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Impact of Genomic Selection on Organizational Structures in Milk Recording and Breeding

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Outline

- Where we came from
  - Progeny test

- **Genomic Selection 1.0**
  - Started 2009 / 2010, classical ‘Interbull’ traits

- **Genomic Selection 2.0**
  - started 2014-2016, Complete herd genotyping, new traits

- **Genomic Selection 3.0**
  - New sources of data

- Where do farmers want to go

- Outlook
Classical dairy cattle breeding programs

- Progeny test: size of AI breeding (testing) programs was limited by size of DHI cow population
  - International marketing of proven bulls via Interbull MACE
- Genomic Selection 1.0 made use of large amount of historic data from progeny testing programs / DHI data

- Classical evaluation HOL Germany (April 2019):

<table>
<thead>
<tr>
<th>Traits</th>
<th>MFP/SCC</th>
<th>Longevity</th>
<th>Fertility</th>
<th>Calving</th>
<th>Conform.</th>
<th>Milk.-speed</th>
</tr>
</thead>
<tbody>
<tr>
<td># records</td>
<td>420 Mio</td>
<td>15 Mio</td>
<td>43 Mio</td>
<td>24 Mio</td>
<td>2.9 Mio</td>
<td>8.6 Mio</td>
</tr>
<tr>
<td># animals with rec.</td>
<td>22 Mio</td>
<td>15 Mio</td>
<td>29 Mio</td>
<td>11 Mio</td>
<td>2.9 Mio</td>
<td>2.7 Mio</td>
</tr>
</tbody>
</table>

EuroGenomics reference bulls include via Interbull MACE phenotypes from about 40 Mio cows

→ Very reliable gEBVs for the ‘historic traits’ for male AND female calves
Use of young genomic Holstein bulls in cow population (DEU)

- % use of young genomic bulls now at 80%
  - Internationally 50-98%

- Increase of market for polled bulls in Germany
DEU: Development of number new HOL A.I. bulls per year

But smaller number of bulls and strong preselection (1 : 40) causes problems in classical genetic evaluation ← input to bull reference population
Increased genetic progress by Genomic Selection

- EBV all used semen straws Holstein bulls in Germany, mean =100, SD = 12

<table>
<thead>
<tr>
<th>HOL</th>
<th>Progress/year</th>
</tr>
</thead>
<tbody>
<tr>
<td>all ins.</td>
<td>1998-2001</td>
</tr>
<tr>
<td>RZM</td>
<td>1,94</td>
</tr>
<tr>
<td>RZE</td>
<td>1,55</td>
</tr>
<tr>
<td>RZS</td>
<td>-0,21</td>
</tr>
<tr>
<td>RZN</td>
<td>0,52</td>
</tr>
<tr>
<td>RZR</td>
<td>-1,68</td>
</tr>
<tr>
<td>RZKm</td>
<td>0,92</td>
</tr>
<tr>
<td>RZG</td>
<td>1,74</td>
</tr>
</tbody>
</table>

- With genomic selection progress in all important traits
  - And more than doubled progress in TMI
  - Progress longevity now same as for milk production
10 Years Genomic Selection for Holstein → Breeding

- Very good selection response
  - Large databases with phenotypes from DHI
  - Combination of reference populations through Interbull MACE

- Number of new AI bulls per year
  - decreased significantly in European AI programs
  - decreased slightly in USA

- Improved international comparability of young AI bulls and females
  - Fully comparable gEBV by exchange of SNP

- High prices for elite females
  - Few individual private farmers that are still breeding AI bulls
    → many belong to AI companies or farms under contract

- New players in the AI market and increased competition
  → less AI companies
**Genomic Selection for herd management**

- **First years of GS**
  - Genotyping relatively expensive
  - Only potential elite females genotyped

- **Now**
  - Genotyping cheaper (25-40 $)
  - Higher selection intensity e.g. by use of sexed semen

