

## 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
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## 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
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## 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  $< 1$
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## 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
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## Objective

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

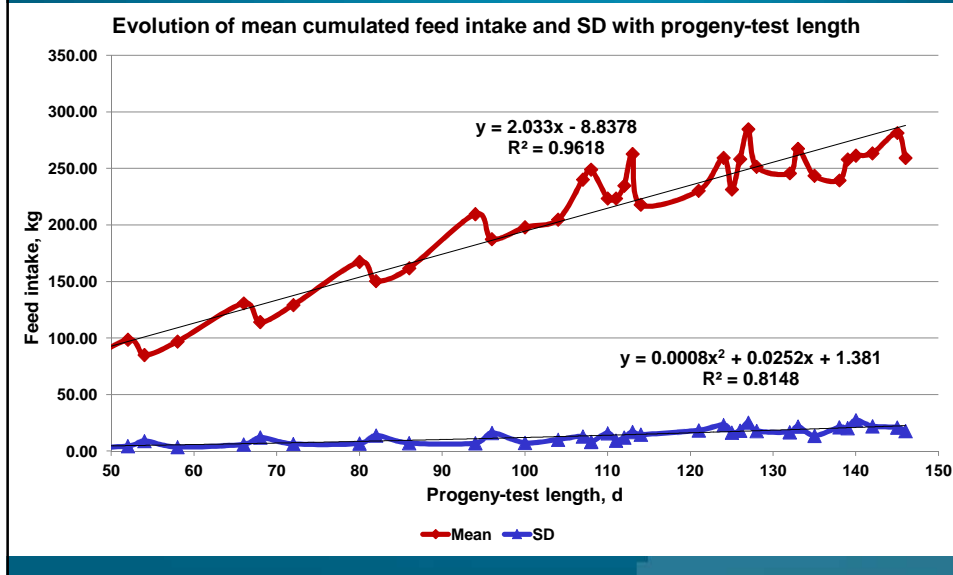
## Data

- 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
  - Heterogeneity 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** ( $x = \text{day of test}$ )

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

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

## Method

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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

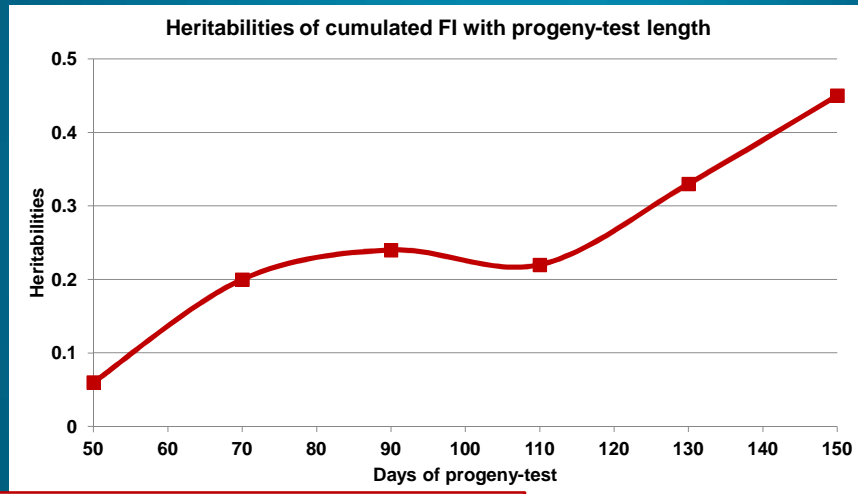
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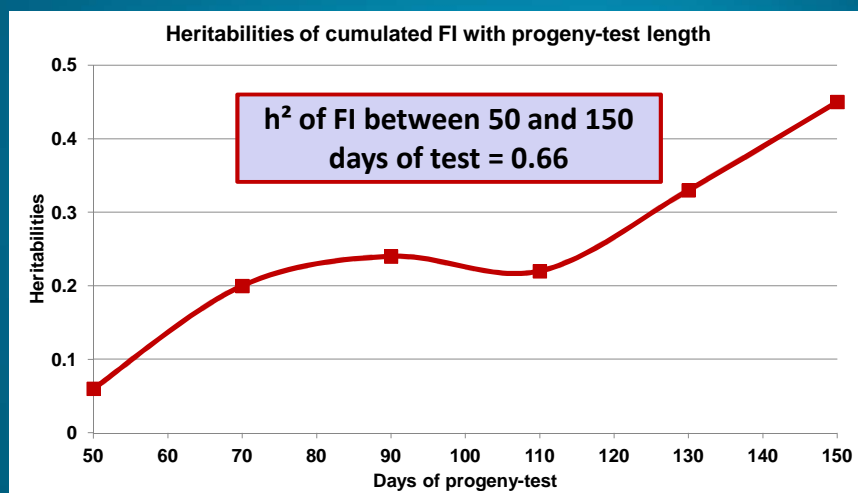
- **a, p** = random regression effects
  - a = additive genetic
  - p = permanent environment
- **l** = vector of random pen effect
- **e** = vector of random residual effect

## Results: heritabilities



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

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$h^2$  of FI between 50 and 150 days of test = 0.66

$h^2$  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

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Genetic correlations decrease with increasing age intervals

## Results: correlations

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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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