



Alternative Residual Feed Intake (RFI) Expressions in Dairy Cattle

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Residual Feed Intake (Koch et al., 1963)

- Residuals from linear regression of feed intake (DMI) on various energy sinks (ECM, MBW) expressed on the phenotypic scale

$$DMI_i = \mathbf{x}_i' \mathbf{b} + \lambda_{ECM} * ECM_i + \lambda_{MBW} * MBW_i + e_i$$

- Estimates of regression coefficients λ_{ECM} and λ_{MBW} are obtained by LS and phenotypes for RFI (e_i) are subsequently used as observations in genetic/genomic evaluation model

Residual Feed Intake (Kennedy et al., 1993)

- Alternatively, and equivalently, λ_{ECM} and λ_{MBW} can be derived as partial regression coefficients from phenotypic co-variances among DMI and the energy sinks
- Define $\mathbf{C} = [\mathbf{C}_{ij}]$ (2x2) phenotypic co-variance matrix for ECM and MBW, $\mathbf{w} = [\mathbf{w}_{ij}]$ vector of phenotypic co-variances between sinks and DMI. Then

$$[\lambda_{\text{ECM}} \lambda_{\text{MBW}}]' = \mathbf{C}^{-1}\mathbf{w}$$

Residual Feed Intake (Lu et al., 2015)

Challenges of using phenotypes for RFI from LS for genetic analyses:

- RFI is not an observable trait
- All covariates (energy sinks) are incorrectly assumed to have no measurement errors
- Impossible to calculate RFI if any sink is missing
- Any genetic or residual correlation between DMI and energy sinks will affect heritability estimate for RFI and interpretation of inferences

Use of Mixed Model Methods for RFI

- EBVs for RFI can be obtained w/o directly using phenotypes for RFI

- Multiple-Trait (MT) model for ECM, MBW and DMI

$$\mathbf{y}_i = \mathbf{X} \mathbf{b} + \mathbf{a}_i + \mathbf{p}_i + \mathbf{e}_i, \text{ with}$$

$v(\mathbf{a}_i) = \mathbf{G}$ - genetic covariance matrix

$v(\mathbf{p}_i) = \mathbf{E}$ - covariance matrix for the PE effects

$v(\mathbf{e}_i) = \mathbf{R}$ - residual covariance matrix

$\mathbf{P} = \mathbf{G} + \mathbf{E} + \mathbf{R}$ - phenotypic co-variance matrix

Use of Mixed Model Methods for RFI

- Let $\mathbf{a} = [a_{\text{ECM}}, a_{\text{MBW}}, a_{\text{DMI}}]'$ be EBVs for DMI and sinks
- Then $\mathbf{a}^* = [a_{\text{ECM}}, a_{\text{MBW}}, a_{\text{RFI}}]' = \mathbf{\Lambda}_p \mathbf{a} =$
 $= [a_{\text{ECM}}, a_{\text{MBW}}, (a_{\text{DMI}} - \lambda_{\text{ECM}} a_{\text{ECM}} - \lambda_{\text{MBW}} a_{\text{MBW}})]$

λ_x = partial **phenotypic** regression coefficient (derived from MT estimate of P) of DMI on X (energy sink)

$$\mathbf{\Lambda}_p = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ -\lambda_{\text{ECM}} & -\lambda_{\text{MBW}} & 1 \end{bmatrix}$$

Recursive Model Approach for RFI

Y_1 , Y_2 , and Y_3 - phenotypes for ECM, MBW and DMI

Recursive Model (RM) equations:

$$Y_1 = \text{fixed}_1 + \text{random}_1 + e_1$$

$$Y_2 = \text{fixed}_2 + \text{random}_2 + e_2$$

$$Y_3 = \lambda_{31} * Y_1 + \lambda_{32} * Y_2 + \text{fixed}_3 + \text{random}_3 + e_3$$

λ_{jk} = recursive coefficient parameter for the effect of change in trait j caused by the phenotype of trait k

