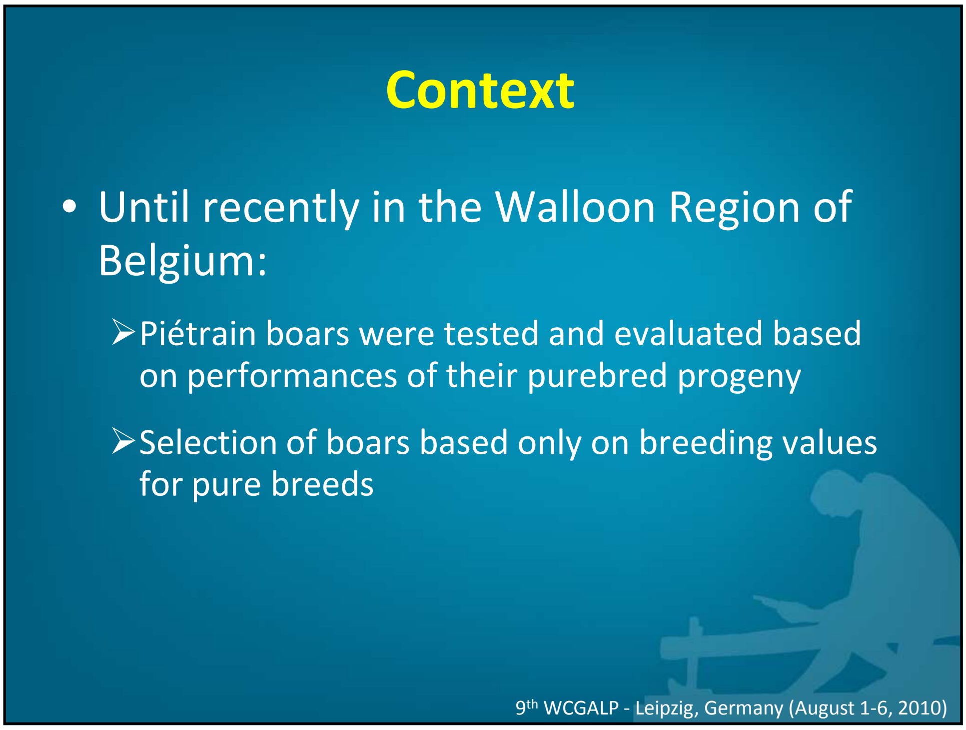
gembloux agro bio tech

Université de Liège ULg

Development of a new genetic evaluation model for carcass quality based on crossbred performances of Piétrain boars in the Walloon Region of Belgium

M. Dufrasne[1] – H. Hammami[1] – V. Jaspart[2] – J. Wavreille[3] & N. Gengler[1,4]

[1] Animal Science Unit, Gembloux Agro-Bio Tech, University of Liege (GxABT-ULg) – Gembloux, Belgium
[2] Walloon Pig Breeders Association (AWEP) – Ciney, Belgium
[3] Walloon Agricultural Research Centre (CRA-W) – Gembloux, Belgium
[4] National Fund for Scientific Research (FRS-FNRS) – Brussels, Belgium



Context

- Until recently in the Walloon Region of Belgium:
  - Piétrain boars were tested and evaluated based on performances of their purebred progeny
  - Selection of boars based only on breeding values for pure breeds

Context

- Production pigs are mostly crossbred
- Genetic correlation between purebred and crossbred performances is considered to be < 1
- Genetic merit of boars used in crossbreeding systems should be estimated from crossbred performances

Context

- Since 2007 in the Walloon Region of Belgium:
  - ➢Development of a new genetic evaluation program of Piétrain boars
  - ➢Crossbred progeny are tested in a test station for fattening and carcass traits (e.g., growth, feed intake, backfat thickness, meat percentage)
  - ➢Dams of progeny are from a hyperprolific Landrace sow line

Objective

- To develop the genetic evaluation system of Piétrain boars based on crossbred performances
  - In particular, development of a genetic evaluation model for carcass quality traits: backfat thickness and meat percentage
- To allow selection of boars that produce carcass with a high meat percentage

Material

- Data
  - From the on-farm performance recording system
  - Pigs on-farm
  - But also pigs fattened in test station
- Recording on live animals by ultrasound
- Traits analysed in this study:
  - Backfat thickness (BF)
  - Meat percentage (%meat)

Material

- Datafile:
  - ➢60 546 records from 56 822 different pigs for each trait (6 % of repeated records)
  - ➢Measured between 150 and 300 days of age
  - ➢Measured on pigs of at least 40 % Piétrain or Landrace to have animals with similar breed composition with animals from the test station

