evaluation

- RFI from research cows already adjusted for phenotypic correlations with milk net energy, metabolic body weight, and weight change

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

- Remove remaining genetic correlations and include 60 million nongenotyped Holsteins

- Genomic model:
  Predict 1.4 million genotyped Holsteins

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

Estimation of genomic reliability

- Correlation of genomic predictions from research cow data ($GEBV_r$) vs. national data ($GEBV_n$) for SCS
  - Observed REL = $corr(GEBV_r , GEBV_n)^2$ * national REL
- 5-way cross-validation
  - Use RFI records of 80% of cows to predict RFI records of remaining 20%
  - Exclude cows from the validation data if they had daughters in the reference data
  - Observed REL = $corr(GEBV_r , RFI)^2$ / heritability
- Choose discount to match computed to observed REL

Computed vs. actual GREL for SCS

- Expected genomic reliability of young animals was 19% for both RFI and SCS using standard discount of 0.7
- SCS GPTA correlated by only 0.39 for national vs. research-cow reference data
- Observed REL of SCS was $(0.39)^2 \times 72\% = 11\%$
- Genomic REL was discounted by a factor of 0.3 to agree with Var(PTA) for RFI and observed REL of SCS

5-way cross-validation

Trait	Reliability		Reliability	
	method	Traditional	Genomic	Difference
RFI	Observed	13.4	18.1	+4.7
	Expected[1]	14.0	21.2	+7.2
SCS	Observed	17.6	23.0	+5.4
	Expected[1]	16.4	24.7	+8.3

[1] Expected REL calculated from parent average for cows not in the reference, or from genomic REL calculated using a discount factor of 0.3.

RFI reliability by animal group

Animal group	**RFI Reliability (%)**	
	Traditional	**Genomic**[1]
3,965 **cows** with RFI phenotypes	30	34
Top 10 **sires** with most RFI daughters	78	85
Top 100 Net Merit **progeny tested** sires	8	16
Top 100 Net Merit **young bulls**	3	12
1.5 million **genotyped** Holsteins	5	13
60 million **non-genotyped** Holsteins	3	3

[1] Computed with discount factor of 0.3

Economic values

Statistic	Milk production (3.5% F, 3.0% P)	Dry matter intake	Residual feed intake
Price/pound	$0.17	$0.12	$0.12
Mean income or cost/lactation	$4,250	–$1,992	0
Lifetime value/pound (2.8 lactations)	$0.253	–$0.336	–$0.336
Relative value (% of NM$)	36%		–16%

- **Since 2000, Net Merit $ has selected for smaller cows using type traits (body weight composite) to reduce expected feed intake (-6% of NM$)**
- **Economic values for yield and BWC already account for correlated feed intake, and RFI measures uncorrelated intake**

Reporting feed efficiency

- Feed efficiency expected from yield and type traits
  - FE$ is milk income – feed cost expected from PTAs for milk, fat, protein, and body weight composite (type)
  - Current definition used in TPI
  - New FE$ = FE$ – RFI$

- Feed saved (used in AUS , also USA proposal)
  - FeedSaved$ combines RFI$ and regression on body weight composite, but not yield trait regressions

Economic progress

- Ratio of progress from new vs. old index is square root of

$$[REL_{NM\$}(194^2) + REL_{RFI}(70^2)]/[REL_{NM\$}(194^2)]$$

- Ratio of progress is small (1.01) because REL_{RFI} (12%) is much lower than $REL_{NM\$}$ (75%)

- Extra 1% faster progress is worth $4.5 million per year to the U.S. dairy industry

Early feed intake studies at USDA

- Hooven et al., JDS 51:1409–1419, 1968
  - 661 lactations of 318 Holstein cows at Beltsville
  - Genetic correlation (feed efficiency, milk energy) = 0.92

- Hooven et al., JDS 55:1113–1122, 1972
  - 10-mo intake trials for 425 cows
  - 30-d trial (month 5) gave 89% of progress

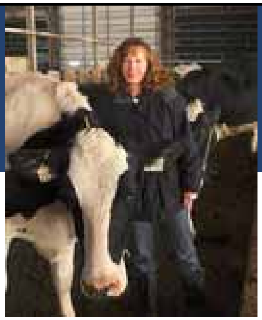
Conclusions

- Producers and researchers have always wanted to measure and select for feed efficiency
- RFI could get ~16% of relative emphasis in net merit, but low REL of ~12% for young animals will limit progress
- Genomics can multiply feed intake information from a few herds to thousands of other herds
- Higher REL will require more research herds or international cooperation

Acknowledgments

- Agriculture and Food Research Initiative Competitive Grant #2011-68004-30340 from USDA National Institute of Food and Agriculture (feed intake funding)
- USDA-ARS project 1265-31000-101-00, “Improving Genetic Predictions in Dairy Animals Using Phenotypic and Genomic Information” (AGIL funding)
- Council on Dairy Cattle Breeding and dairy industry contributors for pedigree and genomic data
- Jim Liesman (MSU) for merging and editing phenotypes
- George Wiggans for managing genotypes

6-week or 4-week trials



	6-week	4-week
Days of feed intake	42	28
Cows recorded	4,621	202
RFI mean	0	0
RFI standard deviation (kg/day)	1.68	1.75
Correlation with 6-week trial	1.00	0.96
Weighted in statistical model	1.00	0.92
Approximate cost of recording (+1 week pre-trial)	$700	$500