The breeding plan and the work for better indices from a global perspective

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NAV
Outline

Status and future:

• Breeding goal
• Registrations
• Breeding value
• Breeding plan
• Genetic progress
Breeding values - abbreviations

- **DGV (SNP effects)**
  - Direct Genomic Value

- **EBV (phenotypic registrations)**
  - Estimated breeding value

- **GEBV (SNP effects + phenotypic registrations)**
  - Genomic Enhanced Breeding value

\[ \text{DGV} \quad \text{EBV} = \text{GEBV} \]
Breeding goal and genomic selection

- Breeding goal is the same with or without genomic selection.

But:

- The composition of the genetic trend is different.
  - More progress in functional traits relative to yield and type.
  - More progress in later lactation relative to first lactation.

Genomic selection can give a more balanced genetic progress.
## Reliability EBVs

<table>
<thead>
<tr>
<th>Trait</th>
<th>DGV* Birth</th>
<th>Cow-3 year</th>
<th>Bull – 5 year</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yield</td>
<td>40-50%</td>
<td>50%</td>
<td>90%</td>
</tr>
<tr>
<td>Fertility</td>
<td>40-50%</td>
<td>22% (PI)</td>
<td>70%</td>
</tr>
<tr>
<td>Mastitis</td>
<td>40-50%</td>
<td>25% (PI)</td>
<td>75%</td>
</tr>
</tbody>
</table>

Note the relationship between reliabilities:

Yield versus functional traits
Registrations

Today
• High quality and lots of data

Future with genomic selection
• High quality and lots of data

Data from practice will still be the key!!
Today

Bulls with known EBVs and SNPs create the "DNA-dictionary" (reference pop.)
SNPs from young animals can be translated to DGVs

- **HOL**: 40-50%
- **JER**: 30-40%
- **RDC**: 25-35%

SNPs from young animals → DNA-dictionary → Genomic EBVs
Bulls with known EBVs and SNPs create the "DNA-dictionary"

The quality of the dictionary is correlated to the size of the reference population.
Bulls with known EBVs and SNPs create the "DNA-dictionary"

Holstein – Eurogenomics
+12,000 reference bulls
+10% reliability (40 to 50%)
Bulls with known EBVs and SNPs create the "DNA-dictionary"

Reference bulls:
- 16,000 Eurogenomics (HOL)
- 12,000 US+CDN (HOL)
- 5,000 Brown Swiss

More cooperations will be established

SNPs ↔ EBVs
Bulls with known EBVs and SNPs create the "DNA-dictionary"

More reference bulls:
RDC: NRF? or HOL (700K)?
DJ: USJ? or HOL (700K)?
SNPs
3K, 50K, 700K (whole genome)

Future

Phenotypes

Number of animals tested depends on prices:
• Today in total about 300 Euro
• Future prices for 3K, 50K, 700K?
Nordisk Avlsværdi Vurdering

• Nordic Cattle Genetic Evaluation

SNPs ↔ EBVs

DNA-dictionary

Future

Low prices → Large scale testing/screening

Large scale DNA collection

DNA available on females with new registrations 3 year ahead!

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It is time to plan for a large scale DNA collection - the first countries make already plans

E.g.

New registrations available in 2014 – DNA collection has to start in 2011, if it takes place along with ear tagging
Future

Statistical methods will be improved

SNPs  DNA-dictionary  EBVs
Combining of DGV and EBV

• Assumptions
  • DGV is robust it means stable from evaluation to evaluation also when reference group is updated
  • Fluctuations in DGV will give fluctuations in GEBV and in worst case raise doubts about genetic evaluation in general

Stability in DGVs are needed
Combining of DGV and EBV

• Assumption
  • We need to know the reliability on DGV and EBV to be able to combine in an optimal way.
  • Critical because we want to compare animals with different information – bulls at 5 year with 100 daughters versus bulls 1 year with genotypic information only.

Estimation of reliabilities for DGV – R&D is still needed
What is included in DGV?

