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**Agroscope**

# **Genetic parameters for genetic variance uniformity in Swiss pigs' birth weight**

**Claudia Kasper, Alfredo Lepori, Juan-Pablo Gutiérrez, Nora Formoso-Rafferty, Ewa Sell-Kubiak, Isabel Cervantes**

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# Heterogeneity in birth weight in pigs

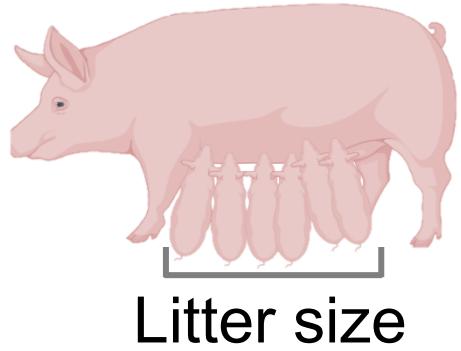
Selection for **increased litter size** → higher within-litter **heterogeneity** of birth weights

- Higher perinatal mortality
- Higher variation in weaning weight and age at slaughter
- Management challenges:
  - cross-fostering
  - match piglets according to weight – immunity concern

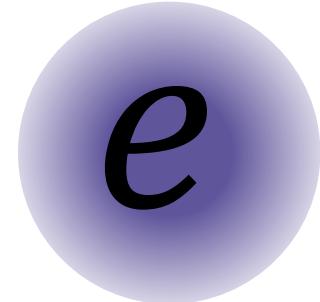
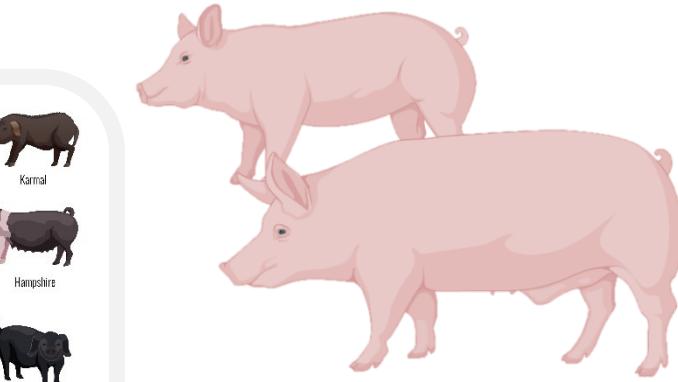


# Heterogeneity in birth weight in pigs

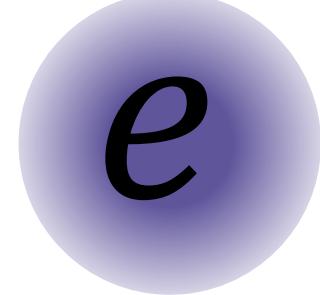
## Factors influencing birth weight



Breed



# Heterogeneity in birth weight in pigs



## Breeding

*“Genetic control of environmental/residual variance”*

(Formoso-Rafferty et al., 2015; de Souza lung et al., 2019)

Homogeneity ~ robustness (Rönnegard et al., 2010; Fathallah et al., 2016)

