Why use robotic milking data?

- **High genetic correlations** (~ 0.90) between udder linear and AMS traits
- high heritabilities of AMS traits
  - → **Increased EBVs accuracy**
  - Information from multiple lactations
    - → **Accurate EBVs for 2nd and 3rd lactations**

- It is possible to get information from more herds than those enrolled in linear classifications today and with a lower cost
Udder coordinates from Lely milking robots (AMS data)

- AMS data from Danish herds (HOL, RDM and JER)
- Multiple observations from udder traits are available:
  - Teat placement front = TPLF
  - Teat placement back = TPLB
  - Udder balance = UB
  - Udder depth = UD

Time span of linear and AMS traits

- Linear traits: TPLF, UD (DNK)
- Linear + TPLB, UB
- AMS traits: TPLF, TPLB, UB and UD
  - 2016
  - ~1985
  - 2006
  - 2008
Means of Udder Depth - Hol

Traits by lactations
• Overlapping number of observations in **udder balance** - between AMS and Linear traits

From the total of cows with AMS data 66.7% also have linear data.

<table>
<thead>
<tr>
<th>Breed</th>
<th>N</th>
<th>% of both AMS and Linear</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Linear</td>
<td>AMS</td>
</tr>
<tr>
<td>HOL</td>
<td>1,762,652</td>
<td>38,664</td>
</tr>
<tr>
<td>JER</td>
<td>164,490</td>
<td>3,595</td>
</tr>
<tr>
<td>RDM</td>
<td>853,678</td>
<td>3,693</td>
</tr>
</tbody>
</table>

**Genetic parameters (lact.1)**

**Source:** Ane M. Closter
Genetic model

- Udder linear traits model as in routine evaluation
- AMS data is included as a correlated trait
- **NEW:** number of milkings per day (AMS)

![Holstein milkings per day](image)

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**Holstein sires with AMS data**

<table>
<thead>
<tr>
<th>Description</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of AMS sires</td>
<td>1824</td>
</tr>
<tr>
<td>Average AMS daughters/sire</td>
<td>14.4</td>
</tr>
<tr>
<td>highest number of AMS dghters/sire</td>
<td>805</td>
</tr>
<tr>
<td>Sires with &gt; 10 AMS dghtrs</td>
<td>15.4% (274)</td>
</tr>
<tr>
<td>Sires with &gt; 50 AMS dghtrs</td>
<td>4.1%</td>
</tr>
<tr>
<td>Sires with &gt; 100 AMS dghtrs</td>
<td>2.3%</td>
</tr>
</tbody>
</table>
HOLSTEIN - EBV correlations between current and new evaluation

What are the changes in breeding values?
Correlations between current evaluation and AMS evaluation - cows with linear traits
Influence of AMS data on breeding value estimation
Correlations between current evaluation and AMS evaluation
- for cows with both AMS and linear traits

Standard deviation of EBVs - HOL cows
HOL- correlation old vs. new
Sires with ams daughters

HOL- correlation old vs. New
Sires with ams daughters
Final remarks

• MORE Data: #3 lactations
• High heritabilities for AMS
• Genetic correlations >90 = same trait
• No change on the genetic trends
• Higher reliability for sires (with AMS daughters) and cows (especially later lactations)
• Plan for implementation in routine (parallel runs in 2016)
• IB test September and implementation Nov’16

NAV

Nordisk Avlsværdi Vurdering • Nordic Cattle Genetic Evaluation