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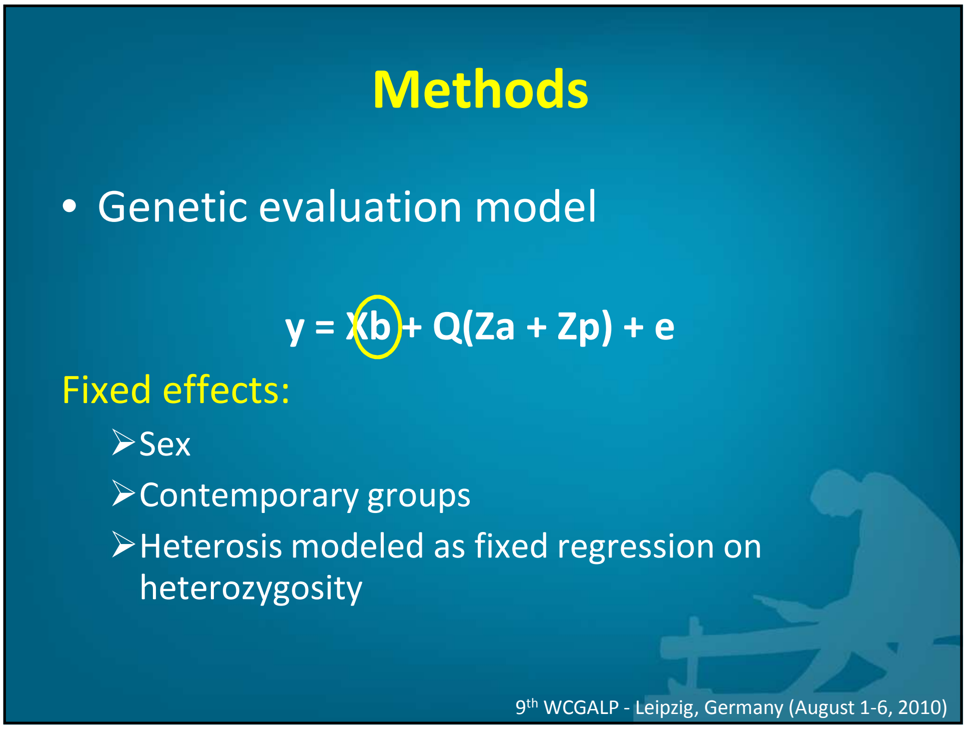
Methods

- Genetic evaluation model

$$\textcircled{y} = Xb + Q(Za + Zp) + e$$

Observations:

- ➢Backfat thickness
- ➢Meat percentage



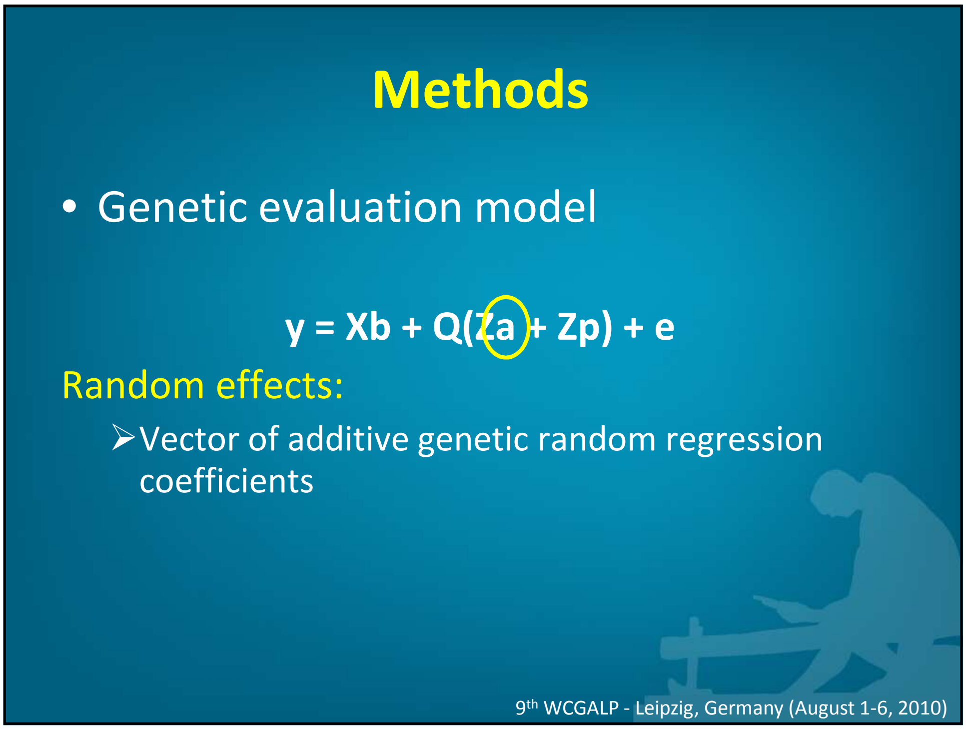
Methods

- Genetic evaluation model

$$y = Xb + Q(Za + Zp) + e$$

Fixed effects:

- Sex
- Contemporary groups
- Heterosis modeled as fixed regression on heterozygosity



