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
  \[ \text{DMI}_i = \mathbf{x}_i' \mathbf{b} + \lambda_{\text{ECM}} * \text{ECM}_i + \lambda_{\text{MBW}} * \text{MBW}_i + e_i \]
- Estimates of regression coefficients \( \lambda_{\text{ECM}} \) and \( \lambda_{\text{MBW}} \) 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, $\lambda_{ECM}$ and $\lambda_{MBW}$ can be derived as partial regression coefficients from phenotypic co-variances among DMI and the energy sinks.
- Define $\mathbf{C} = \begin{bmatrix} C_{ij} \end{bmatrix}$ (2x2) phenotypic co-variance matrix for ECM and MBW, $\mathbf{w} = \begin{bmatrix} w_{ij} \end{bmatrix}$ vector of phenotypic co-variances between sinks and DMI. Then

$$\begin{bmatrix} \lambda_{ECM} & \lambda_{MBW} \end{bmatrix}' = \mathbf{C}^{-1} \mathbf{w}$$
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

\[ y_i = X b + a_i + p_i + e_i, \text{ with} \]

\[ \nu(a_i) = G \] - genetic covariance matrix
\[ \nu(p_i) = E \] - covariance matrix for the PE effects
\[ \nu(e_i) = R \] - residual covariance matrix

\[ P = G + E + R \] - phenotypic co-variance matrix
Use of Mixed Model Methods for RFI

• Let $\mathbf{a} = [a_{ECM}, a_{MBW}, a_{DMI}]'$ be EBVs for DMI and sinks

• Then $\mathbf{a}^* = [a_{ECM}, a_{MBW}, a_{RFI}]' = \Lambda_p \mathbf{a} = $ $\Lambda_p = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ -\lambda_{ECM} & -\lambda_{MBW} & 1 \end{bmatrix} $ 

$\lambda_X =$ partial phenotypic regression coefficient (derived from MT estimate of $P$) of DMI on $X$ (energy sink)
Recursive Model Approach for RFI

\( Y_1, Y_2, \) and \( Y_3 \) - phenotypes for ECM, MBW and DMI

Recursive Model (RM) equations:

\[
Y_1 = \text{fixed}_1 + \text{random}_1 + e_1  \\
Y_2 = \text{fixed}_2 + \text{random}_2 + e_2  \\
Y_3 = \lambda_{31} \cdot Y_1 + \lambda_{32} \cdot Y_2 + \text{fixed}_3 + \text{random}_3 + e_3  \\
\]

\( \lambda_{jk} = \) recursive coefficient parameter for the effect of change in trait j caused by the phenotype of trait k
Mixed linear RM for ECM, MBW and DMI:

\[ \Lambda y_i = X b^* + a_i^* + p_i^* + e_i^*, \text{ with} \]

\[ a_i^* = \Lambda a_i \]

\[ \nu(a_i^*) = \Lambda G \Lambda' \]
\[ \nu(p_i^*) = \Lambda E \Lambda' \]
\[ \nu(e_i^*) = \Lambda R \Lambda' \]

\[ P^* = G^* + E^* + R^* \]

RM for ECM, MBW and DMI + restrictions on certain RM parameters = MT model for these traits
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
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: $\Lambda_P$
- gRFI: $\Lambda_G$
- eRFI: $\Lambda_E$
- rRFI: $\Lambda_R$

with the same structure as shown earlier for $\Lambda_P$
Example of Application

- 1\textsuperscript{st} 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:

<table>
<thead>
<tr>
<th></th>
<th>gRFI</th>
<th>pRFI</th>
<th>eRFI</th>
<th>rRFI</th>
</tr>
</thead>
<tbody>
<tr>
<td>ECM</td>
<td>0.48</td>
<td>0.31</td>
<td>0.28</td>
<td>0.19</td>
</tr>
<tr>
<td>MBW</td>
<td>0.14</td>
<td>0.13</td>
<td>0.11</td>
<td>0.15</td>
</tr>
</tbody>
</table>

