# Estimation of genetic parameters for longitudinal measurements of feed intake in Piétrain sire lines

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## General context

- Importance of feed efficiency (FE) in livestock production
- Feed intake (FI) is a component of FE
- Selection to reduce FI with constant growth rate
- Electronic feeders ➔ Individual daily FI (DFI) records

## General context

- DFI = longitudinal measurements
- Random regression models (RRM) = option for longitudinal data analysis

  ➔estimation of individual and population curves
- Measurement of DFI is expensive

## Context of the study

- Progeny-test of Walloon Piétrain boars in test station
  - Crossbred progeny (Piétrain x Landrace K+)
  - Batches of approximately 100 pigs
  - From 20 kg to 110 kg
  - On average 4 pigs per pen
  - Body weight recorded every 15 days
  - Carcass quality traits recorded on live pigs and on carcasses

# Context of the study

- Development of a new genetic evaluation program in the Walloon Region of Belgium
- Genetic evaluation for production traits
- Estimation of genetic merit of purebred Piétrain boars in crossbreeding
  - Production pigs mostly crossbred
  - Genetic correlation between purebred and crossbred performances < 1

# Context of the study

- FI recording system
  - No facilities to record individual DFI
    - Until 2010: total FI in test station
    - Since 2011: FI recorded every 15 days
    - Total pen FI records
    - Individual mean FI
- FI different
  - Between pigs in same pen
  - During growth period

# Objective

To estimate genetic parameters for longitudinal measurements of feed intake (FI) in a crossbred population of pigs

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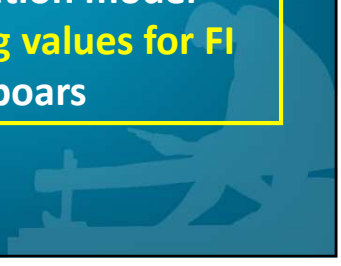
To develop a genetic evaluation model for the estimation of breeding values for FI of Walloon Piétrain boars



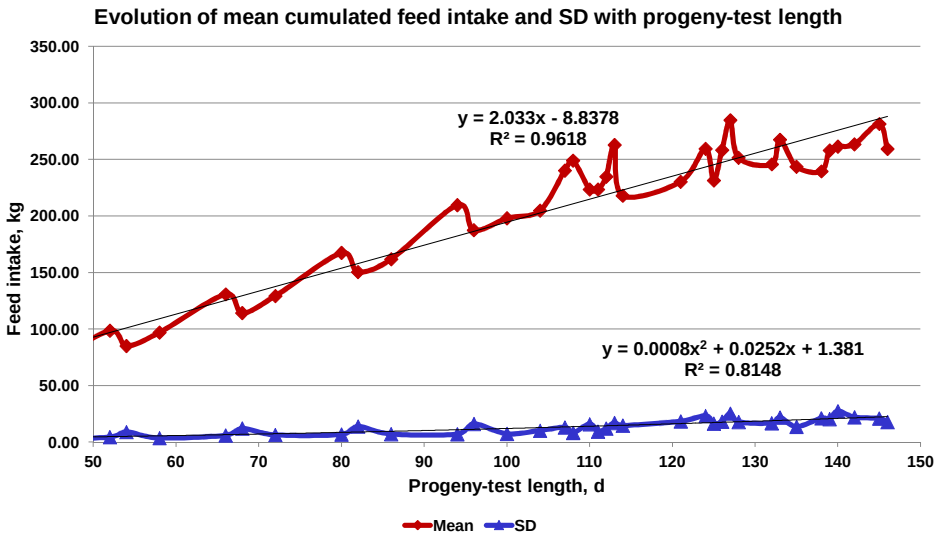
# Data

- Walloon Pig Breeding Association (Belgium)
- 4,095 records of cumulated FI
- 2,127 crossbred pigs Piétrain x Landrace K+
- Walloon test station
- 2007 to 2012

# Description of data

| | |
|---|---|
| No. of records | 4,095 |
| No. of animals in pedigree | 7,897 |
| No. of sires | 84 |
| No. of dams | 163 |
| No. of batches | 22 |
| No. of CG (batch x pen) | 585 |
| No. of pigs per pen | 2-5 |
| Freq. of males (%) | 47.55 |
| Freq. of females (%) | 52.45 |

# Description of data




# Method

- Variance heterogeneity
  - Homogeneity for each day
  - Heterogenity between days
- Pre-adjustment method
  - Standardization with estimated trait mean and SD per day
  - Pre-adjustment at the last day of test (150 d)

# Method

- Estimated mean and SD based on the smoothing curves (x = day of test)

  $m_i = 2.033x - 8.8378$ $(R^2 = 0.96)$

  $\sigma_i = 0.0008x^2 + 0.0252x + 1.381$ $(R^2 = 0.81)$

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- Standardized and pre-adjusted records $y_{ij}^*$

$$y_{ij}^* = \frac{y_{ij} - m_i}{\sigma_i}\sigma_{150} + m_{150}$$

# Model

- Random regression animal model

$$y = Xb + Za + Zp + Wl + e$$

y = vector of observations

- Standardized and adjusted cumulated FI

# Model

- Random regression animal model

$$y = Xb + Za + Zp + Wl + e$$

b = vector of fixed effects

- Sex
- Batch

# Model

- Random regression animal model

$$y = Xb + Za + Zp + Wl + e$$

- a, p = random regression effects
  - a = additive genetic
  - p = permanent environment