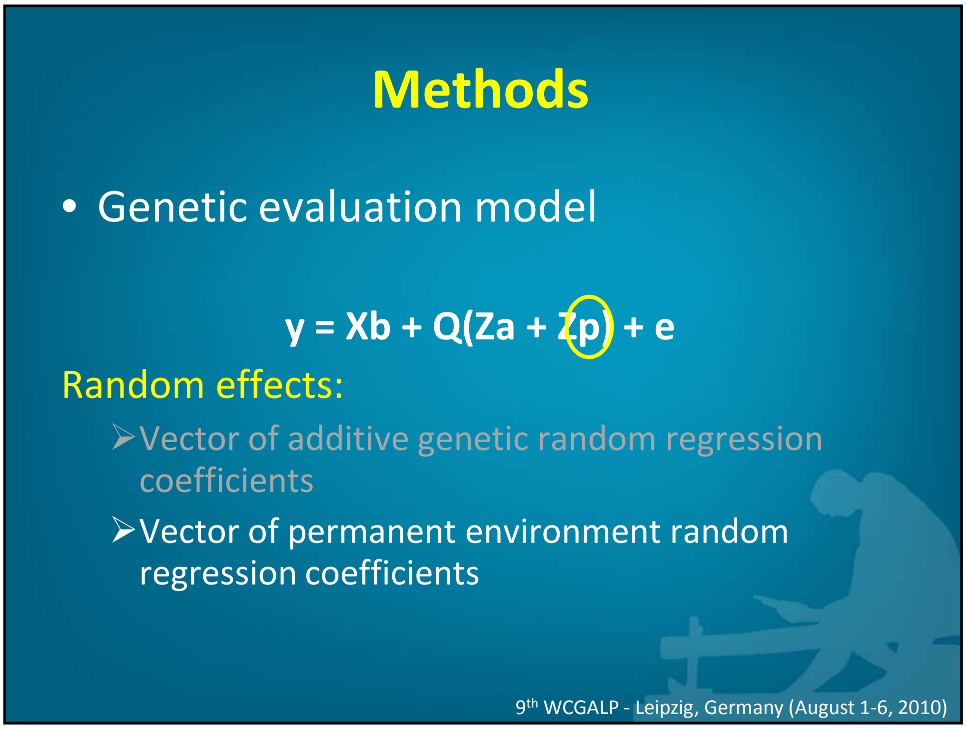
Methods

- Genetic evaluation model

$$y = Xb + Q(Za + Zp) + e$$

Random effects:

- Vector of additive genetic random regression coefficients



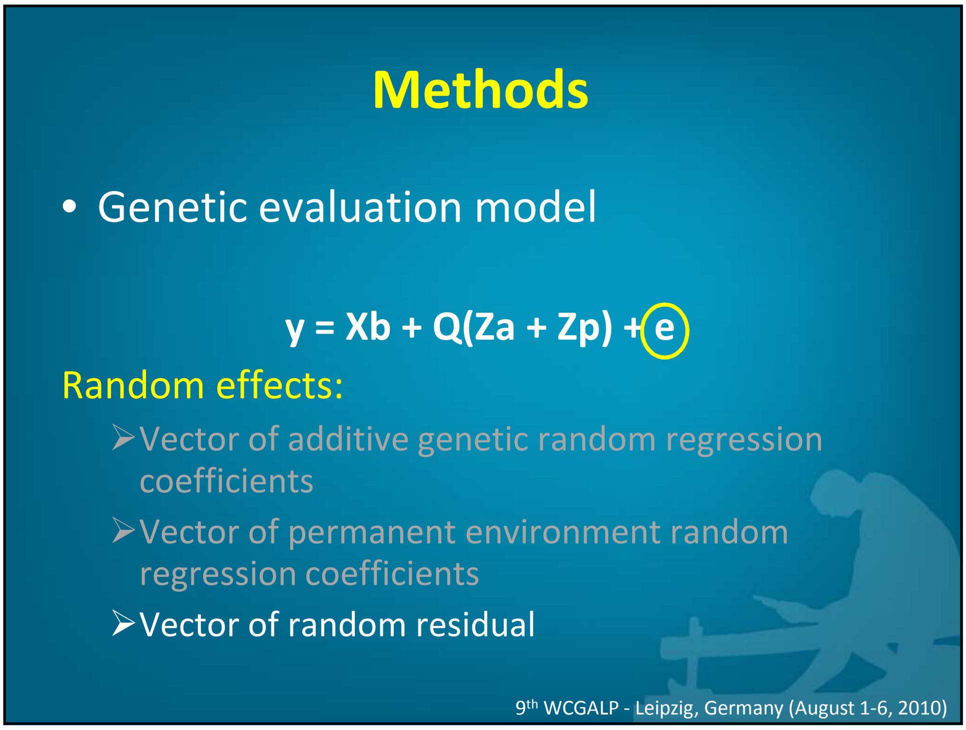
Methods

- Genetic evaluation model

$$y = Xb + Q(Za + Zp) + e$$

Random effects:

  - Vector of additive genetic random regression coefficients
  - Vector of permanent environment random regression coefficients



