Modelling metabolic efficiency

Do we need to understand the biological meaning of residual feed intake breeding values?

M.H. Lidauer[1], T. Andersen[2], U.S. Nielsen[2], E.A. Mäntysaari[1], G.P. Aamand[3]*

[1]Natural Resources Institute Finland (Luke), Jokioinen, Finland

[2]SEGES Innovation P/S, Aarhus N, Denmark

[3]Nordic Cattle Genetic Evaluation, Aarhus N, Denmark

Residual feed intake (RFI)

- Models by its definition (intake – expected intake) the metabolic efficiency in a broad sense that captures variation due to:
  - ability to digesting feed
  - ability to have low energy loss through CH_4 exhalation
  - ability to utilize metabolizable energy for the different energy pathways
- intake: usually measurements for dry matter intake
- expected intake: through modelling of intake requirements for energy sinks (usually by partial regression analyses)

Residual feed intake for Nordic Total Merit Index

- Implemented into Nordic Total Merit in 2020
- Since then, more data is added (CFIT data)
- Along this we have recognized:
    - Partial regression coefficients may vary significantly across time and parities
    - For both CFIT data and research farm data

Aim of the study

Attempt to understand metabolic efficiency

Objective

Study different modelling approaches

Data from 4 herds with CFIT feed intake

- 46,822 weekly records
- 1st to 6th parity
- 1,211 Jersey cows with records
- Years: 2019, 2020, 2021

Means of daily observations

	First parity	Later parities
N	18,221	28,588
DMI	21.3	24.5
MBW	95.0	103.3
ECM	28.9	37.1
MY	22.0	28.5
FY	1.3	1.7
PY	1.0	1.2

DMI = dry matter intake [kg]
MBW = metabolic body weight [$kg^{0.75}$]
ECM = energy corrected milk [kg]
MY = milk yield [kg]
FY = fat yield [kg]
PY = protein yield [kg]

A: Currently used RFI model (RFI_partial_regressions)

First step:

a) partial regression analyses of dry matter intake (DMI)

$$DMI = c_1 \times A + c_2 \times A^2 + LP + LYS + HYS + \gamma_1 \times ECM + \gamma_2 \times MBW + \gamma_3 \times \Delta BW + rfi$$

where

- partial regressions nested within LP classes
- A = calving age
- LP = lactation month x parity classes
- LYS = lactation x year x season
- HYS = herd x year x season

b) raw rfi values adjusted for heterogeneous variance

c) RFI observation = rfi* + estimates for LYS and HYS

A: Currently used RFI model (RFI_partial_regressions)

Second step:

estimating breeding values by a repeatability animal model:

$$RFI = LYS + HYS + pe + a + e$$

where

- LYS = lactation x year x season
- HYS = herd x year x season
- pe = random permanent environmental effect
- a = random additive genetic effect
- e = random residual

B: Regression on requirements (RFI_reg_on_requirement)

- Same as approach A but step 1 model was modified:

  $$DMI = c_1 \times A + c_2 \times A^2 + LP + LYS + HYS + \varphi \times eDMI + rfi$$

  regression on expected dry matter intake (eDMI) instead of partial regressions

- eDMI: firstly calculating energy requirements (ER) in mega joule (MJ):

  $$ER\ [MJ/day] = 4.81 \times ECM + 0.603 \times MBW - 27.6 \times BW\_Loss + 38.3 \times BW\_Gain$$

  (based on Agnew et al., 2003)

  and subsequently:

  $$eDMI = ER \times \text{average of } [DMI\ kg\ /\ (MJ/day)]$$

C: Requirements RFI (RFI_requirements)

- Same as approach A but the raw rfi observations in step 1 were calculated as:
  rfi = DMI – eDMI

D: Regression on expected feed intake (ReFI)

- A different approach where feed intake is regressed on expected feed intake
- Covariables for expected feed intake are calculated using energy requirement estimates from dairy cow nutrition studies
- Allows to model metabolic efficiency from a biological perspective

D: Regression on expected feed intake (ReFI)

- DMI was modelled by a random regression model:

$$DMI = \beta \times eDMI + \eta \times eDMI + \psi \times eDMI + \alpha \times eDMI + \varepsilon$$

with fixed regression coefficients

β nested within herd × year × parity classes

and random regression coefficients

η nested within herd × year × month classes

ψ nested within animal permanent environmental effect

α nested within additive genetic animal effect

Results

- Variance components for different approaches
- Genetic correlations between metabolic efficiency and yield traits
  (multivariate analyses of first parity yield deviations)
- Quick look on phenotype means of 10% genetically superior cows
  (cows selected alternatively based on the 4 different sets of EBV)

Results: Estimates of regression coefficients

	RFI_partial_regressions			RFI_regression_on _requirement	ReFI
Covariables	ECM	MBW	ΔBW	eDMI	eDMI
Coefficient	γ_1	γ_2	γ_3	ϕ	β
First parity estimates	0.31	0.159	-0.28	0.46	1.04
Later parities estimates	0.18	0.196	-0.24	0.32	1.01
Biological expectation	0.49	0.062	3.91	1.00	1.00

Results: Heritability and genetic correlations with yield traits

Approach	h^2	Genetic correlations to:		
		Milk yield	Fat yield	Protein yield
RFI_partial_regressions	0.14	0.47	0.17	0.31
RFI_regression_on_requirement	0.16	0.43	0.24	0.30
RFI_requirement	0.10	-0.01	-0.20	-0.16
ReFI	0.10	0.02	-0.28	-0.10

positive correlation: unfavourable
negative correlation: favourable

Results: Phenotypic means of superior cows

10% best cows based on the EBV by different approaches

	Approach	DMI	MBW	ECM	MY	FY	PY	FCE
All cows		21.2	94.9	28.7	21.8	1.30	0.946	**1.35**
10% best cows	RFI_partial_regressions	18.6	94.7	26.3	18.8	1.22	0.860	**1.41**
	RFI_regression_on_requirement	18.4	92.8	25.3	18.3	1.17	0.833	**1.38**
	RFI_requirement	19.9	93.1	29.1	21.5	1.34	0.966	**1.46**
	ReFI	19.8	93.9	29.8	22.0	1.37	0.982	**1.51**

DMI = dry matter intake [kg]
MBW = metabolic body weight [$kg^{0.75}$]
ECM = energy corrected milk [kg]
MY = milk yield [kg]
FY = fat yield [kg]
PY = protein yield [kg]
FCE = ECM/DMI

Conclusions

- Currently used RFI model favours cows with low production
- ReFI (regression on expected feed intake) favours cows with high production and high efficiency
- Poor performance of the RFI model was due to the inability of the RFI model to properly estimate the partial regression coefficients for the energy sinks

Thank you!