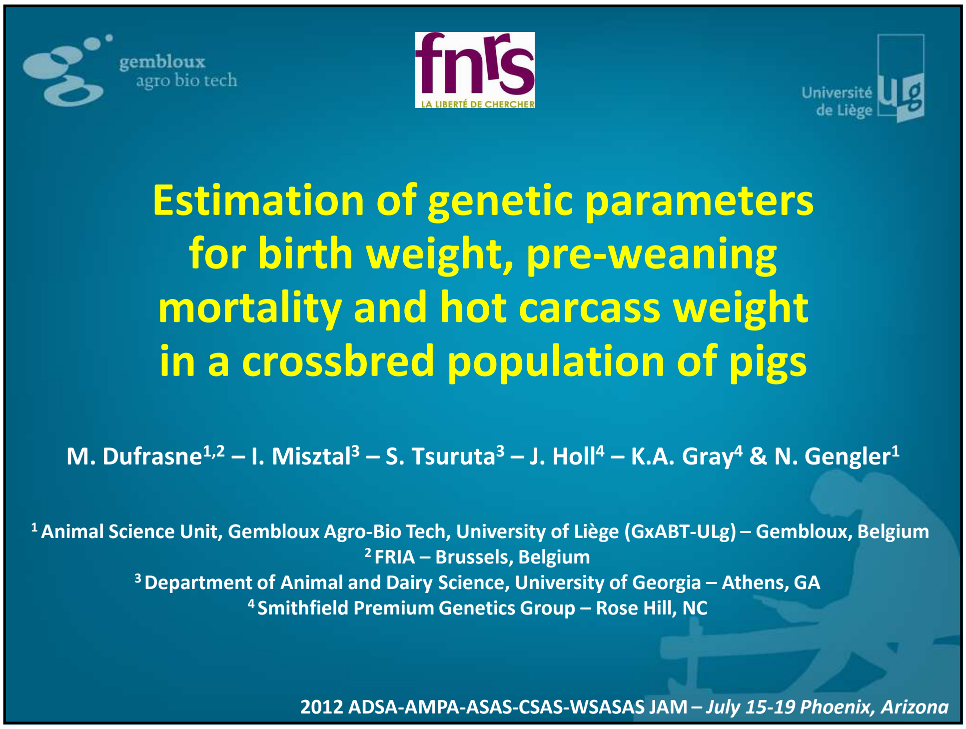

Estimation of genetic parameters for birth weight, pre-weaning mortality and hot carcass weight in a crossbred population of pigs

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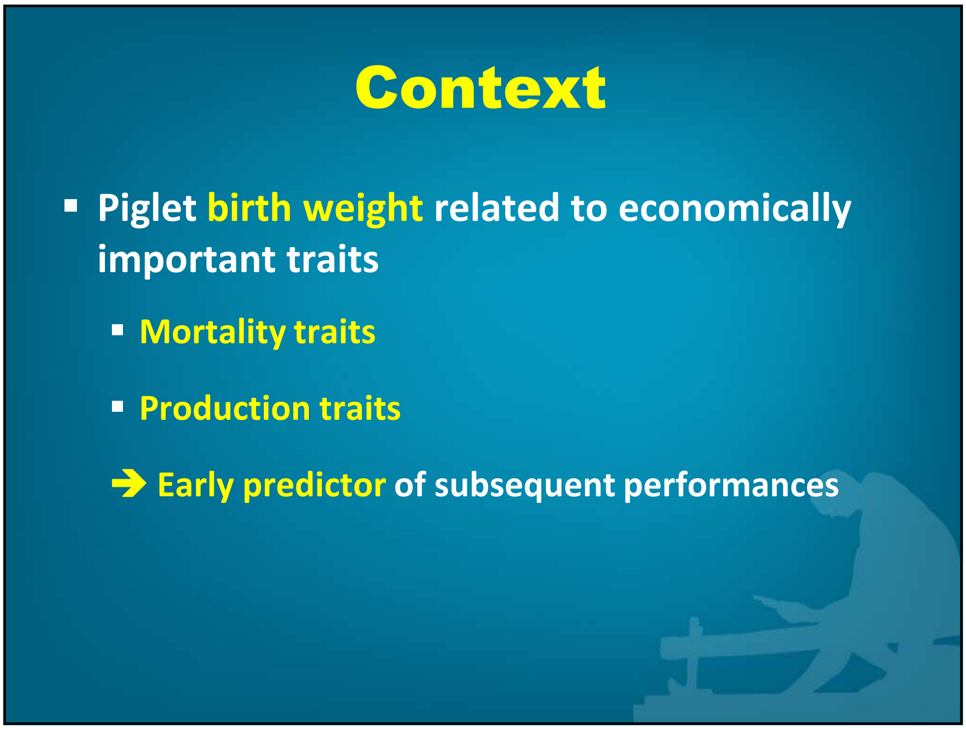


