

Genomic Prediction of Genetic Residual Feed Intake Integrating a Novel Energy Sink for Change in Body Reserves

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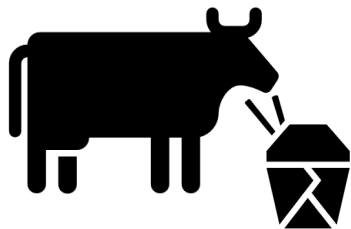
Background

Easy to measure and model

Hard to measure and model

Focus trait in this presentation

Maintenance (**BW**) + Metabolic efficiency (**RFI**)



Background and challenge with RFI

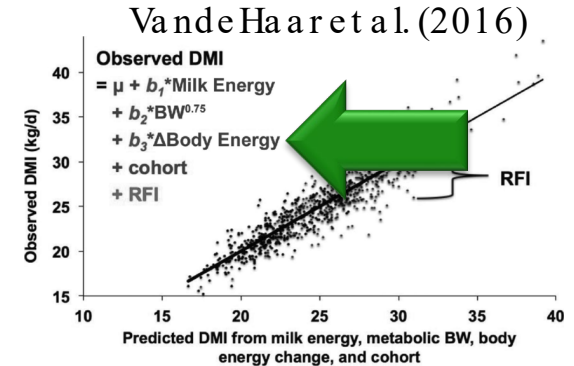
• Definition of **Residual Feed Intake**

- Observed feed intake - **expected** feed intake

- 1st step: $DMI = \mu + \beta_i E_i + \varepsilon$

- 2nd step: $\varepsilon = a + pe + e$

- Challenged in handling **fixed effects** and **missing** observations



- Proposed solution - **genetic RFI** (Kennedy et al. (1993))

- A **multi-trait** setting handles fixed effects and missing records better

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 \\ X_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 \\ Z_2 \end{bmatrix} \begin{bmatrix} \alpha_1 \\ \alpha_2 \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \end{bmatrix}$$

Modelling body reserves

- Important to account for Δ body energy in RFI
- Most evaluations uses Δ BW, but this assumes energy equality
 - mobilization vs. deposition
 - adipose vs. muscle tissues
- Thorup et al. (2018) suggested EB from body reserves (EB_{body})
 - Thorup et al. (2013) tested EB_{body} from frequent BW measurements

Investigated in this study

Objective of this project

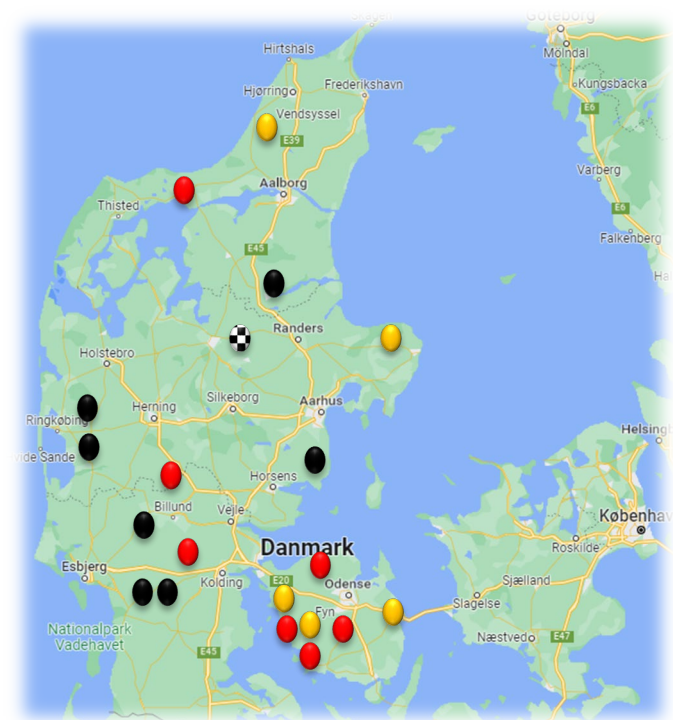
- **Genomic** EBVs are important in modern dairy cattle breeding
 - Limited knowledge on genomic validation of **gRFI** EBVs
- We aimed to test a **genomic** evaluation of **gRFI** in Nordic primiparous dairy cows, including **EB_{body}** as energy sink