Regression curves modelled with quadratic Legendre polynomials

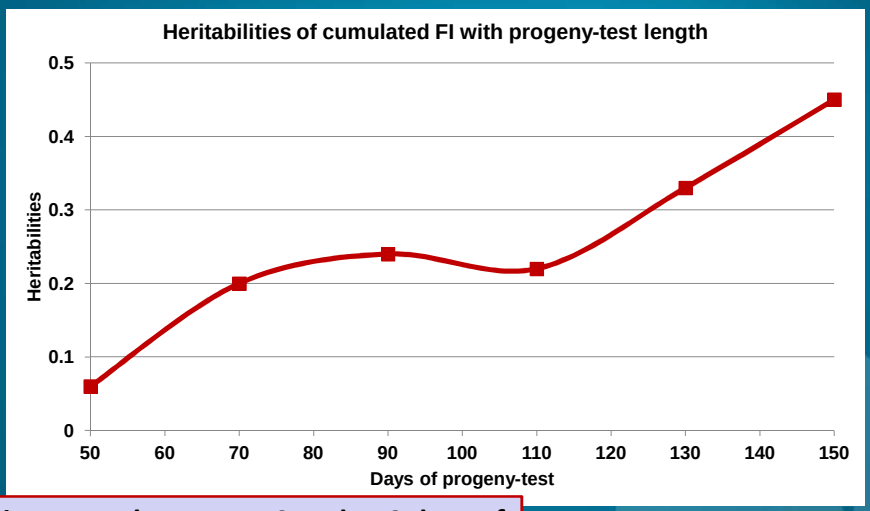
# Model

- Random regression animal model

$$y = Xb + Za + Zp + Wl + e$$

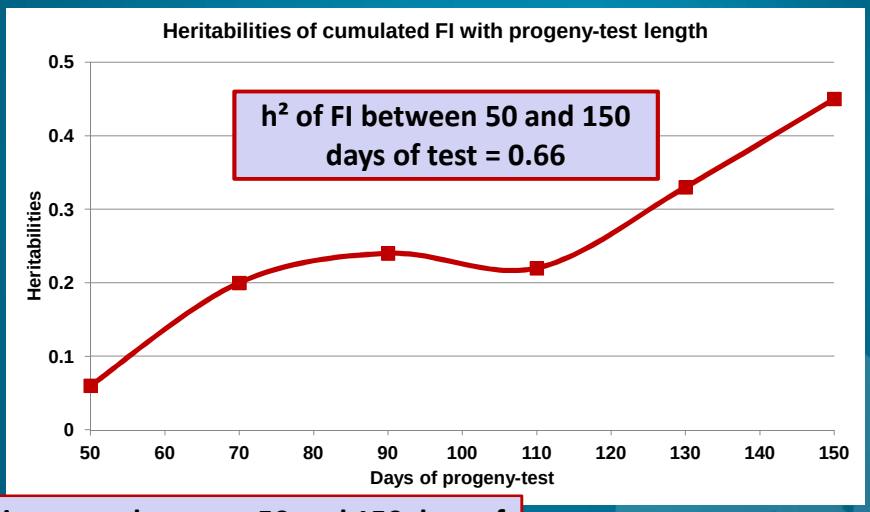
- a, p = random regression effects
  - a = additive genetic
  - p = permanent environment
- l = vector of random pen effect
- e = vector of random residual effect

# Results: heritabilities




$h^2$ increases between 50 and 150 days of progeny-test, from 0.06 to 0.45

# Results: heritabilities




$h^2$ increases between 50 and 150 days of progeny-test, from 0.06 to 0.45

# Results: correlations

| Days | 70 | 90 | 110 | 130 | 150 |
|---|---|---|---|---|---|
| 50 | 0.76 | 0.54 | 0.25 | -0.20 | -0.65 |
| 70 | | 0.96 | 0.82 | 0.49 | 0.01 |
| 90 | | | 0.95 | 0.72 | 0.28 |
| 110 | | | | 0.90 | 0.57 |
| 130 | | | | | 0.87 |

High correlations between adjacent ages

# Results: correlations

| Days | 70 | 90 | 110 | 130 | 150 |
|---|---|---|---|---|---|
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| 70 | | 0.96 | 0.82 | 0.49 | 0.01 |
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Genetic correlations decrease with increasing age intervals

# Results: correlations

| Days | 70 | 90 | 110 | 130 | 150 |
|---|---|---|---|---|---|
| 50 | 0.76 | 0.54 | 0.25 | -0.20 | -0.65 |
| 70 | | 0.96 | 0.82 | 0.49 | 0.01 |
| 90 | | | 0.95 | 0.72 | 0.28 |
| 110 | | | | 0.90 | 0.57 |
| 130 | | | | | 0.87 |

Negatives genetic correlations between the very beginning and the end of the testing period

# Conclusions

- FI is moderately heritable
- Heritability of FI tends to increase with age
- FI data at the end of the growth period seems to be more informative
- High FI at the beginning not related with high FI at the end
- FI seems to be influenced by different genes during the growth period

# Perspectives

- To estimate genetic parameters with more data
- To test different models
- To model FI with growth to individualize FI
- To estimate breeding values and their reliabilities

# Acknowledgments


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