Context

- Piglet birth weight related to economically important traits
  - Mortality traits
  - Production traits
  - ➔ Early predictor of subsequent performances

Context

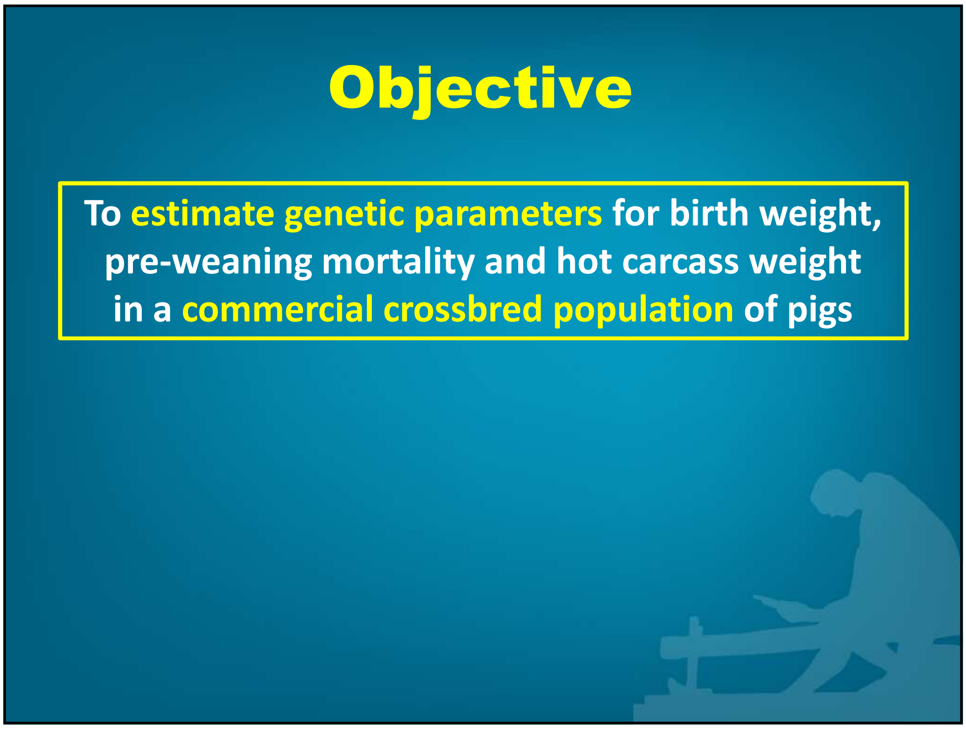
- Commercial swine production
  - Economic gain
  - Full market value pigs
    - Survival, market weight, carcass compostion
  - Low hot carcass weight → alternative market
- Low birth weight
  - Pre-weaning mortality
  - Reduced weight gain
  - Fatter carcass

Context

- Genetic improvement of crossbreds depends on selection of purebred

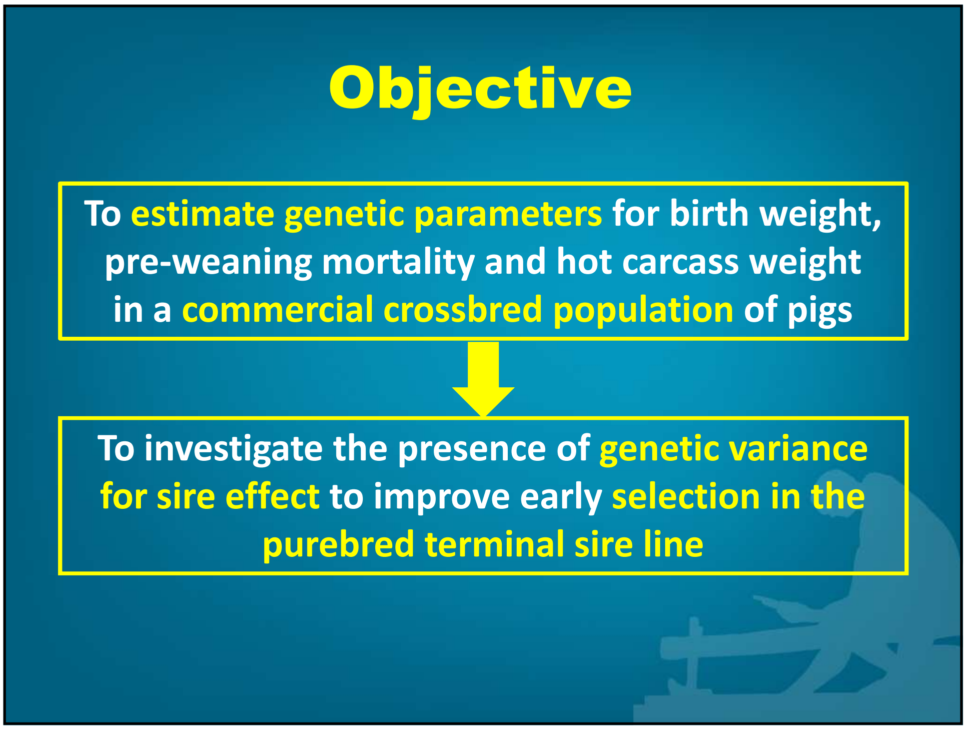
  → Identification of genetic predictors of commercial performances at the nucleus level
- Paternal additive genetic effect