- **herd genotyping and Genomic Selection = Genomic Herd Management has become profitable for commercial dairy herds**
  - e.g. in USA ca. 25% of all (new) Holsteins in DHI
  - e.g. in Germany ca. 11% of all (new) Holsteins in DHI

- **Advantages**
  - Precise selection among calves (saves rearing costs)
  - Precise mating for all traits and for heifers and cows
  - Parentage verification and detection, management of genetic recessives

- **on farm breeding decisions independent from phenotypes (DHI and classification)**
Genomic Selection 2.0

- Introduction of new traits into Genomic Selection not possible by bull reference population
  - Would take to long time
- Introduction of new traits possible by cow reference population
  - Reference cow = genotyped cow/female with phenotype
  - 3-10 reference cows same information content as one reference bull with 100 non-genotyped daughters
- For effective cow reference population just small proportion of all (DHI) cows needed
  - E.g. equivalent of 35,000 bulls = 105,000 – 350,000 reference cows
    - 3-10% of US-HOL DHI cows
    - 5-17% of DEU-HOL DHI cows
  - For Interbull traits by farms with herd genotyping already given
  - For some new traits (e.g. health traits) almost given

- Currently data recording by DHI in genotyping herds is still the base
Started in June 2016 as a joint project by German Holstein breeding associations with vit, later CONVIS (Lux.) and Holstein Austria joined

Now a fast growing standard tool for commercial farmers

- 1,421 farms participating in whole herd genotyping / KuhVision
  - 664 farms providing data on new traits
  - 30-35 new farms every month

- milking >10% of all milk recorded HOL

- 370,000 female HOL genotyped

- >150,000 cows have already calved

3. June 2019:
Mixed cow + bull reference population health traits

- Reference cow: genotyped cow with health record
  - Health records from all lactations for genetic evaluation
- Reference bull: AI bull with daughters (non-genotyped) with health records

Size of mixed reference population health traits (here Mastitis)

<table>
<thead>
<tr>
<th>Date</th>
<th>RP cows</th>
<th>RP bulls</th>
<th>RP total</th>
</tr>
</thead>
<tbody>
<tr>
<td>04-2018 (test)</td>
<td>61,550</td>
<td>5,574</td>
<td>67,124</td>
</tr>
<tr>
<td>08-2018 (test)</td>
<td>77,029</td>
<td>6,159</td>
<td>83,188</td>
</tr>
<tr>
<td>12-2018 (test)</td>
<td>87,809</td>
<td>6,337</td>
<td>94,146</td>
</tr>
<tr>
<td>04-2019</td>
<td>ca. 100,000</td>
<td>ca. 6,500</td>
<td>ca. 106,500</td>
</tr>
</tbody>
</table>
Reliability (rel) of gEBV health traits

- Data just from new cow reference population

<table>
<thead>
<tr>
<th>Trait</th>
<th>Weight in RZhealth</th>
<th>rel. P.I.</th>
<th>rel. dGV</th>
<th>rel. gEBV</th>
</tr>
</thead>
<tbody>
<tr>
<td>RZudderfit</td>
<td>0.40</td>
<td>0.13</td>
<td>0.43</td>
<td>0.48</td>
</tr>
<tr>
<td>DDcontrol</td>
<td></td>
<td>0.14</td>
<td>0.46</td>
<td>0.51</td>
</tr>
<tr>
<td>RZhoof</td>
<td>0.30</td>
<td>0.13</td>
<td>0.41</td>
<td>0.46</td>
</tr>
<tr>
<td>RZrepro</td>
<td>0.20</td>
<td>0.12</td>
<td>0.43</td>
<td>0.48</td>
</tr>
<tr>
<td>RZmetabol</td>
<td>0.10</td>
<td>0.13</td>
<td>0.39</td>
<td>0.43</td>
</tr>
<tr>
<td>RZhealth</td>
<td></td>
<td>0.13</td>
<td>0.42</td>
<td>0.47</td>
</tr>
</tbody>
</table>

- Reasonable reliabilities for gEBV all 4 health trait indices and RZhealth
### Improved reliability (rel) of gEBV health traits

