Genetic evaluation for Saved feed
– Genomic prediction of residual feed intake in the Nordic breeds using data from research herds and 3D cameras in commercial herds

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The overall aim of Saved feed

Saved feed for all Nordic breeds

- Maintenance (Aug ‘19) – (covered by Lidauer et al., 2019)
- Saved feed in NTM (Aug ‘20)
- Metabolic efficiency (Nov ‘20) – Residual feed intake

\[
EBV \text{ (Saved feed)} = EBV \text{ (Maintenance)} + EBV \text{ (Metabolic efficiency)}
\]

Based on weight and correlated info
Based on feed intake, yield, weight, etc.
Weight data (maintenance)

Core trait
- Weight from scales
- Tape measurements
- Weight predicted from pictures (CFIT)

Indicator traits
- Slaughter weight
- Stature
- Chest width
- Body depth

Described by Lidauer et al., 2019
Metabolic efficiency – what is that?

Metabolic efficiency = observed feed intake – predicted feed intake

• Predicted feed intake is based on yield, maintenance, mobilization, etc.
Feed intake data (metabolic eff.)

**Core trait**
- Complete lactations with feed intake data
- Prefer more than one lactation

**Indicator traits**
- Feed intake from parts of the lactation (eg. day 60-120)
- Feed intake only in 1st lactation
- Heifer feed intake

Most reliable information include early lactation

Less reliable – genetic correlation < 1.00 lactation
Feed intake data (metabolic eff.)

- We have access to feed intake data from
  1. 3D camera system from VikingGenetics (CFIT)
     - We gratefully acknowledge VikingGenetics
     - See ICAR2021 - 10.5 Lassen et al - Identification of cows and individual feed intake records using a 3D camera system in commercial farms
  2. EDGP research farm data
     - We gratefully acknowledge the EDGP project
  3. Luke research farm data
     - We gratefully acknowledge Luke
Feed intake data (metabolic eff.)

- Nordic HOL (Foulum+CFIT) | Repeated records from 1st to 6th parity
- HOL abroad (AUS, CAN, USA) | Repeated records from 1st to 6th parity
- Nordic RDC (Luke+CFIT) | Repeated records from 1st to 6th parity
- Nordic JER (CFIT) | Repeated records from 1st to 6th parity

<table>
<thead>
<tr>
<th>Number of cows</th>
<th>Research farms</th>
<th>Private farms April 21</th>
<th>Private farms Dec 2021</th>
</tr>
</thead>
<tbody>
<tr>
<td>Holstein</td>
<td>2,600</td>
<td>430</td>
<td>3,000</td>
</tr>
<tr>
<td><strong>RDC</strong></td>
<td>725</td>
<td>270</td>
<td>2,000</td>
</tr>
<tr>
<td>Jersey</td>
<td>0</td>
<td>1,500</td>
<td>2,000</td>
</tr>
</tbody>
</table>
Descriptive statistics for phenotypes

- All statistics presented as kg per day
- Levels are as expected compared to knowledge from practice and research herds
- Differences on production is caused by distribution of lactations – RDC have majority of data from 1st parity

<table>
<thead>
<tr>
<th></th>
<th>Nordic HOL</th>
<th>Nordic RDC</th>
<th>Nordic JER</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>21.8</td>
<td>20.2</td>
<td>17.4</td>
</tr>
<tr>
<td>SD</td>
<td>3.6</td>
<td>3.6</td>
<td>2.6</td>
</tr>
<tr>
<td>DMI</td>
<td>21.8</td>
<td>20.2</td>
<td>17.4</td>
</tr>
<tr>
<td>ECM</td>
<td>34.0</td>
<td>29.7</td>
<td>34.8</td>
</tr>
<tr>
<td>MBW</td>
<td>128.4</td>
<td>119.2</td>
<td>101.3</td>
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</tbody>
</table>
Pedigree and T-matrix construction

- Pedigrees traced for 5 generations in JER/RDC and 3 generations for HOL
  - Holstein was traced fewer generations since EDGP only deliver 3 generations
  - Genetic groups added – birth year, breed and country
  - All candidates were added to get GEBVs
- Pedigree and genomic information has been incorporated by setting up a ssGTaBLUP model (Strandén and Mäntysaari, 2017)
  - 10% weight on residual polygenic effect
  - QP transformation used
  - Inbreeding coefficients used – calculated with RelaX2 (Strandén and Vouri, 2006)
Metabolic efficiency model – 1st step

- DMI =
  - Linear regression on calving age and calving age$^2$
    - Nested within parity (parity = 1, 2, ..., 6)
  - Lactation period
    - Nested within parity (parity = 1, 2, ..., 6)
  - Herd x Year x Season
  - Year x Season x lactation period
  - Regression on ECM, MBW and ΔBW
    - ECM and ΔBW is nested with in lactation period and 1st or later parities
    - MBW is nested within 1st or later parities
  - Residual used for further analysis
Genetic model – 2nd step

• Heterogenous variance correction for
  • Parity
  • Lactation period
  • Year x season

• Fixed effects of HYS and $Y_{S_lacp}$ from LS-model is back transferred to phenotype
  • Ensure that additive effects not are lost

• Genetic model = HYS + $Y_{S_lacp}$ + PE + A + e

• Single trait model for JER and RDC
• Multi country model for HOL
• Solver used is ssGTaBLUP in MiX99 (MiX99 Development Team, 2019)
Genetic parameters

Assumptions

- Heritability: 15% for all 3 breeds
- Same trait across parities and within lactation
  - It is a rough assumption but a consequence of few data
Extra reliability in addition to pedigree information

- Tested for production traits from research data

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<th>RDC</th>
<th>HOL</th>
</tr>
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<tbody>
<tr>
<td>Extra reliability</td>
<td>1-3%</td>
<td>3-7%</td>
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- Expected increase in reliability for metabolic eff. about the same size as for production traits
- More females in the reference population will increase genomic reliability
The Saved feed index

• The effect of 1 index unit is the same for maintenance and metabolic efficiency
  • RDC = 9.8 kg DMI per annual cow
  • HOL = 8.2 kg DMI per annual cow
  • JER = 6.7 kg DMI per annual cow

• The correlation between the index for maintenance and metabolic efficiency is 0

• Currently, the maintenance breeding values influence the Saved feed index most
Summary

• Both component traits of Saved feed are available
  • Jersey, Red Dairy Cattle & Holstein
• Reliable GEBVs depends on large scale feed intake recording in production herds
• Data from CFIT is used in the genetic evaluation
  • Feed intake data of good quality, whole lactations and data from production herds
• Selection for the Saved feed index will lead to:
  • More profitable and climate friendly cattle