  → Sire selection and breeding scheme optimization?



Objective

To **estimate genetic parameters** for birth weight, pre-weaning mortality and hot carcass weight in a **commercial crossbred population** of pigs



Objective

To **estimate genetic parameters** for birth weight, pre-weaning mortality and hot carcass weight in a **commercial crossbred population** of pigs

↓

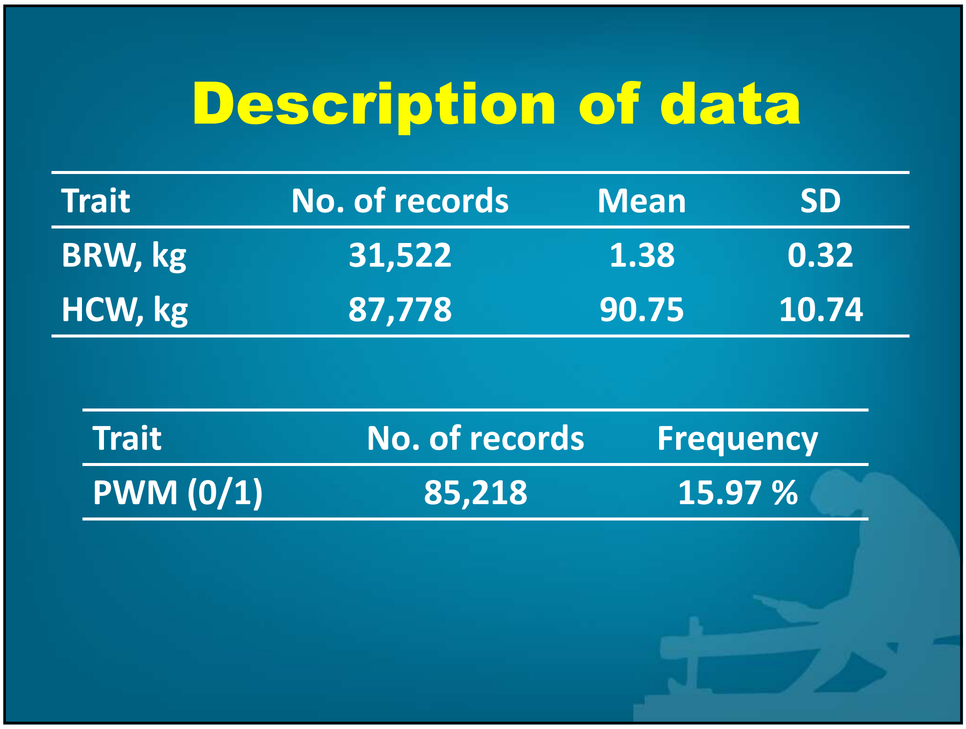
To investigate the presence of **genetic variance for sire effect** to improve early **selection in the purebred terminal sire line**

Data

- Smithfield Premium Genetics Group
- Crossbred Duroc x (Large White x Landrace)
- 134,498 records
- 4 commercial farms
- 2004 to 2011
- Traits:
  - Birth weight (BRW)
  - Pre-weaning mortality (PWM)
  - Hot carcass weight (HCW)