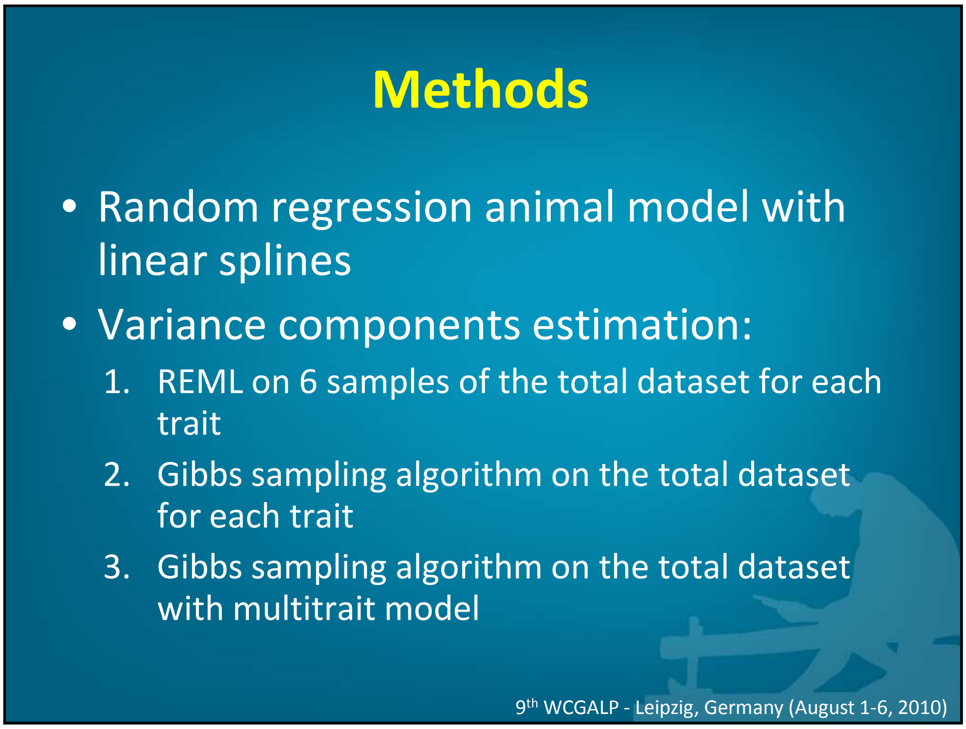
Methods

- Genetic evaluation model

$$y = Xb + Q(Za + Zp) + e$$

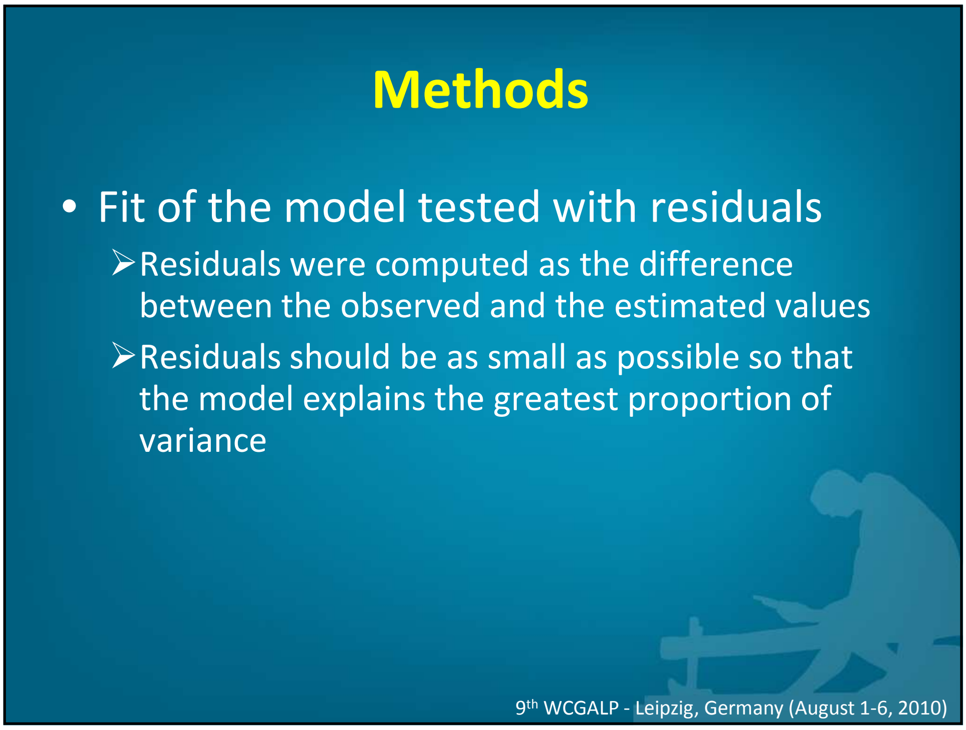
Random effects:

  - Vector of additive genetic random regression coefficients
  - Vector of permanent environment random regression coefficients
  - Vector of random residual