## Mouse as model

*What can be expected when selecting for increased homogeneity?*



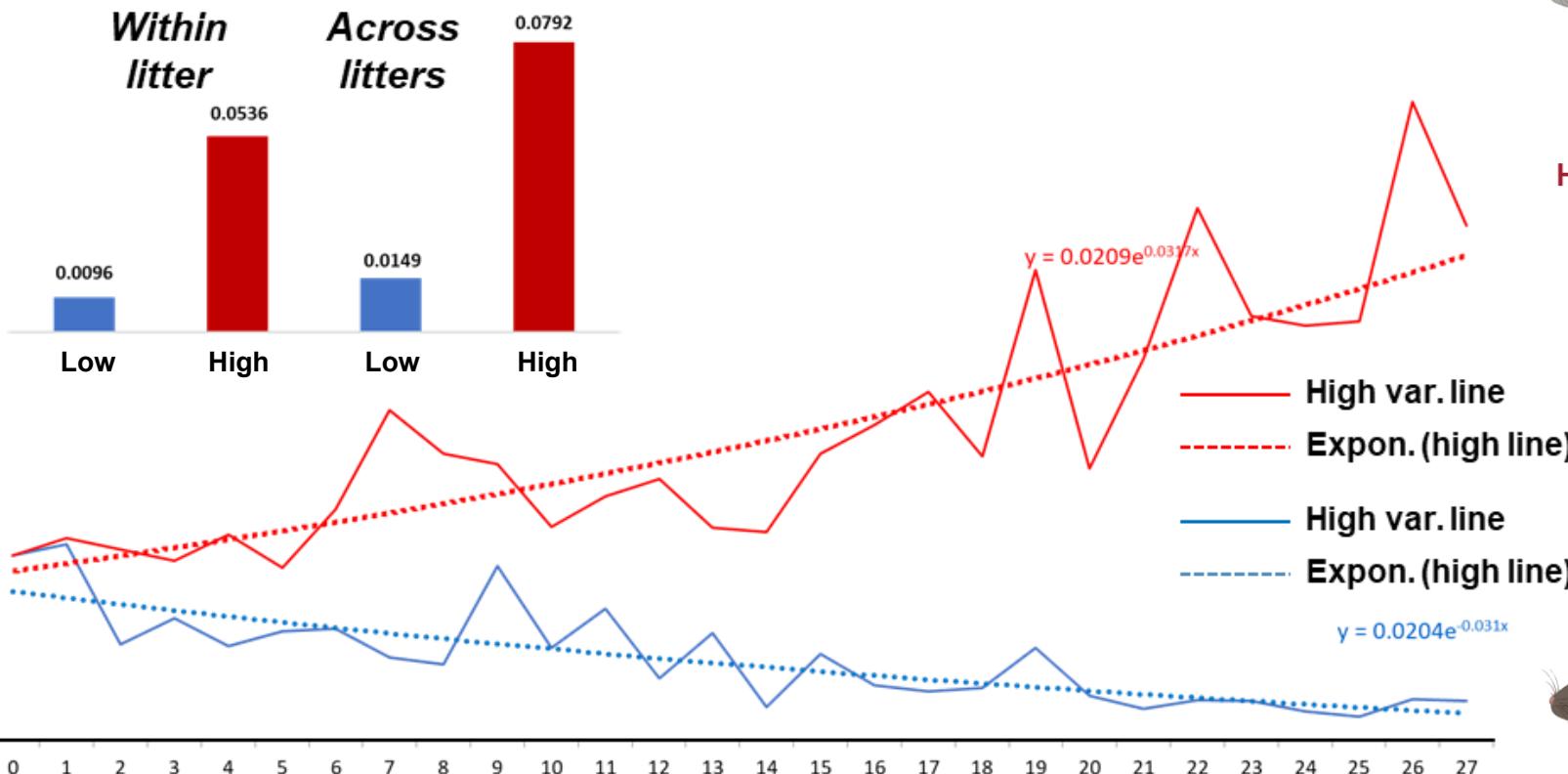
Low-variability line



High-variability line

(Formoso-Rafferty et al., 2015)

# Heterogeneity in birth weight in mice



Claudia Kasper | EAAP 2023  
Genetic variance of uniformity in piglet birth weight



High-variability line

Low variability line:

- Higher survival
- Larger litter size
- Higher reproductive longevity



Low-variability line

# Data set

- 2 commercial farms
- Free farrowing
- Suisag
- Individual birth weights ( $\leq$  24 hrs of birth)
- 24,720 piglets, 1,744 litters, 813 sows
- Pedigree: 27,285 individuals



# Homoscedastic vs. heteroscedastic model

- Assumption: residual variance is not homogeneous
  - different for each level of random and systematic effect
- Homoscedastic → heteroscedastic model (GSEVM software)

$$y_i = x_i b + z_i a + w_i c + e_i \rightarrow y_i = x_i b + z_i a + w_i c + e^{1/2(x_i b^* + z_i a^* + w_i c^*)} \varepsilon_i$$

\* environmental variability  
correlation  $\rho$

b: systematic (fixed) effects:

- Sex (male or female)
- Survival at weighing (alive/dead)
- Age of the sow (from 300 to 1956 days)
- Farm \* Month \* Year (75 levels)
- Litter Size (17 levels: 2-5, 6, 7... 20, >20)
- Breed (4 levels)