Description of data

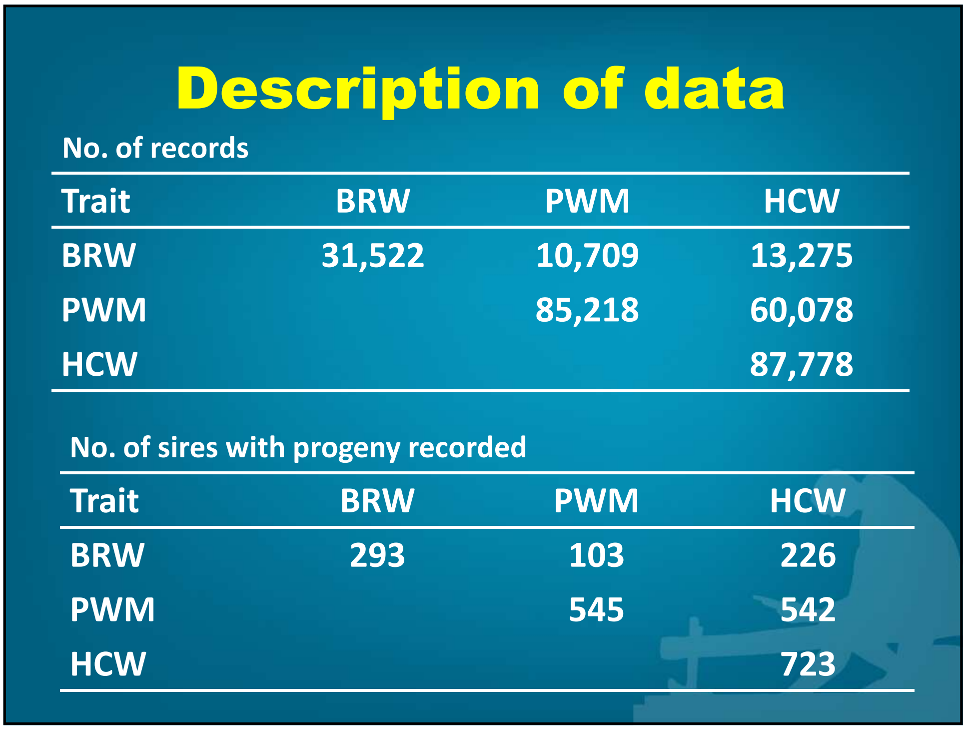
No. of records	134,498
No. of animals in pedigree	143,779
No. of litters	15,055
No. of dams	8,351
No. of sires	791
No. of contemporary groups	94
Average number of parities per dam	3.67



