"Genetic progress in pigs: innovating for the 2025 industry and markets"

Eveline Willems DVM
AMVEC 2015
July 31st
Genetic progress

\[ \Delta G_{\text{year}} = \sigma_H \times r_{IH} \times \frac{i}{L} \]

- **Accuracy of selection**
  - Data collection / traits
  - BVE technology

- **Selection intensity**
  - Population sizes
  - Selection work

- **Genetic variation**

- **Generation interval**
  - Replacement rate
  - Age at 1st service
Data collection
Genetic progress

\[ \Delta G_{\text{year}} = \sigma_H \times r_{IH} \times \frac{i}{L} \]

- **Accuracy of selection**
  - Data collection / traits
  - BVE technology

- **Selection intensity**
  - Population sizes
  - Selection work

- **Genetic variation**

- **Generation interval**
  - Replacement rate
  - Age at 1st service
Genomic selection

Connecting data
Genotyping tools
Some terms and definitions in the era of genomics
SNP’s
DNA and genes

QTL = Quantitative Trait Loci = Gene

E.g. a piece of DNA with a positive effect on meat quality
Marker / SNP

QTL

SNP’s define a position on the genome
SNP panel

QTL

Set of markers

Many SNP’s = many markers = high density
Training

Markers explaining phenotypic performance:

1. Inside the causative mutation

2. Near the causative mutation
Recombination

Oocyte/sperm production: mixing DNA of grandparents

(= *Mendelian sampling / crossing-over* )

Marker/SNP – QTL relation can break → **repeat training**
Genotyping

Different densities:

• Full genome sequence (~1M SNPs)
• HD-chip (80k SNPs)
• LD-chip (10k SNPs)
GWAS

# of teats

highly significant in all phenotyped lines
Genomic selection

Connecting data

+ 30-40% genetic progress
Added value

- More reliable breeding values
- Faster genetic improvement (30-40%)
- New selection traits
- More predictable performance in client herds
Reliable pedigree

- Parental Identification

[Images showing different pig genotypes (AA CG TT, AA CG AT, AG CC TT, AG GG AA)]
Specific Markers

E.g. total number born

- T-T-G-T-A-C-A-
  - A-A-C-A-T-G-T-

- T-T-G-A-A-C-A-
  - A-A-C-A-T-G-T-
More accurate relations ($A^{-1} \rightarrow H^{-1}$)

Classical breeding values ($A^{-1}$)

Population average (0)
Traditional family relations ($A^{-1}$)

Halfsibs: 25%  
Full sibs: 50%
Traditional + DNA relations ($H^{-1}$)

Halfsibs

18%

28%

+1.5

Full sibs

56%

43%

1.0

1.2
More accurate relations = more accurate EBV

Accuracy H-1 versus A-1

Parents

Own performance

Relatives

Offspring
Added value

• More $\Delta G$, via higher accuracy
  – Late in life
  – Low heritability
  – Single sex
  – Expensive/difficult to measure

• Highest added value in dam lines
Reliability without genomics

Dam line boar

Genomics

Own performance

Parent info

Selection

Age d

Reliability%

Reliability Fattening

Reliability Fertility

- Reliability Fattening
- Reliability Fertility

- Dam line boar

- Parent info

- Own performance

- Genomics

- Offspring
## Reliability breeding values

<table>
<thead>
<tr>
<th>Trait</th>
<th>OP BLUP</th>
<th>GS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Feed intake</td>
<td>62</td>
<td>9</td>
</tr>
<tr>
<td>Gain</td>
<td>65</td>
<td>10</td>
</tr>
<tr>
<td>Deboned ham weight</td>
<td>50</td>
<td>27</td>
</tr>
<tr>
<td>Meat color</td>
<td>41</td>
<td>22</td>
</tr>
<tr>
<td>Number born</td>
<td>24</td>
<td>29</td>
</tr>
<tr>
<td>Survival</td>
<td>21</td>
<td>25</td>
</tr>
<tr>
<td>Birth weight</td>
<td>43</td>
<td>37</td>
</tr>
</tbody>
</table>

**Reliability %**
New breeding goal traits

Examples:

• Disease resistance requires infection
  – e.g. PRRS.

• Cured ham quality
  – e.g. Incarlopsa project

• Boar taint
  – e.g. Nador SNP-panel
What could bring this in relation with welfare and robustness traits?
Robustness and animal welfare

- General robustness
- Heat stress + day length
- Disease resistance & tolerance
- Social interactions & welfare
- Piglet survival
- Conformation
- Osteochondrosis
- Defects
What will the future bring?
Stem cell technology

Recipe:
- Kill semen producing cells of AI boar
- Replace with similar cells from high genetic value week old boar piglets
- Save 6 months (or so) of male generation interval

\[ \Delta G_{year} = \frac{\sigma_H \cdot r_{IH} \cdot i}{L} \]
**In vitro** challenge using blood sample

Susceptibility to PMWS (Circo virus)

- **Group 1:** Higher susceptibility
- **Group 2:** Lower susceptibility

\[ \Delta G_{year} = \frac{\sigma_H \cdot r_{IH} \cdot i}{L} \]

Source: Metadis (2011)
Organoids

Source: Sato and Clevers. Science 340, 1190 (2013);
Gene editing?

- Ultimate goal: find animal with desired genotype for all SNPs
  - Chance of desired genotype:
    - 25% (in case of 50% allele frequency)
    - Reduces rapidly with increasing # SNPs
  - Today:
    - Sum of SNP-effects
    - Normal distribution
    - Part of selection index

- Gene editing: future solution?
• Existing variation!
• Healing!
• Still: ethical discussion (and high price...)

• Increases genetic standard deviation

Examples of use?
- F4 (Ecoli receptor)
- PRRS QTL

\[ \Delta G_{year} = \frac{\sigma_H \cdot r_{IH} \cdot i}{L} \]
Wrapping up:

- Pick up client data (Big Data)
- Precision phenotyping
- Genomics

- Keep it? (optimum cont.)
- Gene editing?

\[ \Delta G_{\text{year}} = \frac{\sigma_H \cdot r_{IH} \cdot i}{L} \]

Reduce generation interval

More selection candidates to choose from (Blueprint)
Questions?