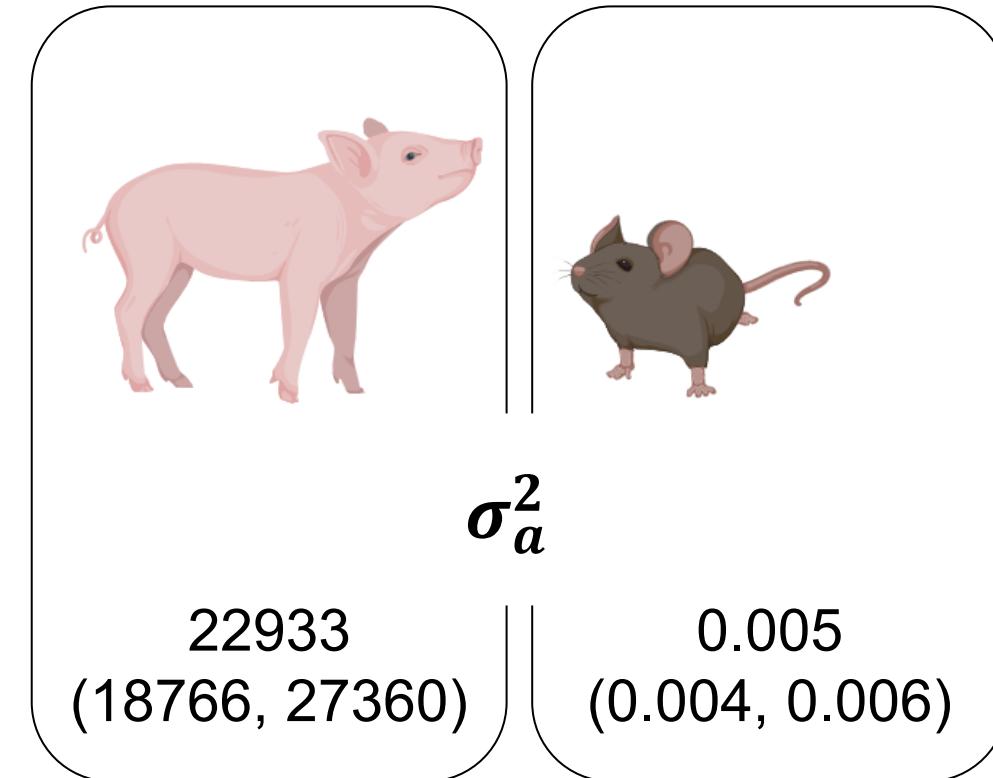
random effects

- a: sow genetic effects
- c: litter effects

e

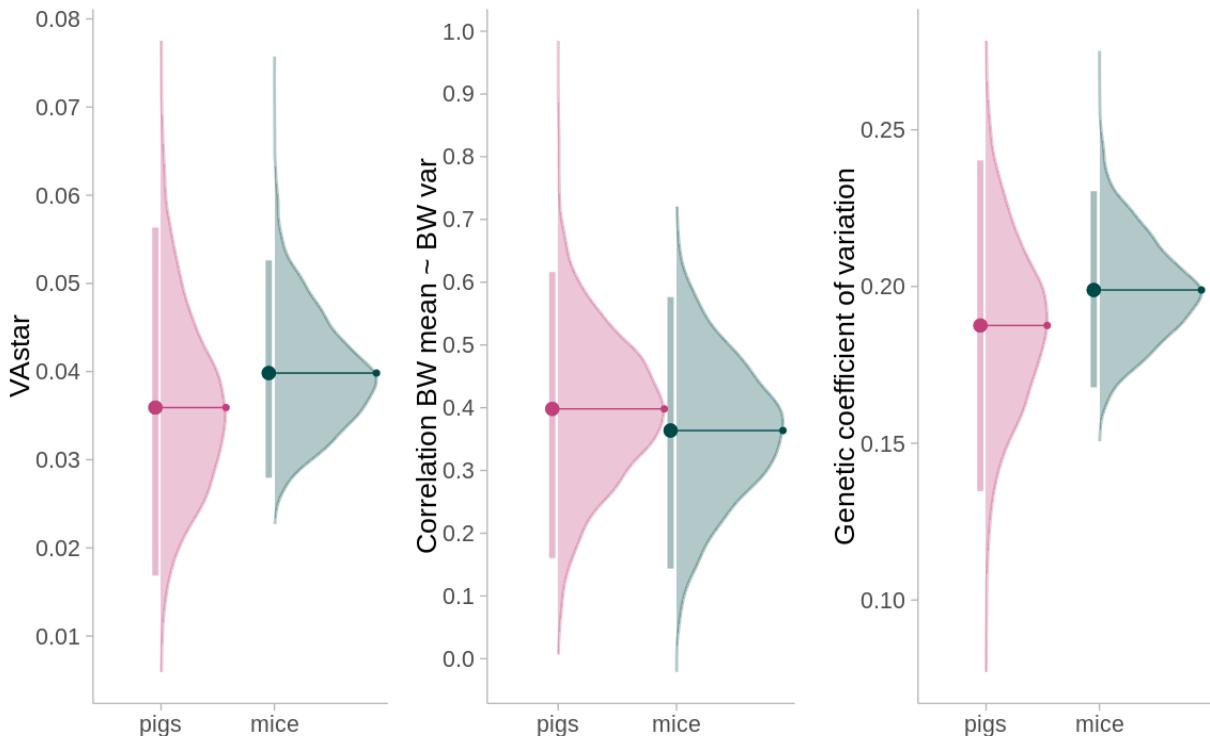