Description of data

Trait	No. of records	Mean	SD
BRW, kg	31,522	1.38	0.32
HCW, kg	87,778	90.75	10.74

Trait	No. of records	Frequency
PWM (0/1)	85,218	15.97 %



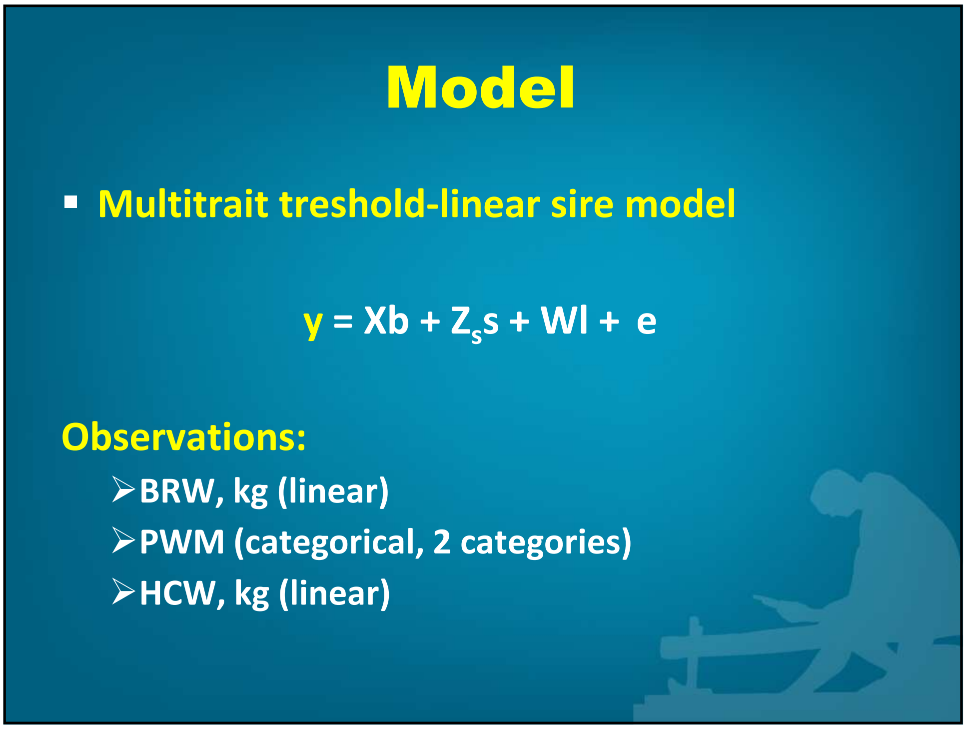
Description of data

No. of records

Trait	BRW	PWM	HCW
BRW	31,522	10,709	13,275
PWM		85,218	60,078
HCW			87,778

No. of sires with progeny recorded

Trait	BRW	PWM	HCW
BRW	293	103	226
PWM		545	542
HCW			723



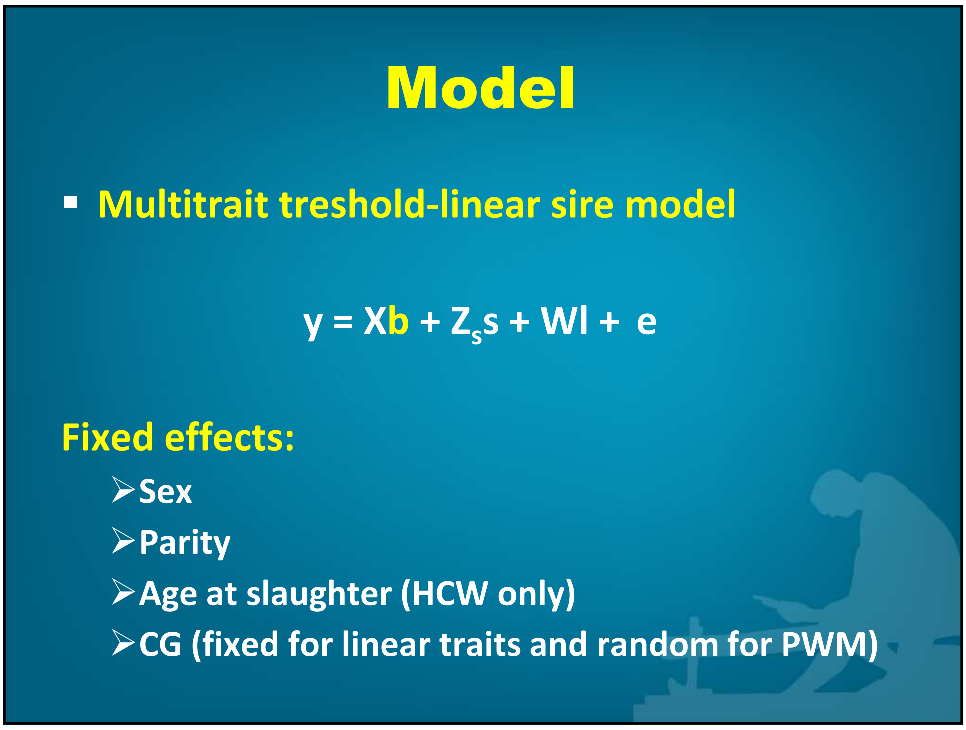
Model

- Multitrait treshold-linear sire model

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

Observations:

- BRW, kg (linear)
- PWM (categorical, 2 categories)
- HCW, kg (linear)



Model

- Multitrait treshold-linear sire model

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

Fixed effects:

- Sex
- Parity
- Age at slaughter (HCW only)
- CG (fixed for linear traits and random for PWM)

