

Genetic analysis of pig survival in a crossbred population

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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**



Context

- **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:**
 - **Prewaning mortality (PWM)**
 - **Farrow dock (FAD)**
 - **Nursery dock (NUD)**
 - **Finisher dock (FID)**
 - **Hot carcass weight (HCW)**



Data

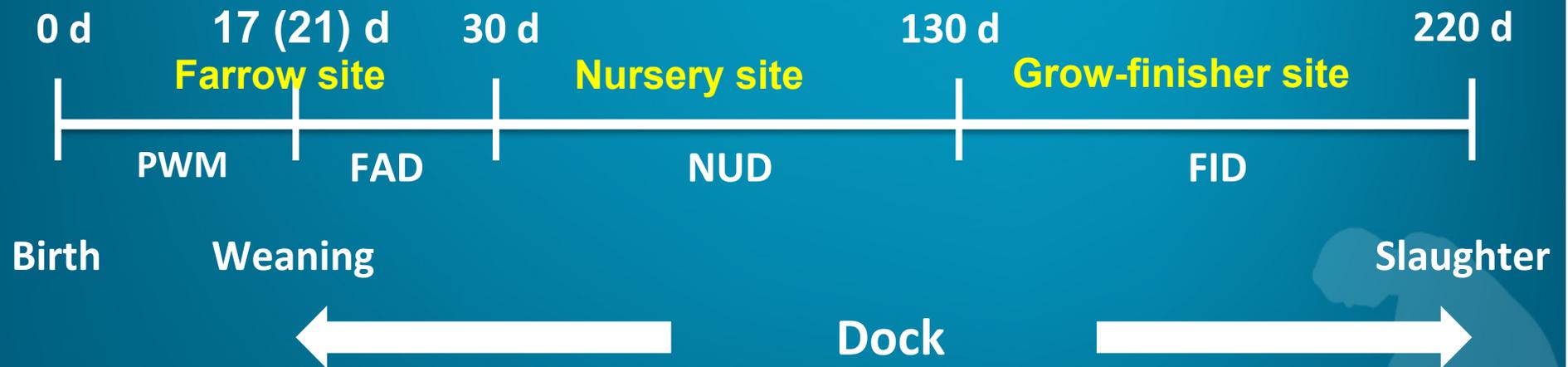
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} Dock



Description of data

- Trait definition



Description of data

Trait	PWM	FAD	NUD	FID	HCW
No. of records	99,384	58,989	58,856	58,691	51,933
No. of litters	11,144	8,225	8,225	8,224	8,186
No. of dams	4,388	3,556	3,556	3,556	3,549
No. of sires	302	229	229	229	229
No. of contemporary groups	31	24	24	24	24

Description of data

Trait	No. of records	Frequency
PWM	99,384	24.47 %
FAD	58,989	0.23 %
NUD	58,856	0.28 %
FID	58,691	0.32 %

Trait	No. of records	Mean	SD
HCW, kg	51,933	92.30	9.08

Description of data

Trait	No. of records	Frequency
PWM	99,384	24.47 %
FAD	58,989	0.23 %
NUD	58,856	0.28 %
FID	58,691	0.32 %
Dock (FAD+NUD+FID)	58,989	0.82 %

Trait	No. of records	Mean	SD
HCW, kg	51,933	92.30	9.08

Model

- **Multitrait threshold-linear sire model**

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_s\mathbf{s} + \mathbf{W}\mathbf{c} + \mathbf{e}$$

Observations:

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

Model

- **Multitrait threshold-linear sire model**

$$y = X\mathbf{b} + Z_s\mathbf{s} + W\mathbf{c} + e$$

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**

$$y = Xb + Z_s s + Wc + e$$

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 10th samples to compute mean and SD of the posterior distribution



Results

3-traits model

Effect	PWM	Dock	HCW
h² additive	0.07 (0.003)	0.11 (0.127)	0.14 (0.055)
Sire genetic	0.02 (0.015)	0.03 (0.035)	0.03 (0.016)
Litter	0.28 (0.017)	0.22 (0.045)	0.14 (0.004)

5-traits model

Effect	PWM	FAD	NUD	FID	HCW
h² additive	0.02 (0.004)	0.07 (0.035)	0.12 (0.058)	0.10 (0.121)	0.15 (0.017)
Sire genetic	0.01 (0.001)	0.02 (0.009)	0.03 (0.010)	0.02 (0.011)	0.04 (0.005)
Litter	0.16 (0.005)	0.17 (0.044)	0.16 (0.047)	0.12 (0.033)	0.14 (0.004)

Results

Correlations	Dock	HCW
PWM	-0.83 (0.44)	0.07 (0.50)
Dock		-0.08 (0.57)

- Selection to improve survival before weaning may not improve survival at later ages
- Different genes seem to influence survival and growth traits

Results

Correlations	Dock	HCW
PWM	-0.83 (0.44)	0.07 (0.50)
Dock		-0.08 (0.57)

Correlations	FAD	NUD	FID	HCW
PWM	0.18 (0.31)	-0.62 (0.12)	0.13 (0.17)	0.03 (0.13)
FAD		0.33 (0.35)	0.37 (0.21)	-0.40 (0.18)
NUD			0.58 (0.13)	0.01 (0.17)
FID				-0.24 (0.14)

Favorable genetic correlations exist between the growing periods

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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

Results

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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
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- A faint, light blue silhouette of a person sitting on a log, possibly operating a sawmill, is visible in the bottom right corner of the slide.

Acknowledgements

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