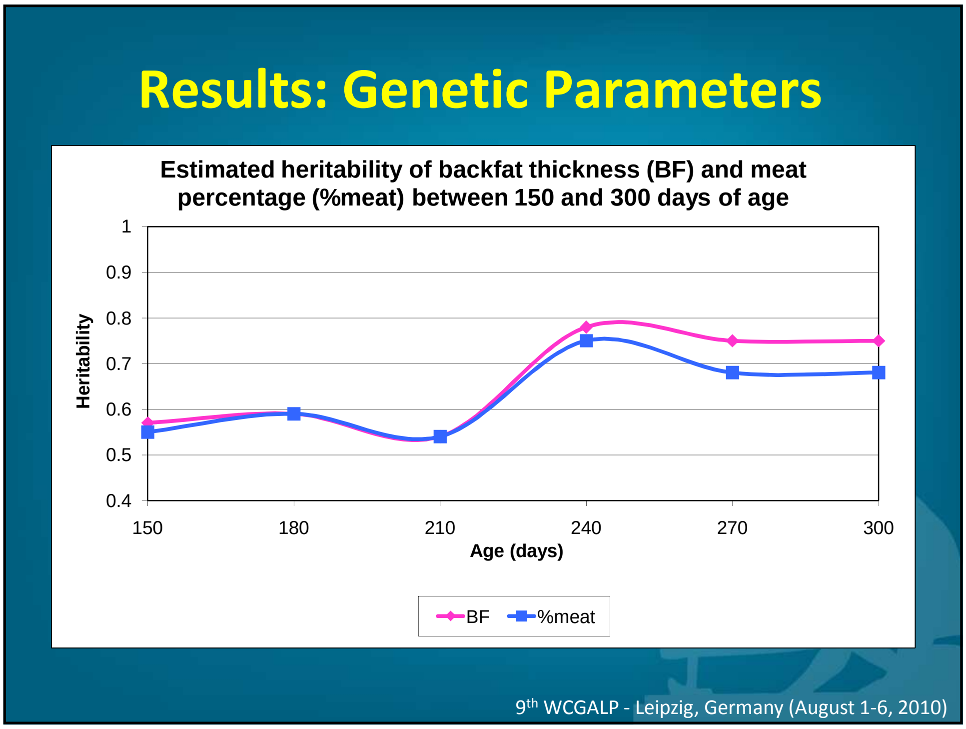
Methods

- Random regression animal model with linear splines
- Variance components estimation:
  1. REML on 6 samples of the total dataset for each trait
  2. Gibbs sampling algorithm on the total dataset for each trait
  3. Gibbs sampling algorithm on the total dataset with multitrait model



Methods

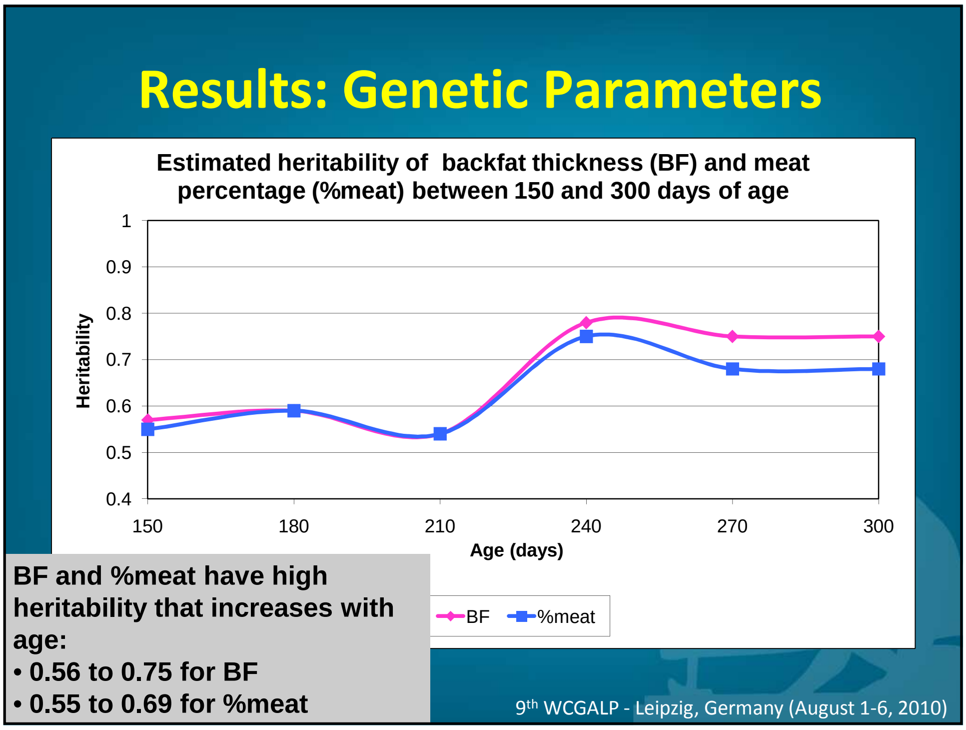
- Fit of the model tested with residuals
  - ➢Residuals were computed as the difference between the observed and the estimated values
  - ➢Residuals should be as small as possible so that the model explains the greatest proportion of variance