Model

- Multitrait treshold-linear sire model

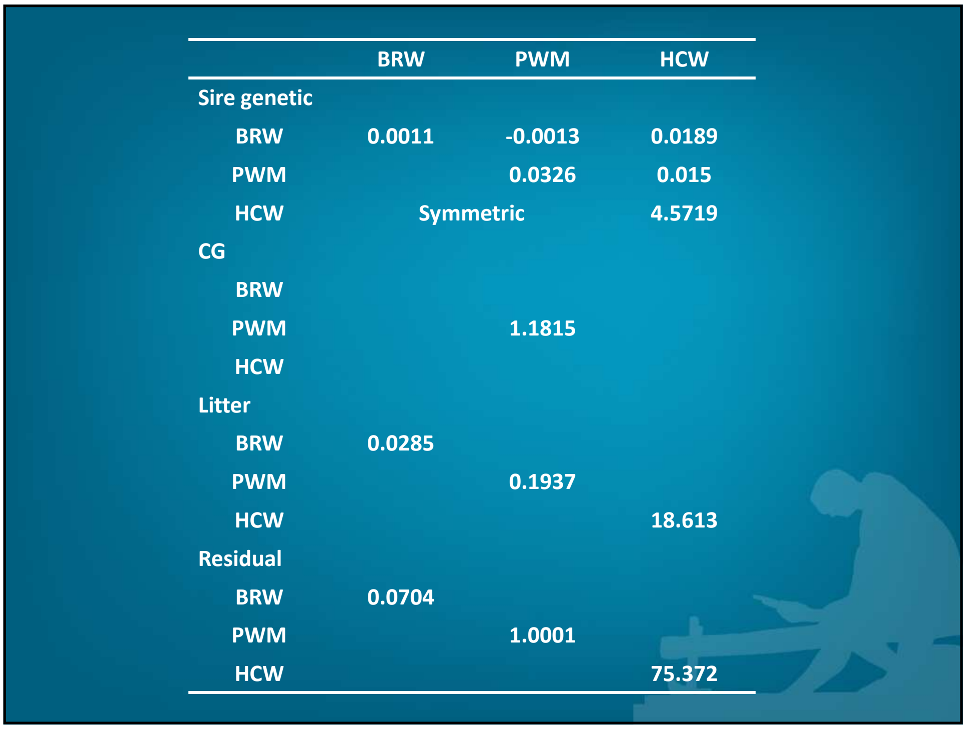
$$y = Xb + Z_s s + Wl + e$$

Random effects:

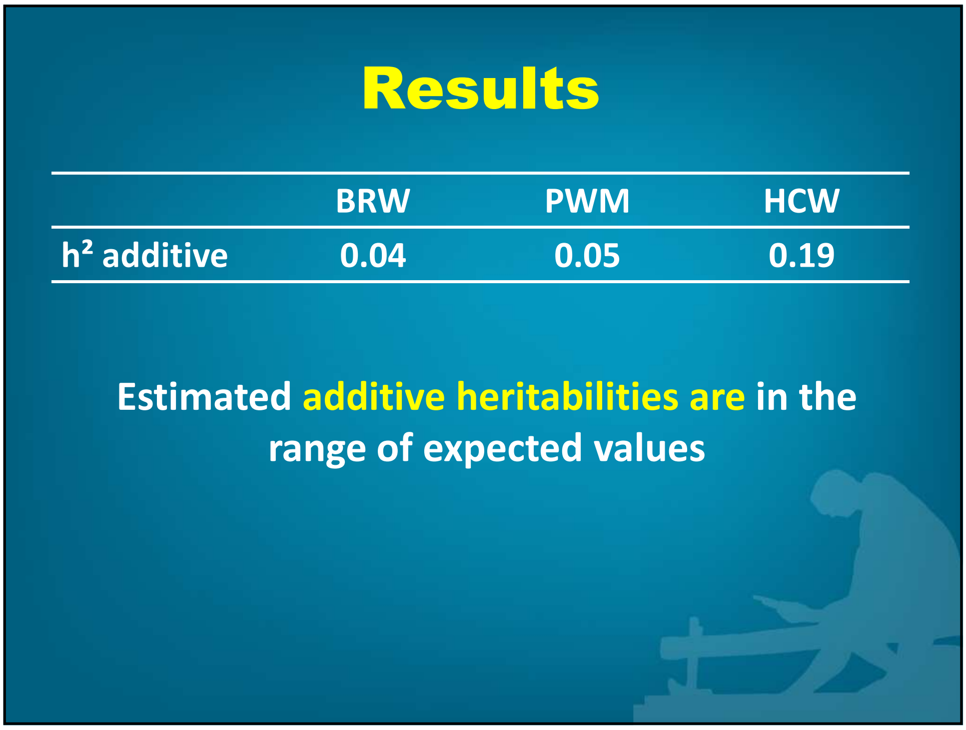
- Sire additive genetic effects (s)
- Litter effects (l)
- Residual effects (e)

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 10,000
  - Every 10th samples to compute mean and SD of the posterior distribution



