

# Genomic prediction for feed intake in UK Holstein dairy cattle

Bingjie Li<sup>1</sup>, Raphael Mrode<sup>1</sup>, Marco Winters<sup>2</sup>, Mike Coffey<sup>1</sup>

<sup>1</sup>Scotland's Rural College (SRUC), Roslin Institute Building, Easter Bush, Midlothian, UK

<sup>2</sup>Agriculture and Horticulture Development Board (AHDB), Stoneleigh Park,  
Kenilworth, Warwickshire, UK

# Outline

- Feed efficiency (FE) as a new trait
- Dairy feed intake data in UK
- Genomic prediction for dry matter intake (DMI) in Holstein dairy cattle
- Publication of dairy feed efficiency evaluations
- Summary

# Feed efficiency (FE) as a new trait

- Feed cost is the largest part of operating costs in dairy production
- Global interest in including FE into dairy breeding goal
- Including FE into the UK dairy evaluation will result in additional profit and reduced environmental footprint of dairy industry



# Feed intake data in UK

- Dry matter intake (DMI) have been recorded for individual cows in Langhill research herd over 30 years
- DMI records for 4,328 lactations of 1,763 Holstein cows (Lactation 1-4)
  - A total of 155,026 daily DMI records averaged on a weekly basis
- 80k imputed genotypes available
  - 1,213 genotyped and phenotyped animals
  - 396 genotyped sires/grandsires in pedigree

## The Award Winning Langhill Herd

*High and low genetic merit dairy cows split between two production systems*

### The Challenge

SRUC maintains a genetically unique dairy herd, offering a wealth of information dating back to its establishment in the 1970s. It provides researchers with a data and living resource to undertake controlled genetic, nutritional, fertility, productivity and environmental studies that are not possible on a commercial farm.



Milking cow shed at SRUC Dairy and Innovation Centre

# Genomic prediction for dry matter intake

- Single-step GBLUP method
- Animal repeatability model

$$DMI = Parity + Lact\_month[Parity] + Age\_calv + Feeding\_grp + YM\_Rec + a + pe + e$$

- Phenotype: Daily DMI (kg/d) averaged by month (in period of ~305 DIM)
- a for additive genetic effect
- pe for permanent environmental effect
- Heterogeneous residual variances by 4 stages over lactation

# Estimation of prediction reliability

- Theoretical reliability of GEBV for each individual was calculated by inverting the coefficient matrix of the MME
  - $REL_i = 1 - (PEV_i/G_i)$
- Validation
  - Cows were divided into training and testing dataset in 3 scenarios
  - Corrected phenotype (yc) was used, and prediction accuracy =  $cor(GEBV, yc)$  in the testing dataset

Scenarios	Training dataset	Testing dataset
Old to predict young	Cows born before 2015	Cows born $\geq$ 2015
Prediction between two genetic lines <sup>1</sup>	Cows in selection or control line	Cows in the other genetic line
Prediction between two feeding groups <sup>1</sup>	Cows in one feeding group	Cows in the other feeding group

<sup>1</sup>Cows in Langhill research herd are under 2 genetic lines (selection and control line) and 2 feeding groups for over 30 years

# Genetic parameters for dry matter intake

- Genetic correlations (DMI\_1 and DMI\_2+) > 0.9
- Genetic parameters estimated from pedigree and genomics agree with each other taking account of standard errors

	<b>DMI_1</b>	<b>DMI_2+</b>
<b>DMI_1</b>	0.16 (0.03)	0.94 (0.05)
<b>DMI_2+</b>		0.19 (0.03)

Table. Genetic parameters for DMI in first lactation (DMI\_1) and in other lactations (DMI\_2+) from pedigree analyses.

# Prediction accuracy from validation

Scenarios	Accuracy = $\text{cor}(\text{GEBV}, y_c)$	Bias
Old to predict young	0.62	0.94
Prediction between genetic lines	0.34	1.04
Prediction between two feeding groups	0.68	1.09

- $y_c$  = corrected phenotypes (i.e., DMI correcting for fixed effects and pe effect)
- Bias was estimated as the regression coefficient of  $y_c$  on GEBV to approximate regression of TBV on GEBV



# GEBV reliability by animal groups

Animal group	Mean GEBV Reliability <sup>1</sup> (%)
1,763 phenotyped animals	37
396 genotyped bulls (sires, grandsires and so on) in 5-gen pedigree	22
Top 10 genotyped sires with most phenotyped daughters <sup>2</sup>	60
1,689 currently active bulls in UK	9

<sup>1</sup>Theoretical reliability of GEBV was calculated by inverting the coefficient matrix of MME,  $REL = 1 - (PEV/G)$

<sup>2</sup>The top 10 genotyped sires have  $\geq 20$  phenotyped daughters

# Publication of feed efficiency evaluations

- GEBV of “**Wasted feed (WF)**” as a basis (Meyer et al., 2017, Interbull Bulletin)

$$\text{WF} = \text{DMI} - \text{MilkEnergy} * k_{\text{DMI\_MilkEnergy}} - \text{Maintenance} * k_{\text{DMI\_LW}}$$

- DMI, MilkEnergy, Maintenance are on GEBV level for DMI, milk energy, and live weight
  - $k_{\text{DMI\_MilkEnergy}}$  and  $k_{\text{DMI\_LW}}$  reflect correlations between DMI and MilkEnergy/LW
- **Publication of GEBV for feed efficiency**
    - Based on WF, and possibly reverse for positive value
    - Using predictor traits (e.g., milk, LW) to improve GEBV prediction for DMI
    - Similar way as “FeedSaved” is also an alternative

# Summary

- Feed intake data has been recorded in UK research herd for over 30 years and will continue being recorded
- It's feasible to include feed intake as the basis of improving FE in the UK national dairy index
- Incorporating predictor traits (e.g., milk, LW) has potential to improve prediction for DMI
- Feed intake data from daughters of active bulls and from more herds or international collaboration will further improve prediction reliability

*Thank you* 😊