Positive and Negative Impacts of Genomic Selection

Ignacy Misztal and Daniela Lourenco

University of Georgia
Changes after genomics - dairy

- > 2x after genomics for Holsteins

Guinan et al. (2023)
Negative effects of genomic selection

• Informal industry reports:
  – Deteriorating sow survival in pigs
  – Deteriorating feet & legs in beef
  – Short teats and increased calf mortality in dairy
  – Increased sensitivity to heat stress in dairy
  – Deteriorating disease resistance across species

• Recessive genes or pleiotropy?
Genetic selection as optimization

- Selection for one trait or an index
- Gains on selected traits
- Losses on correlated antagonistic traits
- Losses compensated by improved environment/management
History of selection strategies

- Domestication
- Unformal
- Large-scale single-trait for production traits
- Multi-trait with fitness traits
- Genomic
Genetics of adaptation and domestication in livestock

Sandrine Mignon-Grasteau, Alain Boissy, Jacques Bouix, Jean-Michel Faure, Andrew D. Fisher, Geoffrey N. Hinch, Per Jensen, Pierre Le Neindre, Pierre Mormède, Patrick Prunet, Marc Vandeputte, Catherine Beaumont

Domestication

Winners

Growth
Milk
Mating procedures

Losers

Food finding
Seasonal reproduction
Predator avoidance
Brain size
Example of effects of mostly single-trait selection

Zuidhof et al. (2014) http://dx.doi.org/10.3382/ps.2014-04291
Side effects of intensive selection for growth in broiler chicken

• Unlimited appetite / obesity ➔ artificial lightning
• Poor survival of males ➔ male supplementation
• Increased susceptibility to diseases ➔ antibiotics
• Low hatchability ➔ alternate heating/cooling of incubators
• ...

All companies – similar problems at same time

Eitan and Soller, 2014
Undesirable side effects of selection for high production efficiency in farm animals: a review

W.M. Rauw\textsuperscript{a,*}, E. Kanis\textsuperscript{b}, E.N. Noordhuizen-Stassen\textsuperscript{c}, F.J. Grommers\textsuperscript{c}

\textsuperscript{a}Department of Animal Science, Agricultural University of Norway, P.O. Box 5025, 1432 Ás, Norway
\textsuperscript{b}Animal Breeding and Genetics Group, Wageningen Institute of Animal Science, Wageningen Agricultural University, P.O. Box 338, 6700 AH Wageningen, The Netherlands
\textsuperscript{c}Department of Herd Health and Reproduction and Interdepartmental Section Veterinary Medicine and Society, University of Utrecht, P.O. Box 80151, 3508 TD Utrecht, The Netherlands

Received 4 July 1997; accepted 29 April 1998

\ldots over 100 references on undesirable(cor)related effects of selection for high production efficiency, \ldots with respect to metabolic, reproduction and health traits, in broilers, pigs and dairy cattle\ldots.

Future application \ldots DNA-techniques \ldots may increase production levels even faster \ldots more dramatic consequences for behavioral, physiological and immunological traits.

Selection for more than production traits alone may prevent such.
Multitrait selection

- Decline in some traits too hard to be compensated by management
- New trait recording
- Progress in computing – multitrait animal models
- Selection index
Changes in US dairy index

Miglior et al., 2017
Do we need to select for heat tolerance – or use better management?

• Genetic selection for heat stress with data from weather stations (Ravagnolo et al., 2001)
  – Negative correlations \(\sim -0.4\) ➔ continuous deterioration

• National evaluation for heat stress in Holsteins (Aguilar et al., 2011)
  – 90 million test days
  – 9 million animals
  – 3-trait RRM
Genetic trends of daily milk yield for 3 parities – regular effect

First

Second

Third
Genetic trends for heat stress effect at $5.5^\circ C$ over the threshold

Negative selection for heat stress partially compensated by correlated selection for fertility and survival

High accuracy EBV for old bulls only
Industry approach to heat stress in 2010s

- Poor milk and fertility ➔ better sprinklers and fans
- Still poor fertility and poor heat detection ➔ timed AI
- Low survival and not enough replacements ➔ sexed semen
Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps

T. H. E. Meuwissen, * B. J. Hayes† and M. E. Goddard†,‡

Strategy for applying genome-wide selection in dairy cattle

L.R. Schaeffer
Effects of genomic selection

• High accuracy for well recorded traits
• Low accuracy for low $h^2$ traits with little information
• GEBV for young genotyped animals – lowered generation interval
• Acceleration of trends for selected traits
• Acceleration of correlated responses
• Changes in genetic parameters
Hypothetical trend with genomics – fitness not in index