- Relative impact (%) of ECM versus MBW:

<table>
<thead>
<tr>
<th></th>
<th>gRFI</th>
<th>pRFI</th>
<th>eRFI</th>
<th>rRFI</th>
</tr>
</thead>
<tbody>
<tr>
<td>ECM</td>
<td>63</td>
<td>62</td>
<td>63</td>
<td>62</td>
</tr>
<tr>
<td>MBW</td>
<td>37</td>
<td>38</td>
<td>37</td>
<td>38</td>
</tr>
</tbody>
</table>
Heritability & Repeatability (x100) of RFI

Heritability
- gRFI: 5%
- pRFI: 9%
- eRFI: 11%
- rRFI: 15%

Repeatability
- gRFI: 38%
- pRFI: 40%
- eRFI: 42%
- rRFI: 45%
Correlations (x100): RFI – Sinks & DMI

<table>
<thead>
<tr>
<th></th>
<th>gRFI</th>
<th>pRFI</th>
<th>eRFI</th>
<th>rRFI</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Genetic</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ECM</td>
<td>0</td>
<td>62*</td>
<td>67</td>
<td>80</td>
</tr>
<tr>
<td>MBW</td>
<td>0</td>
<td>4</td>
<td>11</td>
<td>-11</td>
</tr>
<tr>
<td>DMI</td>
<td>37</td>
<td>82**</td>
<td>88</td>
<td>83</td>
</tr>
<tr>
<td><strong>Phenotypic</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ECM</td>
<td>-33</td>
<td>0</td>
<td>6</td>
<td>23</td>
</tr>
<tr>
<td>MBW</td>
<td>-4</td>
<td>0</td>
<td>3</td>
<td>-6</td>
</tr>
<tr>
<td>DMI</td>
<td>59</td>
<td>81**</td>
<td>85</td>
<td>88</td>
</tr>
</tbody>
</table>

*pRFI strongly genetically correlated with ECM

**pRFI genetically and phenotypically more similar to DMI than gRFI
**Genetic & Phenotypic Correlations (x100) Between Different RFI Expressions**

<table>
<thead>
<tr>
<th></th>
<th>gRFI</th>
<th>pRFI</th>
<th>eRFI</th>
<th>rRFI</th>
</tr>
</thead>
<tbody>
<tr>
<td>gRFI</td>
<td>-</td>
<td>84*</td>
<td>72</td>
<td>68</td>
</tr>
<tr>
<td>pRFI</td>
<td>94</td>
<td>-</td>
<td>92</td>
<td>99</td>
</tr>
<tr>
<td>eRFI</td>
<td>84</td>
<td>92</td>
<td>-</td>
<td>92</td>
</tr>
<tr>
<td>rRFI</td>
<td>84</td>
<td>98</td>
<td>91</td>
<td>-</td>
</tr>
</tbody>
</table>

* 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)

Significant re-rankings between gRFI and pRFI
Correlations (x100) Between GEBV for RFI and Other Traits for Official Sires (N = 298)

<table>
<thead>
<tr>
<th></th>
<th>ECM</th>
<th>MBW</th>
<th>DMI</th>
</tr>
</thead>
<tbody>
<tr>
<td>gRFI</td>
<td>-1</td>
<td>-8</td>
<td>21</td>
</tr>
<tr>
<td>pRFI</td>
<td>75*</td>
<td>14</td>
<td>83*</td>
</tr>
<tr>
<td>eRFI</td>
<td>80</td>
<td>23</td>
<td>89</td>
</tr>
<tr>
<td>rRFI</td>
<td>88</td>
<td>1</td>
<td>82</td>
</tr>
</tbody>
</table>

*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. Δ BW

• Heterogeneity of RFI between and across lactation(s) (random regression model)
EDGP & RDGP Participating Organizations & Data Contributors
Thank You