Results: Genetic Parameters

Estimated heritability of backfat thickness (BF) and meat percentage (%meat) between 150 and 300 days of age

9th WCGALP - Leipzig, Germany (August 1-6, 2010)



Results: Genetic Parameters

Estimated heritability of backfat thickness (BF) and meat percentage (%meat) between 150 and 300 days of age

BF and %meat have high heritability that increases with age:

- **0.56 to 0.75 for BF**
- **0.55 to 0.69 for %meat**

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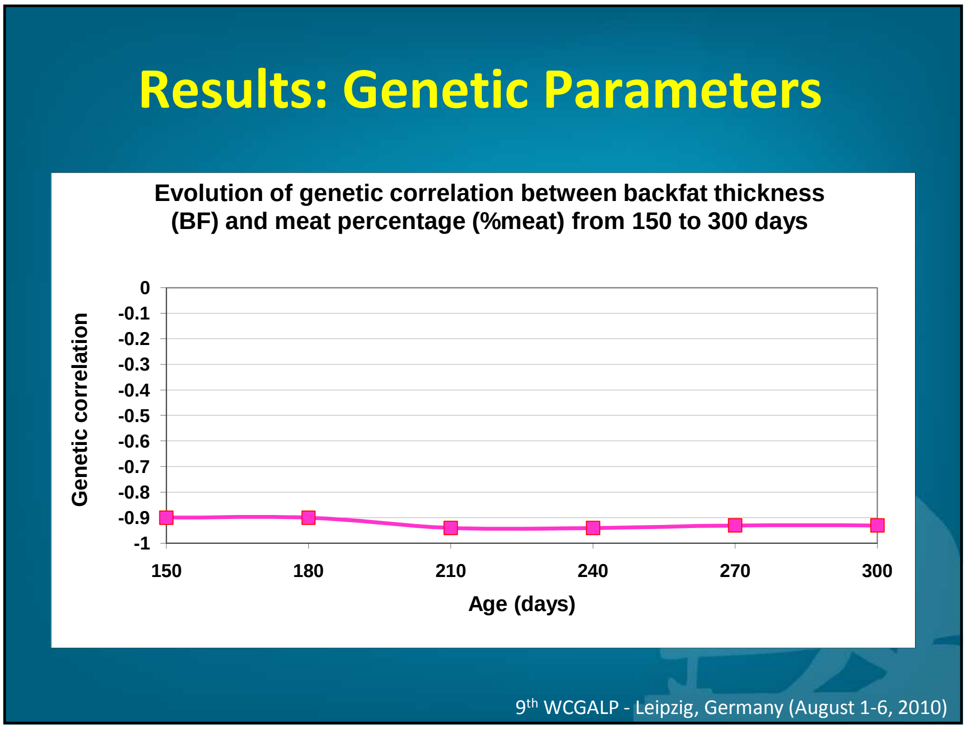

Results: Genetic Parameters

Evolution of genetic correlation between backfat thickness (BF) and meat percentage (%meat) from 150 to 300 days

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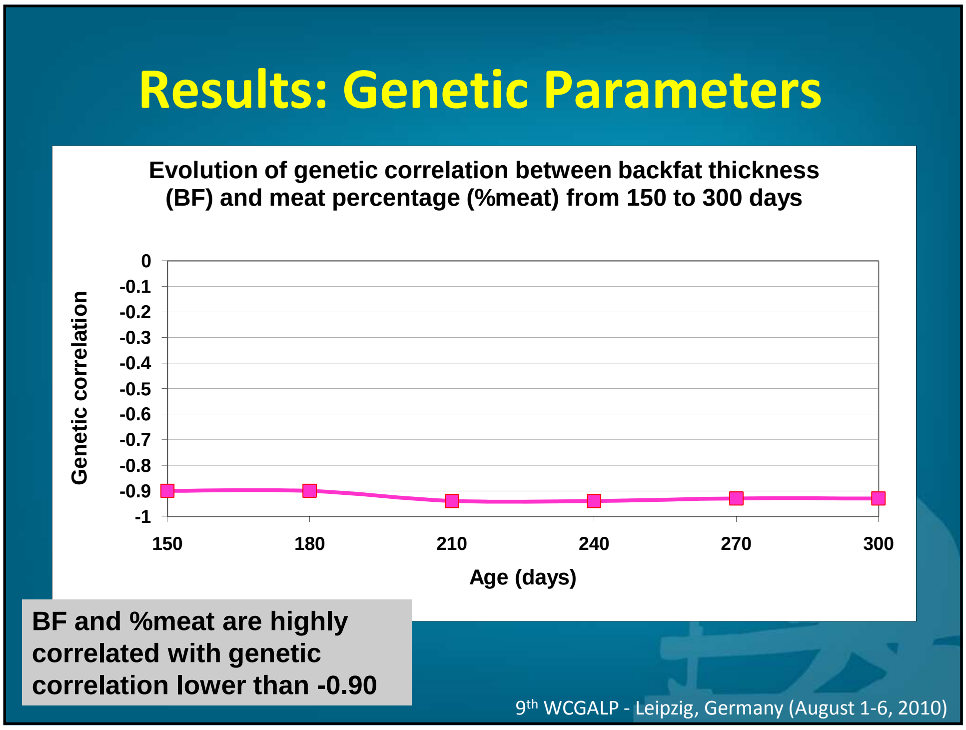