Data overview

Individual weekly **feed intake** measures from

- **Cattle Feed InTake, Viking Genetics**
 - 3,873 HOL cows with 161K records, (2,564 primi)
 - 2,068 JER cows with 93K records, (1,505 primi)
 - 3,235 RDC cows with 139K records, (2,006 primi)
- **Danish Cattle Research Center, AU-Foulum**
 - 878 HOL cows with 50K records, (835 primi)



Pedigree and Genotypes

- Pedigrees **pruned** to remove non-informative animals
 - HOL: 18,432
 - JER: 7,249
 - RDC: 12,423
 - **Genetic groups**: with sex, breed, country & birth year classes
- Genotypes used from **NAV** evaluation system
 - Genotype rate for cows with data
 - 92% for JER and RDC
 - 81% for HOL

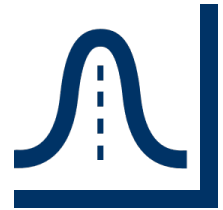
Multi-variate model for DMI, ECM, BW and EB_{body}

- Multi-variate and multi-parity model (primi- & multiparous)
- This presentation now on focus on **primiparous** part

Model effects	
Year x Experiment/ CFIT version	Fixed
Lactation curve (4 th order Legendre Polynomial), nested by herd	Fixed
Age at calving (2 nd order Legendre Polynomial)	Fixed
Herd x year x week	Random
Additive Genetic effect (2 nd order Legendre polynomial)	Random
Permanent Environmental effect (2 nd order Legendre polynomial)	Random
Residual	Random

Genetic model & output

- Variance components estimated with **Gibbs** sampler
 - **RJMC** module in DMU using A-matrix
 - 50K burn-in
 - 500K iterations, **sampling** every 250
 - Trace plots evaluated for **satisfying** convergence
- Matrix notations for gRFI, as in **Islam et al. (2020)**



Genomic validation

- **Legarra Reverter** method applied

$$GEBV_{\text{whole}} = \mu + \beta \times GEBV_{\text{partial}}$$

- **Partial** data sets created by omitting **herds** (~1,000 cows)
 - 3 HOL groups, 2 JER groups, & 2 RDC groups
- **Lactation-wise GEBVs** estimated with DMU5
 - Polygenetic effect of **20%**



Results h^2 and r_G - HOL

	DMI	gRFI	ECM	BW	EB _{body}
DMI	0.46 (0.05)				
gRFI	0.50 (0.05)	0.24 (0.05)			
ECM	0.61 (0.05)	0.00 (0.00)	0.53 (0.04)		
BW	0.53 (0.05)	0.00 (0.00)	-0.10 (0.06)	0.55 (0.04)	
EB _{body}	-0.13 (0.11)	0.00 (0.00)	-0.42 (0.09)	0.06 (0.10)	0.23 (0.04)

Results genomic validation

• Results for genomic LR-validation cows

- $\mu_{w,p}$ = Bias
- $\beta_{w,p}$ = Dispersion
- $\rho_{w,p}$ = Correlation

		HOL	JER	RDC
DMI	$\mu_{w,p}$	-0.36	3.64	-1.15
	$\beta_{w,p}$	0.92	0.75	0.96
	$\rho_{w,p}$	0.68	0.51	0.66
gRFI	$\mu_{w,p}$	0.34	1.69	-2.00
	$\beta_{w,p}$	0.87	0.69	0.85
	$\rho_{w,p}$	0.59	0.46	0.54

Take home messages

- We can estimate **primiparous gRFI**GEBVs for Nordic dairy breeds
- EB_{body} is **heritable** and can be incorporated into gRFI
- **Dispersion** was in an acceptable range
 - Over dispersion was observed in **Jersey** (fewest records)
- Moderate high **correlations** between whole and partial GEBVs
 - Follows a pattern in **number** of records
- Next step – work on **multi-parous** group



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SEGES
INNOVATION

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Thank you for your attention