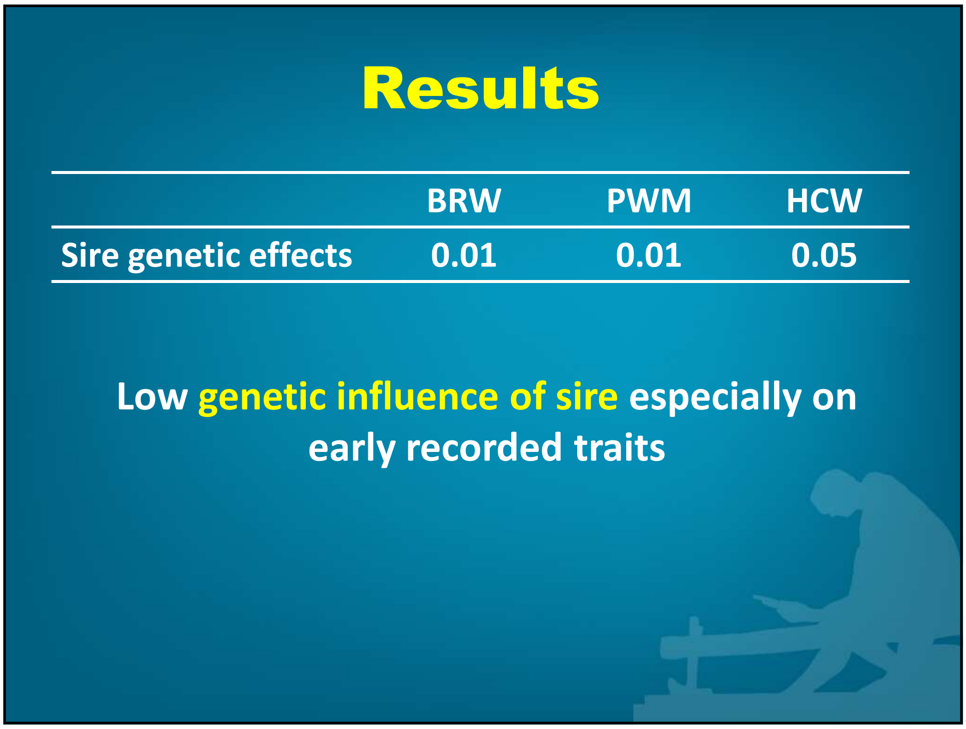
	BRW	PWM	HCW
Sire genetic			
BRW	0.0011	-0.0013	0.0189
PWM		0.0326	0.015
HCW	Symmetric		4.5719
CG			
BRW			
PWM		1.1815	
HCW			
Litter			
BRW	0.0285		
PWM		0.1937	
HCW			18.613
Residual			
BRW	0.0704		
PWM		1.0001	
HCW			75.372



Results

	BRW	PWM	HCW
h^2 additive	0.04	0.05	0.19

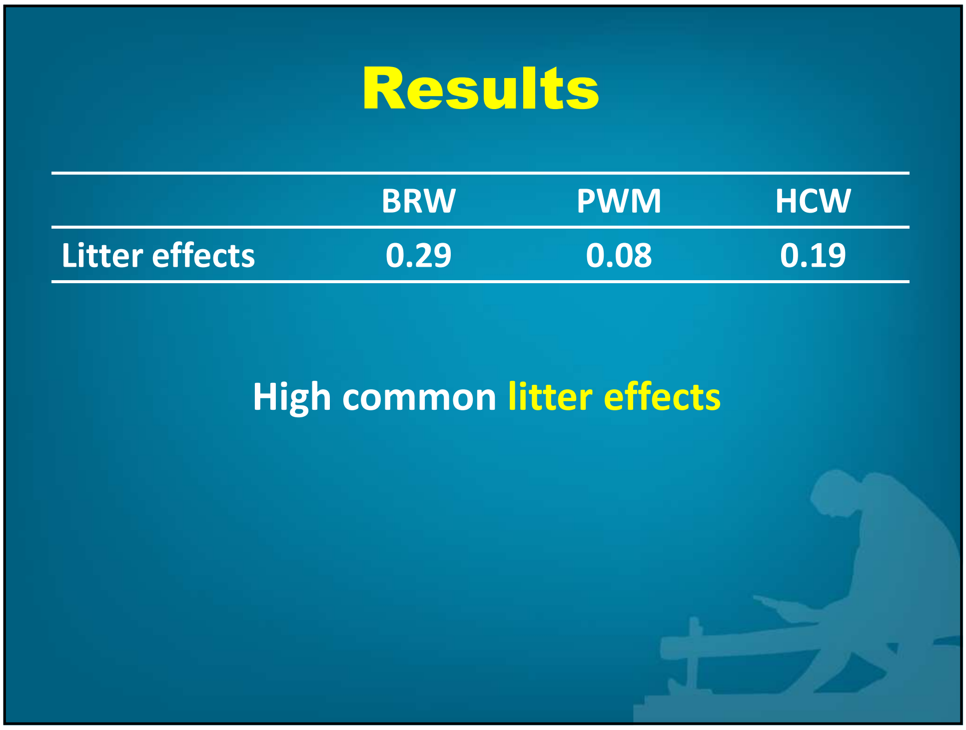
Estimated additive heritabilities are in the range of expected values