Recursive Model Approach for RFI

Mixed linear RM for ECM, MBW and DMI:

$$\Lambda \mathbf{y}_i = \mathbf{X} \mathbf{b}^* + \mathbf{a}_i^* + \mathbf{p}_i^* + \mathbf{e}_i^*, \text{ with}$$

$$\mathbf{a}_i^* = \Lambda \mathbf{a}_i$$

$$v(\mathbf{a}_i^*) = \Lambda \mathbf{G} \Lambda'$$

$$v(\mathbf{p}_i^*) = \Lambda \mathbf{E} \Lambda'$$

$$v(\mathbf{e}_i^*) = \Lambda \mathbf{R} \Lambda'$$

$$\mathbf{P}^* = \mathbf{G}^* + \mathbf{E}^* + \mathbf{R}^*$$

RM for ECM, MBW and DMI + **restrictions on certain RM parameters** = MT model for these traits

Recursive Model Approach for RFI

- Restrictions on phenotypic co-variances i.e. setting $p_{13}^* = p_{23}^* = 0$ of the co-variance matrix $\mathbf{P}^*$ of RM will yield the same estimates of partial regression coefficients as shown in the simple re-parametrization of the EBVs from the MT model
- Given the estimates of partial regression coefficients and the known co-variance structure of the model, EBV for RFI can be derived using estimates of EBV for DMI and sinks from a regular MT model for these traits

Alternative RFI Definitions

- **pRFI** - RFI defined on the **phenotypic level** (feed intake phenotypically independent of energy sinks)
- This can be extended to other random variables affecting DMI, leading to different definitions with different interpretation of RFI:
 - **Genetic RFI (gRFI)** - feed intake genetically independent of energy sinks
 - **PE RFI (eRFI)** - feed intake adjusted for systematic environmental effects on repeated measurements for an animal over time
 - **Residual RFI (rRFI)** - feed intake adjusted for all effects in the model

Alternative RFI Definitions

- Different expression of RFI = partial regression coefficients (recursive model restrictions) for **different source of variability** for DMI and energy sinks (**G, P, E, R**)
 - EBV and co-variance components for specific RFI derived using
 - **pRFI**: Λ_P
 - **gRFI**: Λ_G
 - **eRFI**: Λ_E
 - **rRFI**: Λ_R
- with the same structure as shown earlier for Λ_P

Example of Application

- 1st lactation Feed Efficiency model for Canadian Holsteins
- International data: 7 EDGP + 8 USA herds (6 countries)
- Linear animal MT model for 6 traits: ECM, MBW and DMI in 5 – 60 and 61 – 305 DIM
- Random effects:
 - Additive genetic (G), Perm. Env. (E), Residual (R)
- MC-EM-REML (MiX99 software)
- Four different RFI expressions in 61- 305 DIM:
pRFI, gRFI, eRFI, rRFI