- Production (high $h^2$)
- Raw fitness (low $h^2$)
- Management
- Realized fitness

Genomic selection
Hypothetical trend changes in 3 stages of genetic selection

Production (high $h^2$)
Raw fitness (low $h^2$)
Management
Realized fitness

Single trait selection  Multiple trait selection  Genomic selection

Fitness unselected
Fitness selected Small data
Fitness selected Large data
Phenotypic trends for milk and daughter pregnancy rate in Holsteins

Brito et al., 2021
Trends for daughter pregnancy rate

Environmental - management

Phenotypic

Genetic

Brito et al., 2021
Changes in (co)variances in pigs due to genomic selection

Heritability for growth

Genetic correlation with reproduction

Hidalgo et al. (2019)

Heritability decreases, antagonistic correlations intensify
Selection and resource allocation theory

- Van der Waaij, 2004; Rauw, 2012; Knapp, 2014

- More energy for production $\rightarrow$ fitness more antagonistic
  - Genetic correlations $\rightarrow$ -1
  - $h^2$ of selection index decline

- Fast selection $\rightarrow$ unbalanced animals (Huber, 2015)
Problems and species

• Genomic selection efficient with large data

• Fraction of performance to fertility data in species
  • ~ 1 in cattle
  • 1/15 in pigs
  • 1/200 in layers

• More problems expected in pigs and chickens than in dairy

• Problems with early mortality/morbidity when affected animals not genotyped
Genomic gain for production and fitness traits – example in pigs

• 1000 sows per generation
• 15 piglets per sow
• 4 generations

• Gain per generation:
  • 0.65 phenotypic SD for growth
  • 0.02 phenotypic SD for number of born dead

• Genomic favors bigger populations with better recording
How to mitigate negative effects of genomic selection?

• Identify declining traits, record, evaluate and include in selection index
  – Need updated index with current genetic parameters
  – Need methods for parameter estimation with large-scale genomics
  – Lag from action to market

• If recording difficult, use general fitness traits: survival, productive life...
Possible changes in heritability

\[ h^2 \]

**good**

**bad**

**time**
Possible changes in genetic correlations

\( h^2 \)

- acceptable
- bad

(time)
How to estimate $h^2$ and $r_g$ by generations

- REML or Bayesian
  - High computing cost
  - Base population parameters
- Need method that will work with national population and by recent time slices

$$acc_i = \frac{\text{corr}(y_i - Xb_i, \hat{u}_i)}{h}$$  

$$\text{corr}(y_i - Xb_i, \hat{u}_j) = ? \quad acc_j \quad corr_{ij} \quad h_i$$

$$corr_{ij} = \frac{\text{corr}(y_i - Xb_i, \hat{u}_j)}{h_i \ acc_j} \pm \frac{1}{h_i \ acc_j \ \sqrt{N_{\text{val}}}}$$

Legarra et al. (2008)
Estimation of heritabilities

\[ \hat{h}^2 = \frac{c^2 + \sqrt{c^4 + 4c^2M_e/N}}{2}, \quad c = \text{corr}(y - Xb, \hat{u}) \]

- \( N \) – # animals in reference population
- \( N_{\text{val}} \) – number of animals in validation
- \( M_e \) – number of independent chromosome segments (about 15k in Holsteins)

**US Holsteins -- milk -- 1 million genotyped**

<table>
<thead>
<tr>
<th></th>
<th>Initial ( h^2 )</th>
<th>Estimated ( h^2 )</th>
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<tbody>
<tr>
<td>US Holsteins</td>
<td>0.35</td>
<td>0.33</td>
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**Broiler chicken -- growth -- 150k genotyped**

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<tbody>
<tr>
<td>Broiler chicken</td>
<td>0.30</td>
<td>0.14</td>
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Found correct by company
Conclusions

• Selection as optimization – winner and loser traits

• Decline in low $h^2$ traits compensated by improved management

• Low $h^2$ traits can be improved with selection, to a limit

• With genomic selection
  – Variances change
  – Faster progress for high $h^2$ traits
  – Faster decline for antagonistic unselected traits
  – Management improvements cannot catch up

• Higher risks for pigs and chickens, lower for dairy