Results: Genetic Parameters

Evolution of genetic correlation between backfat thickness (BF) and meat percentage (%meat) from 150 to 300 days

BF and %meat are highly correlated with genetic correlation lower than -0.90

9th WCGALP - Leipzig, Germany (August 1-6, 2010)

Results: Genetic Parameters

- Observed variations in the evolution of genetic parameters
- Probably due to random regression model with linear splines to model variance components

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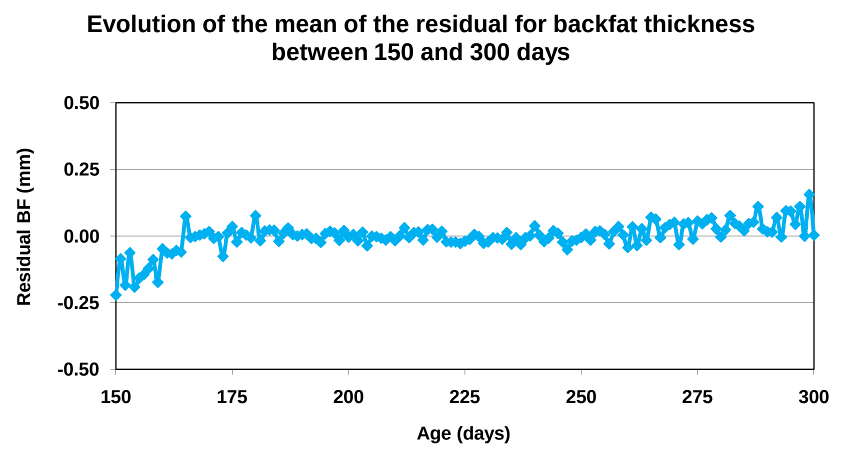
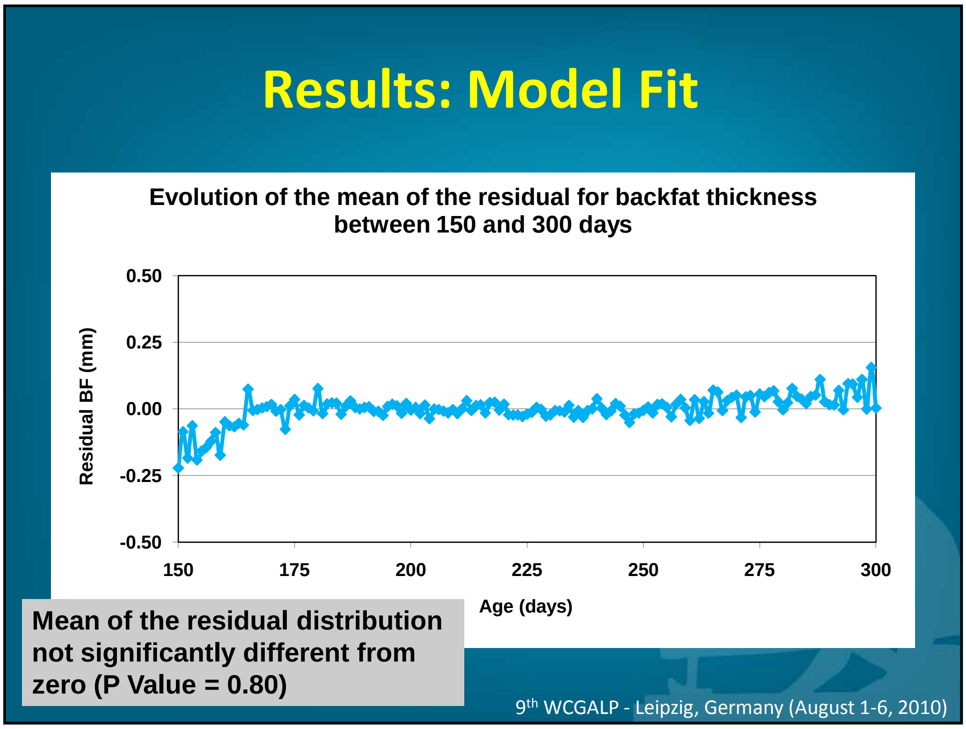
Results: Model Fit