- Lots of pedigree information, which also are in traditional parent average index
- Important information about mendelian sampling
NAV’s plan

1. Test the methods on fertility and yield on Holstein data

2. Participate in Interbulls test run with GEBV’s in sep (Holstein only)

3. Combine PA og DGV for young genomic tested animals and change from unofficial DGV’s and official EBV’s (today) to official GEBV’s (autumn 2010)

4. Blend DGV in the traditional EBVs for all animals (during 2011)
INTERBULLs plans for international evaluation based on EBVs including genomic information

<table>
<thead>
<tr>
<th>Time schedule</th>
<th>What will happen?</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spring 2010</td>
<td>Data delivered – 7 countries</td>
</tr>
<tr>
<td></td>
<td>GMACE ready</td>
</tr>
<tr>
<td></td>
<td>Pilot run GMACE</td>
</tr>
<tr>
<td>June 2010</td>
<td>Discussion of GMACE results</td>
</tr>
<tr>
<td></td>
<td>Validation criteria ready</td>
</tr>
<tr>
<td>Sep 2010</td>
<td>GMACE test run</td>
</tr>
<tr>
<td>Dec 2010</td>
<td>GMACE routine run</td>
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</tbody>
</table>
## Reliabilities, NTM

<table>
<thead>
<tr>
<th></th>
<th>Yesterday</th>
<th>Today</th>
<th>Future</th>
</tr>
</thead>
<tbody>
<tr>
<td>5 year old bulls</td>
<td>80%</td>
<td>80%</td>
<td></td>
</tr>
<tr>
<td>3 year old bull dams</td>
<td>35%</td>
<td>35-55%</td>
<td></td>
</tr>
<tr>
<td>Heifer and bull calves</td>
<td>25%</td>
<td>30-50%*</td>
<td>Higher*</td>
</tr>
</tbody>
</table>

* With GS
Variation in NTM among bulls

NTM

2004 2005 2006 2007 2008 2009 2010

Sire, birth/year

80% 40%

25 +25 29

20 +5 15

15 +1

10 -15

5

0

-5

-10

-15

-20

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Variation in NTM among bulls

Sire, birth/year
Variation in NTM among bulls

Sire, birth/year

NTM

2004 2005 2006 2007 2008 2009 2010

-20 0 5 10 15 20 25 30

80% 50%

+25 +31 +15 -1

+5

-15

-15

-10

-5
Future variation in NTM among bulls

- Future variation in NTM among bulls

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## True breeding values versus EBVs

<table>
<thead>
<tr>
<th>EBV</th>
<th>+25 NTM</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Reliability</td>
</tr>
<tr>
<td>Min</td>
<td></td>
</tr>
<tr>
<td>Max</td>
<td></td>
</tr>
</tbody>
</table>

Low reliabilities means large standard errors (min-max)
Do not use the single bulls too intensive, but use more bulls with nearly the same DGV
## Breeding plan

<table>
<thead>
<tr>
<th></th>
<th>Yesterday</th>
<th>Today</th>
<th>Future</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bull sire and</td>
<td>5 year old &gt;100 daughters</td>
<td>Mixture (1 and 5 year) depending on reliability of GS</td>
<td>1 year old</td>
</tr>
<tr>
<td>Proven bulls</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bull dams</td>
<td>Mainly lactating cows</td>
<td>Mixture (age classes) depending on reliability of GS</td>
<td>Mainly heifers</td>
</tr>
</tbody>
</table>

Reliability 30% ➔ Reliability 50%

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### Breeding plan

<table>
<thead>
<tr>
<th>Use of semen</th>
<th>Yesterday</th>
<th>Today</th>
<th>Future</th>
</tr>
</thead>
<tbody>
<tr>
<td>% Proven bull</td>
<td>70%</td>
<td>50%</td>
<td>0%</td>
</tr>
<tr>
<td>% Genvik plus bull</td>
<td>0%</td>
<td>30%</td>
<td>80%</td>
</tr>
<tr>
<td>% Young bull</td>
<td>30%</td>
<td>20%</td>
<td>20% (Ref)</td>
</tr>
</tbody>
</table>

Selection of Genvik plus bulls depends on reliability of DGV:
- Higher reliability stronger selection
- Lower reliability use relatively more bulls as Genvik plus
Genomic test of animals

- Advantage to test both bull calves and female candidates – more bull calves than females
- 5-6 times the number of selected animals a good starting point
  - Trade off – money and response
  - Progress per test decrease by increasing number of tests, but total progress increase still!
2010

• More balanced and higher genetic progress
• Genomic EBVs have higher reliability than pedigree index but lower than progeny – take care in practice – see Genvik plus bulls as a team
• Genomic prediction has a short history and is still under development – has to be remembered in practice
• Official EBVs will include genomic information in 2010
• Breeding plan will gradually change – shorter generation intervals
Future

• “GS technology” will improve further – cheaper more K’s
• Genomic EBVs will be more reliable
• Breeding animals young animals mainly
• More cooperation across countries/organisations
• Interbulls role might change
• Collection of DNA from all/lots of animals will be standard in the near future – 3K might initiate it
• We need to start thinking/test how to do it
• Still lots of high quality phenotypic registrations are needed – it is the key