- By information from national DHI recording of culling reasons

<table>
<thead>
<tr>
<th>Trait</th>
<th>Weight in RZhealth</th>
<th>rel. P.I.</th>
<th>rel. dGV</th>
<th>rel. gEBV</th>
<th>gen. corr.</th>
<th>rel. gEBV</th>
<th>rel. gain</th>
</tr>
</thead>
<tbody>
<tr>
<td>RZudderfit</td>
<td>0.40</td>
<td>0.13</td>
<td>0.43</td>
<td>0.48</td>
<td>0.85</td>
<td>0.61</td>
<td>(+0.13)</td>
</tr>
<tr>
<td>DDcontrol</td>
<td>0.14</td>
<td>0.46</td>
<td>0.51</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RZhoof</td>
<td>0.30</td>
<td>0.13</td>
<td>0.41</td>
<td>0.46</td>
<td>0.60</td>
<td>0.51</td>
<td>(+0.05)</td>
</tr>
<tr>
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<td>0.20</td>
<td>0.12</td>
<td>0.43</td>
<td>0.48</td>
<td>0.55</td>
<td>0.52</td>
<td>(+0.04)</td>
</tr>
<tr>
<td>RZmetabol</td>
<td>0.10</td>
<td>0.13</td>
<td>0.39</td>
<td>0.43</td>
<td>0.80</td>
<td>0.55</td>
<td>(+0.12)</td>
</tr>
<tr>
<td>RZhealth</td>
<td>0.13</td>
<td>0.42</td>
<td>0.47</td>
<td></td>
<td>0.57</td>
<td></td>
<td>(+0.10)</td>
</tr>
</tbody>
</table>

- Higher reliabilities for gEBV all 4 health trait indices and RZhealth
Classes of gEBV claw ulcer ↔ % incidence

- untere 25% gZW
- 25-49%
- 50-74%
- beste 25% gZW

N = 9821
φ gZW-KGS = 106
φ KGS-Inzidenzrate% = 11%
Genomic Selection 3.0

- New traits based on new ways of data recording
  - on farm (and often independent from DHI)
- i.e. (mass) data recording by sensors
- Dynamic developments driven by
  - Market for dairy management solutions
  - Breeding programs, too
- From the viewpoint of breeding programs
  - Possibility to differentiate from competitors not just by the better bull for same trait ➔ more by new important traits
  - But investment of breeding programs needed in own data recording systems in cooperation with innovative farms
- First results are in the market

- In principal: if sensors can record data on challenging new trait, they can do for classical traits, too
Automatic Milking Systems (AMS) / Robots

- Increasing use in dairy farms

- Reduced time for visual inspection of animals
  → Interest in sensor data for
    - Milkability, Temperament
    - Udder health
    - Volume and content of milk
    - Further traits
What About Robotic Teat Placement Sensors?

- Actual teat location based on successful attachment
- Can we improve trait heritability?
### Udder conformation traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>$h^2$ ams</th>
<th>$h^2$ class.</th>
<th>$r_g$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Front teat distance</td>
<td>0.66</td>
<td>0.46</td>
<td>-0.96</td>
</tr>
<tr>
<td>Rear teat distance</td>
<td>0.56</td>
<td>0.45</td>
<td>-0.97</td>
</tr>
<tr>
<td>Udder depth</td>
<td>0.74</td>
<td>0.49</td>
<td>0.91</td>
</tr>
<tr>
<td>Distance front-rear</td>
<td>0.69</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Udder balance</td>
<td>0.48</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Udder balance left-right</td>
<td>0.03</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Unevenness</td>
<td>0.45</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Note:** Not corrected for stature!