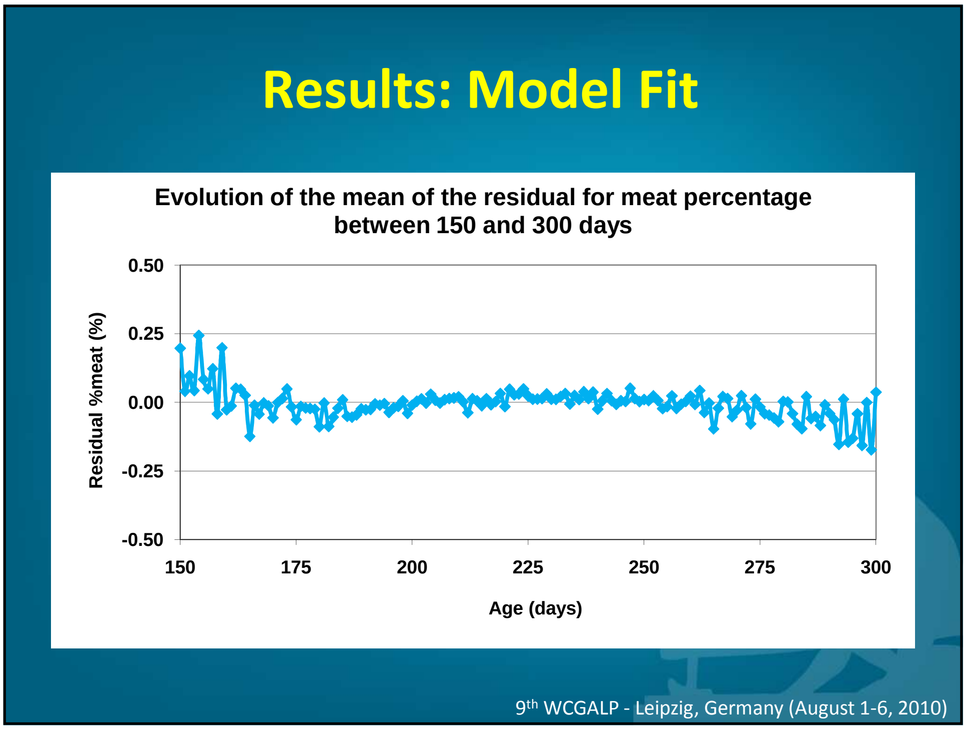


Results: Model Fit

Evolution of the mean of the residual for backfat thickness between 150 and 300 days

Mean of the residual distribution not significantly different from zero (P Value = 0.80)

9th WCGALP - Leipzig, Germany (August 1-6, 2010)

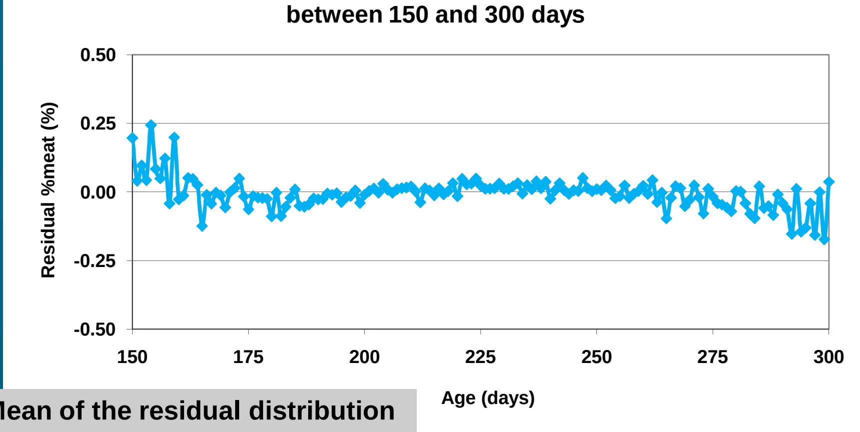


Results: Model Fit

Evolution of the mean of the residual for meat percentage between 150 and 300 days

9th WCGALP - Leipzig, Germany (August 1-6, 2010)

Results: Model Fit



Mean of the residual distribution not significantly different from zero (P Value = 0.15)

Results: Model Fit

- Observed lost of fit of the model at very low and very high ages:
  - ➢Less data available at these ages
  - ➢Extrapolation of splines outside their optimal range

Results: Heterosis Effect

- Solutions for heterosis effect:
  - 13 % lower backfat thickness
  - 1.6 % higher meat percentage

for crossbred animals than the mean of the population

Conclusions

- Backfat thickness and meat percentage have high heritability and are highly correlated
  - Genetic improvement of carcass quality is possible based on these traits
  - Selection could be based only on one of these traits
- According to the study of residuals model developed seems to fit well the data
- Crossbred animals have better performances compared to the whole population

Thank You For Your Attention!

- Collaboration:
  - Walloon Pig Breeders Association (AWEP)
  - Walloon Agricultural Research Centre (CRA-W)

AWEP

CRA-W Gembloux

- Study supported by:
  - Walloon Region of Belgium
  - National Fund for Scientific Research (FRS-FNRS)

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- Author's contact: marie.dufrasne@ulg.ac.be

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