Regression Coefficients: DMI on Energy Sinks

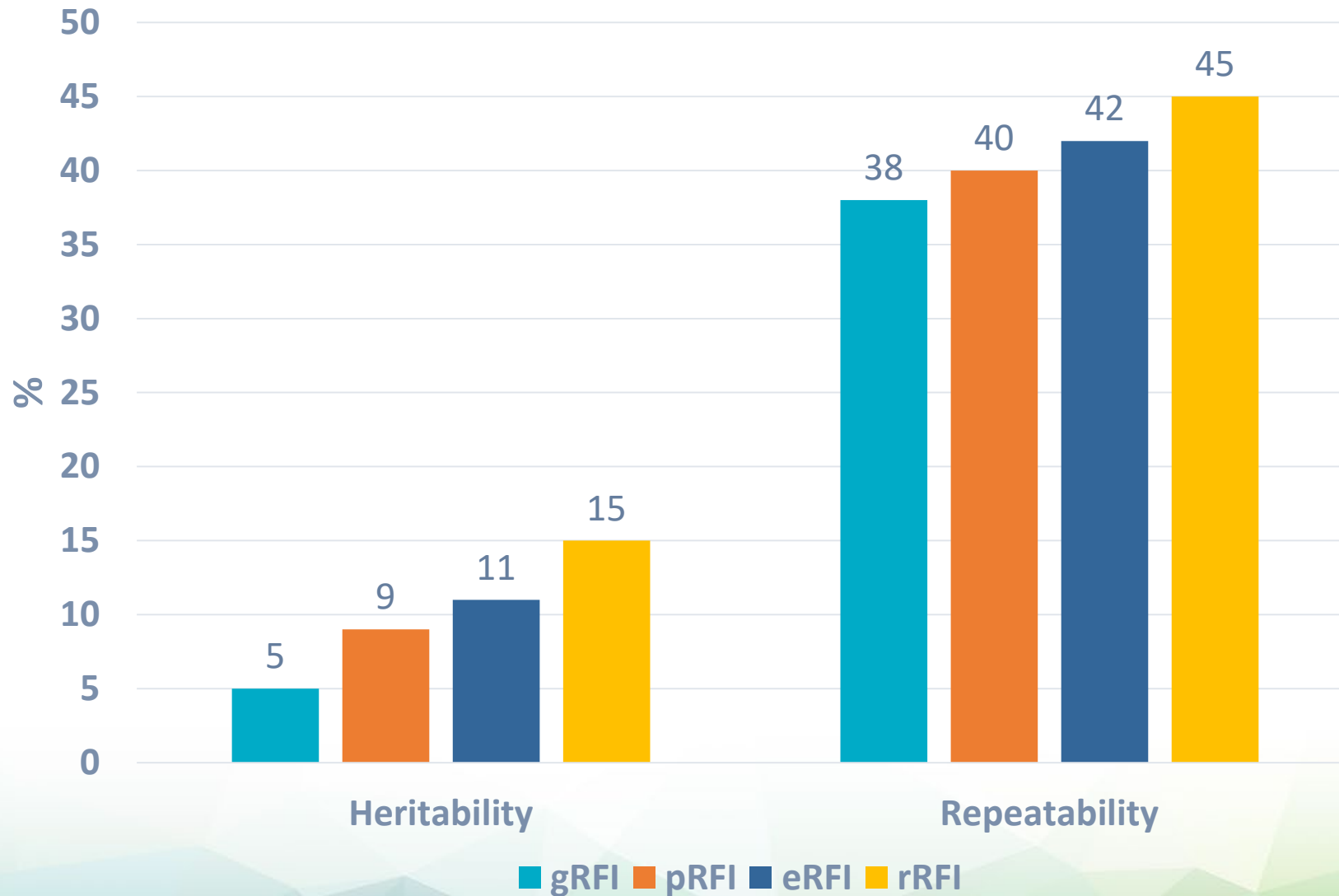
- Regression coefficients:

	gRFI	pRFI	eRFI	rRFI
ECM	0.48	0.31	0.28	0.19
MBW	0.14	0.13	0.11	0.15

- Relative impact (%) of ECM versus MBW:

	gRFI	pRFI	eRFI	rRFI
ECM	63	62	63	62
MBW	37	38	37	38

Heritability & Repeatability (x100) of RFI



Correlations (x100): RFI – Sinks & DMI

		gRFI	pRFI	eRFI	rRFI
Genetic	ECM	0	62 [*]	67	80
	MBW	0	4	11	-11
	DMI	37	82 ^{**}	88	83
Phenotypic	ECM	-33	0	6	23
	MBW	-4	0	3	-6
	DMI	59	81 ^{**}	85	88