Results

	BRW	PWM	HCW
Sire genetic effects	0.01	0.01	0.05

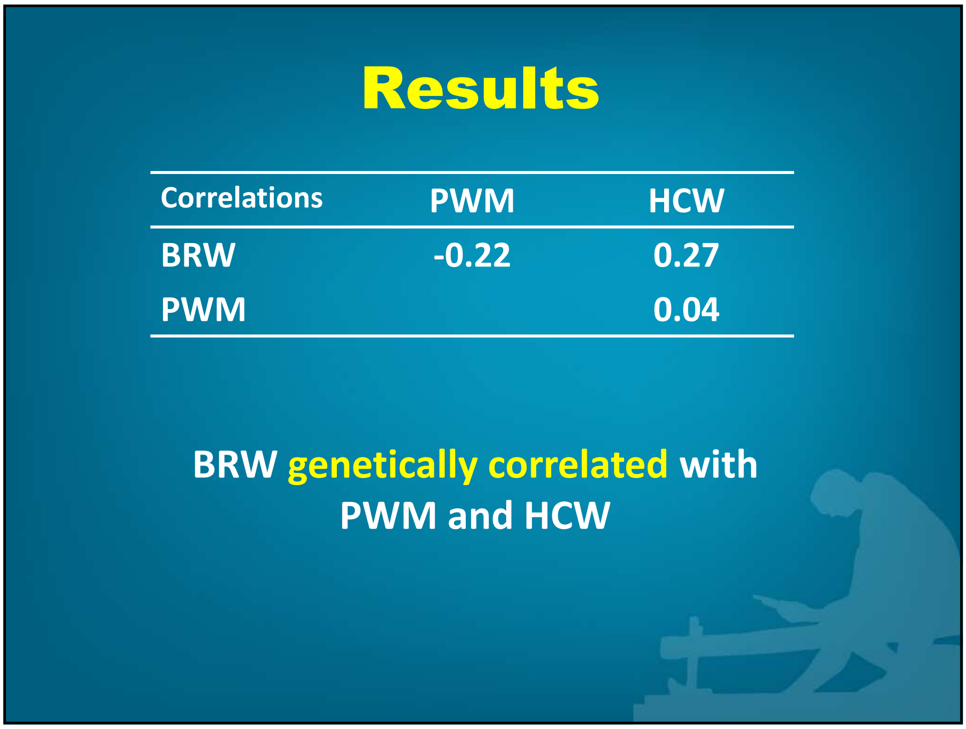
Low genetic influence of sire especially on early recorded traits



Results

	BRW	PWM	HCW
Litter effects	0.29	0.08	0.19

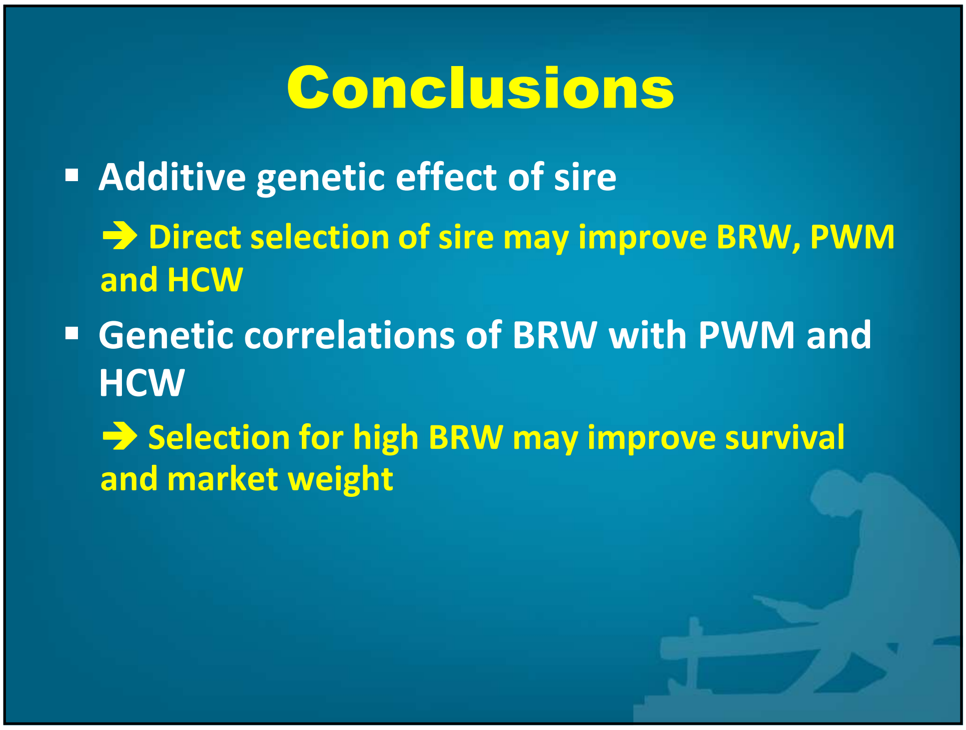
High common litter effects



Results

Correlations	PWM	HCW
BRW	-0.22	0.27
PWM		0.04

BRW genetically correlated with PWM and HCW



Conclusions

- Additive genetic effect of sire

  ➔ Direct selection of sire may improve BRW, PWM and HCW
- Genetic correlations of BRW with PWM and HCW

  ➔ Selection for high BRW may improve survival and market weight

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