Genomic selection in German Landrace

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Session 29

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3 Bayerische Landesanstalt für Landwirtschaft, Institut für Tierzucht, 85586 Poing
Genomic Selection

Successfully implemented in cattle but not yet in pig breeding
Objective

• Investigate the potential for an application of genomic selection in the breeding program for German Landrace in Bavaria

• Focus on fertility traits

• Calibration- and validation samples including boars and sows
• 1,982 animals were genotyped

• Traits analyzed were number of piglets born alive (NBA) and lean meat percentage (LMP)

• After editing of data, 1,868 pigs (314 boars, 1,554 sows) remained in the analysis

• Genotyping was done by Tierzuchtforschung e.V. using SNP60-Illumina Bead-Chips
Data

• Boar samples stored since 1995
  - Living and slaughtered boars
  - Stored by GeneControl GmbH

• Sow samples stored since 2006
  - Mainly from living animals
  - From nucleus and 13 downstream multiplier farms
Data

Sample

Number of sows

Year of Birth


Number of boars

0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100

Sows  Boar

Sample
Sample

Number of sows over the years:
- Sows and Boar graph with years from 1995 to 2011.

Number of sows:
- Year of Birth from 1995 to 2011.
- Number of sows ranging from 0 to 750.

Number of Boar:
- Year of Birth from 1995 to 2011.
- Number of Boar ranging from 0 to 100.

Data
Characterization of genotyped animals

<table>
<thead>
<tr>
<th></th>
<th>Boars</th>
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<th>Sows</th>
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<tbody>
<tr>
<td></td>
<td>mean</td>
<td>min/max</td>
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<td>Progeny on station</td>
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NBA : Number of piglets born alive
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NBA : Number of piglets born alive
Reliability of Total Merit Index

- Red line: Sows
- Black line: Boar

Year of Birth

- 1995
- 1996
- 1997
- 1998
- 1999
- 2000
- 2001
- 2002
- 2003
- 2004
- 2005
- 2006
- 2007
- 2008
- 2009
- 2010
- 2011

Reliability

- 100
- 95
- 90
- 85
- 80
- 75
- 70
- 65
- 60
- 55
- 50
- 45
- 40
- 35
- 30
Data

Reliability of Total Merit Index

Year of Birth

Reliability


Sows
Boar
Data

• Traits
  - number of piglets born alive (NBA; $h^2 = 0.24$)
  - lean meat percentage (LMP; $h^2 = 0.60$)

→ NBA is the mean average of the breeding value of first litters (NBA 1) and the breeding value of second and higher litters (NBA 2+)

→ Phenotypic data from herdbook farms and piglet-producers

→ LMP data was recorded on progeny test station in Schwarzenau and Grub
Method

• Validation via forward-prediction according to Interbull validation-test (Mäntysaari et al., 2011)

• Two different data-sets:
  - Reduced run: all animals since 2011 without own performance
  - Complete run: all available phenotypic information
Method

Size of calibration and validation datasets

- NBA Calibration: 1244 (285 Boars, 959 Sows)
- LMP Calibration: 658 (289 Boars, 369 Sows)
- NBA Validation: 153 (5 Boars, 148 Sows)
- LMP Validation: 305 (17 Boars, 288 Sows)
Method

Size of calibration and validation datasets

- NBA Calibration: 1244 (285 Boars, 960 Sows)
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Size of calibration and validation datasets

- NBA Calibration: 1244 (Boars 285, Sows 959)
- LMP Calibration: 658 (Boars 289, Sows 369)
- NBA Validation: 153 (Boars 5, Sows 148)
- LMP Validation: 305 (Boars 17, Sows 288)
Method

Size of calibration and validation datasets

NBA Calibration: 1244 Boars, 285 Sows
LMP Calibration: 658 Boars, 289 Sows
NBA Validation: 153 Boars, 5 Sows
LMP Validation: 305 Boars, 17 Sows
• Deregressed estimated breeding values were used as response variable (Garrick et al. 2009)

• Direct genomic values (DGV) were calculated using the gBLUP approach (VanRaden 2008)

• Genomic breeding values (GEBV) were calculated by blending direct genomic values with conventional parent averages (VanRaden et al., 2009)

• Reliability was corrected for prior selection on PA with ‘realized genomic reliabilities’ according to VanRaden (2008)
# Results

Realized genomic reliabilities ($R^2$)

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NBA: Number of piglets born alive  
LMP: Lean meat percentage
# Results

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Not on the same scale as reliability of conventional EBVs
Discussion

- Realized reliabilities of GEBV for NBA are higher (0.58) than the parent-average (0.38)

- For LMP, the gain in reliability (0.44) is small from PA (0.41)

- Calibration with boars and sows in one sample is feasible
Outlook

• Genomic selection can be beneficial for maternal traits.

• Genomic selection may also be attractive for traits like boar-taint or intra-muscular-fat

• Realized reliabilities for carcass traits may hardly justify additional costs of Genomic Selection

• Short-term implementation of Genomic Selection is feasible
Thank You!

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Christian-Albrechts-Universität zu Kiel
LKV Bayern
Tierzuchtforschung München e.V.

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