*pRFI strongly genetically correlated with ECM

**pRFI genetically and phenotypically more similar to DMI than gRFI

Genetic & Phenotypic Correlations (x100) Between Different RFI Expressions

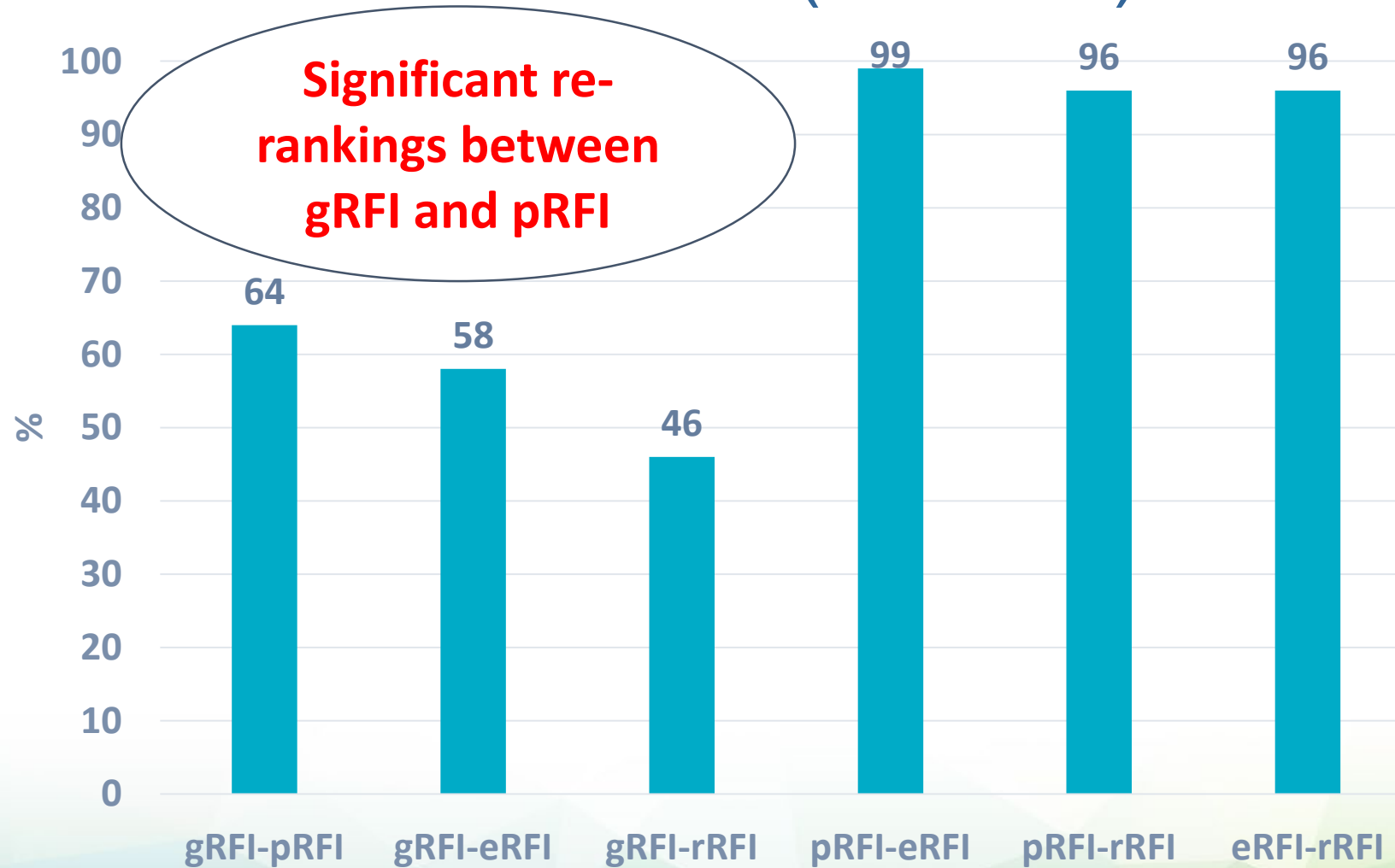
	gRFI	pRFI	eRFI	rRFI
gRFI	-	84*	72	68
pRFI	94	-	92	99
eRFI	84	92	-	92
rRFI	84	98	91	-

*gRFI and pRFI are genetically different traits

Genomic Evaluation

- 111,857 weekly records
- 5,325 (4,313 genotyped) cows
- 1,160 (943 genotyped) sires
- 19,137 (8,375 genotyped) animals in pedigree
- Same model as for VCE
 - ECM and MBW as sinks for DMI, 4 definitions of RFI
- Method:
 - ssGBLUP
 - MiX99 software

Correlations (x100) Between GEBV of RFI for Official Sires (N = 298)



Correlations (x100) Between GEBV for RFI and Other Traits for Official Sires (N = 298)

	ECM	MBW	DMI
gRFI	-1	-8	21
pRFI	75*	14	83*
eRFI	80	23	89
rRFI	88	1	82

*relative to gRFI, pRFI rankings are much more like ECM and DMI rankings

Conclusions

- Using recursive modelling as operational tools (re-parametrization of multiple-trait model parameters) allowed for definition, derivation and interpretation of different expressions of RFI in dairy cattle
- Substantial differences between different definitions of RFI
 - Genetic parameters
 - Genomic evaluation results
- Consequences of using Genetic vs Phenotypic RFI for genetic selection

Generalizations

- 'Producing Ability' RFI derived from G + PE co-variance components
- 'Herd' RFI derived from model with random herd effect
- Other residual (or ratio) traits e.g. residual CH_4 production, CH_4 yield or intensity
- Other (more) energy sinks e.g. ΔBW
- Heterogeneity of RFI between and across lactation(s) (random regression model)

EDGP & RDGP Participating Organizations & Data Contributors



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Thank You

