Effect of genomic pre-selection on the stability of EBVs from traditional BLUP procedure for production traits – a practical illustration

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Current status for genomic selection
HOL, (DNK, FIN, SWE)

• One out of ten bulls selected for total merit (selection intensity 1.8 and selection differential 1.4)
• Selection intensity for the single traits in total merit is lower (Protein: selection intensity 1.0 selection differential 0.8)
• Second batch bulls are used less intensively. Only 10-20% of inseminations is done with second batch bulls.
• Genomic selected bulls are used intensively as bull sires
• Progeny test by traditional BLUP procedure is done per trait or trait group
Traditional BLUP evaluation

Unbiased, if all data on which selection is based is included

• Ignoring genomic selection

In theory:

– Evaluations are biased because in BLUP, progenies are assumed to be average of their parents, i.e. $E[MS-term]=0$

– Leads into problems of separating environmental and genetic levels, i.e. genetic trend is underestimated and environmental trend is overestimated

– as a result: young bulls in progeny test are underestimated
Question: how robust is our evaluation model against unaccounted selection?

• Phenotypic trend = Environmental + genetic trends

• Genetic trend estimation in BLUP:
  – Selection of parents (and now Mendelian term)

• Environmental trend estimation in BLUP:
  – Animals from different generations/birth years are producing in same environment classes
    1. First crop vs. second crop daughters
    2. Same bulls having daughters in consecutive years
    3. Same cows having records in consecutive years
Objective

• Test the effect of bull second crop daughters for the robustness
• Try to test the effect of genomic selection on accuracy of evaluations
• Mimic the effect of bias from pre-selection on real data for a strongly selected trait. Protein is chosen
Material

• Nordic Test Day model for production trait (Multi trait, multi lactation, single breed model. Test day records since 1988)
• Protein yield for Holstein is investigated
  – P-index, relative index
    • Base = 100, cows born in 1990 and 1991
    • STD = 10, genetic std. app. 10.5
Material

- Data is from February 2012
- Results has been presented at Interbull meeting in Cork 2012
Senarios

• Rout: Routine evaluation with all animals included
  • Y_1990-2003: Pre-selection of young bulls born 1990-2003:
    AI bulls with progeny test above average selected
    Selection intensity 0.8, selection differential 0.75
    Records from daughters of discarded bulls were set to missing (no progeny test)
  • Y_2000-: Same as in previous scenario but for young bulls born 2000 and onwards
Senarios (continued)

• Sec_1995-: No pre-selection for young bulls, but second crop daughters born in 1995 and onwards have their records set to missing

• Y_Sec_2000-: Daughters born year 2000 and onwards:
  - No second crop daughters with records
  - Pre-selection of young bulls above average
  - Daughter records were set to missing but pedigree information kept

All senarios: No changes for private and foreign bulls
<table>
<thead>
<tr>
<th>Birth year</th>
<th>Rout</th>
<th>Y_1990-03</th>
<th>Y_2000-</th>
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## Largest progeny group size

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Genetic trend protein Nordic A.I. bulls

Different no of bulls in trend estimation

Genetic std.: 10.5

Year of birth

P-index


160
150
140
130
120
110
100
90

Preselection

Rout

Y_1990_2003

Y_2000-

Sec_1995-

Y_sec_2000-
Difference to routine run, protein

Only selected bulls included

Genetic std.: 10.5

Year of birth

P-index

Y_1990-2003
Y_2000-
Sec_1995-
Y_Sec-2000-
Correlation with routine run

Year of birth

P-index:
- Y_1990-2003
- Y_2000-
- Sec_1995-
- Y_Sec-2000-
Difference in P-index in scenario **Y_Sec_2000**- compared to routine run for bulls born after 2000. No correction for differences in trend

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Conclusion

• Pre-selection of young bulls with a reliability of 0.90 and a selection intensity of 0.8 has negative effect on the genetic trend
  – Bias in expected direction, i.e. trend is underestimated
  – Effect less than was expected
• Omitting second crop daughters has less effect on trend.
• Pre-selection of young bulls in combination with omitting second crop daughters has bigger but still minor effect
• Likely: Genomic selected bulls will be used over a longer time span than young bulls in the old young bull system, and some genomic tested bulls are used for nearly a year
• Selection intensity for a single trait is lower than for the Total Merit Index
• Genomic selection will not ruin traditional estimation of breeding values in the first years