- **Low heritability**
- **Less useful trait**

### AMS
- Objective (exact) score
- Measuring multiple times
- Easy to measure extra traits

### Classifiers
- Subjective score
- Measuring only once

Higher heritability for AMS traits
Type traits collected by cameras

- Movement scores
- Cow condition scores and cow size

WRA – Wiederristhöhe
SBR – Schulterbreite
KBH – Kreuzbeinhöhe
HBR – Höckerbreite
BBR - Beckenbodenbreite
SBB - Steißbeinbreite
New data sources arrive rapidly

- From big manufacturers (blue, grey, red)
- Specialised Manufacturers (e.g., activity sensors)
- From startups
  - Using the camera of a regular smartphone
- Many more
How do practical farmers look onto this?

- Looking for some examples that have made use of these new possibilities
- Opinion on future development
Herd management in times of GS and sensor data

Two examples from US and Germany:

- No-Fla Holsteins, Florida/USA (owner Don Bennink)
- Benninghoff Holsteins, North Germany (owner Marc Benninghoff)
Herd management in times of GS and sensor data

Two examples from US and Germany:

<table>
<thead>
<tr>
<th></th>
<th>No-Fla</th>
<th>Benninghoff</th>
</tr>
</thead>
<tbody>
<tr>
<td>HOL milking cows</td>
<td>6,500</td>
<td>1,200</td>
</tr>
<tr>
<td>Herd genotyping</td>
<td>since 2014</td>
<td>since 2016</td>
</tr>
<tr>
<td>Use genomic bulls</td>
<td>&gt;90%</td>
<td>100%</td>
</tr>
<tr>
<td>Cows/heifers with embryos</td>
<td>50%</td>
<td>25%</td>
</tr>
<tr>
<td>Heifers as donors</td>
<td>90%</td>
<td>100%</td>
</tr>
<tr>
<td>Use beef bulls</td>
<td>0%</td>
<td>25%</td>
</tr>
<tr>
<td>DHI participation</td>
<td>yes</td>
<td>yes</td>
</tr>
</tbody>
</table>
## What changed?

<table>
<thead>
<tr>
<th>Selection/Breeding</th>
<th>Before Genomics</th>
<th>Current</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>DHI results, pedigree, conformation (on cows)</td>
<td>Genomics, pedigree, conformation (on calves/heifers)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Management decisions</th>
<th>Before</th>
<th>Current</th>
</tr>
</thead>
</table>
|                            | Daily milk yield, monthly DHI results (SCC) | No-Fla: Daily milk yield, monthly DHI results (SCC)  
Benninghoff: Daily milk yield, activity data, SCC from DHI |
| Future                     | More on-farm measures (fat, prot., SCC, ketosis, progesteron) |                                                                         |

<table>
<thead>
<tr>
<th>Value of DHI</th>
<th>Before</th>
<th>Current</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Monthly data recording, statistics (actions, benchmarking)</td>
<td>Statistics (actions, benchmarking)</td>
</tr>
<tr>
<td>Future</td>
<td>Statistics and advise based on combination of all (central and on-farm recorded) data</td>
<td></td>
</tr>
</tbody>
</table>
Summary

- Genomic Selection based on bull reference populations
  - changed Holstein breeding programs
  - increased genetic progress
  - Increased competition among AI breeding programs
    - some impact on organizational structures in breeding
    - no impact on structures of DHI

- Genomic Selection based on female reference populations
  - Needs only data from small proportion of cow population/herds
  - Offers opportunities for new important traits
  - Genomic data is already given by herd genotyping for management
  - Sensor data are on the way to provide (all) necessary data
    - impact on organizational structures in breeding
    - possibly severe impact on structures of DHI
    - possibly severe impact on structures of (national) genetic evaluations
Outlook

- Genotyping of all females will become a well used standard tool.

- Farmers will use more technical devices in day to day management → big role/task for ICAR to evaluate the properties of this new data.

- Herd Genotyping AND new on-farm tools are a big threat to traditional farmer owned service organisations.

- Progressive farmers:
  - Role of DHI / Labs with more flexible test plans (early lactation)
  - Benchmarking
  - Use of spectral data

  - AI and DHI → jointly help them to integrate data from different sources → iDDEN
  - Farmers are willing to share on farm data if the novel services are of value to them.
IT-Solutions for Animal Production