Genetic analysis of pig survival in a crossbred population

M. Dufrasne¹,² – I. Misztal³ – S. Tsuruta³ – K.A. Gray⁴ - N. Gengler¹

¹ Animal Science Unit, Gembloux Agro-Bio Tech, University of Liège (GxABT-ULg) – Gembloux, Belgium
² Fonds pour la Formation à la Recherche dans l’Industrie et dans l’Agriculture (FRIA) – Brussels, Belgium
³ Department of Animal and Dairy Science, University of Georgia – Athens, GA
⁴ Smithfield Premium Genetics Group – Rose Hill, NC
Context

- Mortality and docking
  - Economic loss
  - Animal health and welfare implications
- Main causes
  - Low body condition
  - Health issues
  - Hernia
Context

- Genetic studies mainly focused on
  - Farrowing mortality
  - Preweaning mortality
- Mortality during grow-finisher phase
  - High financial implications
    - Increasing rearing costs with age
    - Older and more valuable pigs
- Pigs reaching full market weight
Environmental effects exist but change over time

Genetic effects permanent and cumulative
  → Genetic variations need to exist

Genetic improvement of crossbreds depends on selection of purebred
  → Identification of genetic predictors of commercial performance at the nucleus level

Paternal additive genetic effect
  → Sire selection and breeding scheme optimization?
Objective

To estimate genetic parameters for survival traits at different steps of the fattening period and their relationships with market weight.
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To estimate genetic parameters for survival traits at different steps of the fattening period and their relationships with market weight.

To investigate the presence of genetic variance for sire effect to improve early selection for survival in purebred terminal sire line.
Data

- Crossbred Commercial Pigs
  - Duroc x (Commercial Female)
- 99,384 records
- 1 commercial farm
- 2008 to 2010
- Traits:
  - Preweaning mortality (PWM)
  - Farrow dock (FAD)
  - Nursery dock (NUD)
  - Finisher dock (FID)
  - Hot carcass weight (HCW)
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Description of data

- Trait definition

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>0 d</td>
<td>Birth</td>
</tr>
<tr>
<td>17 d</td>
<td>Farrow site</td>
</tr>
<tr>
<td>30 d</td>
<td>Nursery site</td>
</tr>
<tr>
<td>130 d</td>
<td>Grow-finisher site</td>
</tr>
<tr>
<td>220 d</td>
<td>Slaughter</td>
</tr>
</tbody>
</table>

PWM | FAD | NUD | FID | Dock | Slaughter
### Description of data

<table>
<thead>
<tr>
<th>Trait</th>
<th>PWM</th>
<th>FAD</th>
<th>NUD</th>
<th>FID</th>
<th>HCW</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of records</td>
<td>99,384</td>
<td>58,989</td>
<td>58,856</td>
<td>58,691</td>
<td>51,933</td>
</tr>
<tr>
<td>No. of litters</td>
<td>11,144</td>
<td>8,225</td>
<td>8,225</td>
<td>8,224</td>
<td>8,186</td>
</tr>
<tr>
<td>No. of dams</td>
<td>4,388</td>
<td>3,556</td>
<td>3,556</td>
<td>3,556</td>
<td>3,549</td>
</tr>
<tr>
<td>No. of sires</td>
<td>302</td>
<td>229</td>
<td>229</td>
<td>229</td>
<td>229</td>
</tr>
<tr>
<td>No. of contemporary groups</td>
<td>31</td>
<td>24</td>
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</tr>
</tbody>
</table>
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<th>Trait</th>
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<tbody>
<tr>
<td>PWM</td>
<td>99,384</td>
<td>24.47 %</td>
</tr>
<tr>
<td>FAD</td>
<td>58,989</td>
<td>0.23 %</td>
</tr>
<tr>
<td>NUD</td>
<td>58,856</td>
<td>0.28 %</td>
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<td>0.32 %</td>
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<th>SD</th>
</tr>
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<tbody>
<tr>
<td>HCW, kg</td>
<td>51,933</td>
<td>92.30</td>
<td>9.08</td>
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<td>FID</td>
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<td>0.32 %</td>
</tr>
<tr>
<td>Dock (FAD+NUD+FID)</td>
<td>58,989</td>
<td>0.82 %</td>
</tr>
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Model

- Multitrait threshold-linear sire model

\[ y = Xb + Z_s s + Wc + e \]

Observations:
- PWM, FAD, NUD, FID, or Dock (categorical, 2 categories)
- HCW, kg (linear)
Model

- Multitrait threshold-linear sire model

\[ y = Xb + Z_s s + Wc + e \]

Fixed effects:
- Sex
- Parity
- Age at slaughter (HCW only)
- CG (fixed for linear trait and random for categorical traits)
Model

- Multitrait threshold-linear sire model

\[ y = Xb + Z_s s + W_c + e \]

Random effects:
- Sire additive genetic effects \((s)\)
- Litter effects \((c)\)
- Residual effects \((e)\)
Method

- Variance components estimated using THRGIBBSF90 program
  - Bayesian approach via Gibbs sampling
  - Combination of categorical and continuous traits
  - Total of 250,000 samples with burn-in period of 50,000
  - Every 10\textsuperscript{th} samples to compute mean and SD of the posterior distribution
## Results

### 3-traits model

<table>
<thead>
<tr>
<th>Effect</th>
<th>PWM</th>
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<th>HCW</th>
</tr>
</thead>
<tbody>
<tr>
<td>h² additive</td>
<td>0.07 (0.003)</td>
<td>0.11 (0.127)</td>
<td>0.14 (0.055)</td>
</tr>
<tr>
<td>Sire genetic</td>
<td>0.02 (0.015)</td>
<td>0.03 (0.035)</td>
<td>0.03 (0.016)</td>
</tr>
<tr>
<td>Litter</td>
<td>0.28 (0.017)</td>
<td>0.22 (0.045)</td>
<td>0.14 (0.004)</td>
</tr>
</tbody>
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### 5-traits model

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<tr>
<td>h² additive</td>
<td>0.02 (0.004)</td>
<td>0.07 (0.035)</td>
<td>0.12 (0.058)</td>
<td>0.10 (0.121)</td>
<td>0.15 (0.017)</td>
</tr>
<tr>
<td>Sire genetic</td>
<td>0.01 (0.001)</td>
<td>0.02 (0.009)</td>
<td>0.03 (0.010)</td>
<td>0.02 (0.011)</td>
<td>0.04 (0.005)</td>
</tr>
<tr>
<td>Litter</td>
<td>0.16 (0.005)</td>
<td>0.17 (0.044)</td>
<td>0.16 (0.047)</td>
<td>0.12 (0.033)</td>
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Results

<table>
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<tr>
<th>Correlations</th>
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<tbody>
<tr>
<td>PWM</td>
<td>-0.83 (0.44)</td>
<td>0.07 (0.50)</td>
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- Selection to improve survival before weaning may not improve survival at later ages
- Different genes seem to influence survival and growth traits
## Results

### Correlations

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Favorable genetic correlations exist between the growing periods.
## Results

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Lowest genetic correlations were between PWM and the other periods

⇒ Different genes control mortality in early and late growing stages
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Lowest genetic correlations were between PWM and the other periods:

- Different genes control mortality in early and late growing stages
- Improvement of survival before weaning may not improve NUD
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Survival and growth traits are controlled by different genes.
Conclusions

- **Heritabilities** for survival traits were lower in early life and increased as pigs grew older.

- **Sire genetic influences were low**, especially on early recorded traits.
  - Direct selection of sire may improve survival until market weight.

- **Common litter effects** had a large influence, however, it slightly decreases with age.
Conclusions

- Different genes seem to control mortality in early life and late growing stages.
- Selection to improve survival before weaning may not improve survival between 30 and 130 days (nursery phase).
- Genetic correlations between HCW and the other traits indicate that survival and growth traits might be influenced by different genes.
- Docking decisions are difficult and should be taken very carefully.
Acknowledgements

- Animal and Dairy Science (ADS) Department, University of Georgia (UGA), for advising
- Smithfield Premium Genetics Group, for providing data, advising and support
- National Fund for Scientific Research (FRS-FNRS), for F.R.I.A. scholarship
- Animal Breeding and Genetics Group of Animal Science Unit, Gembloux Agro-Bio Tech, University of Liège (ULg-GxABT)

Author’s contact: marie.dufrasne@ulg.ac.be