# Genetic parameters

in **pigs** and **mice**





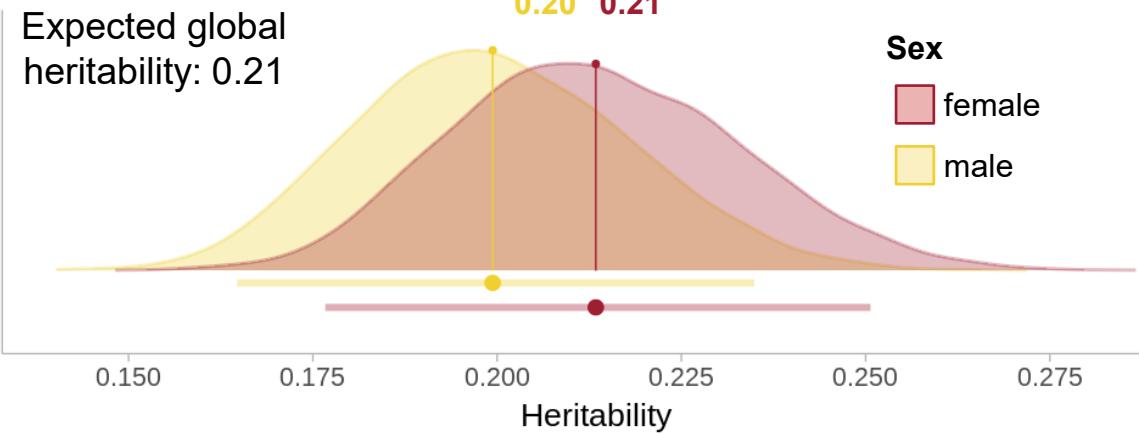
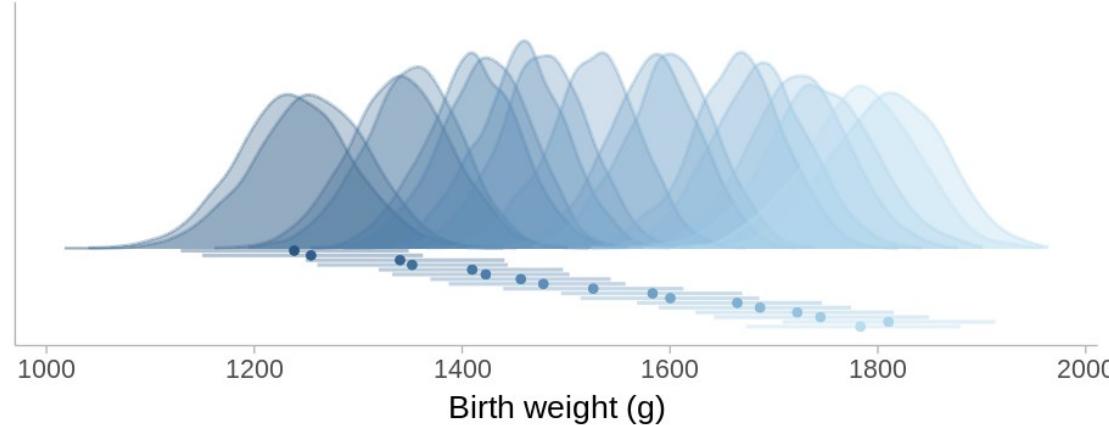
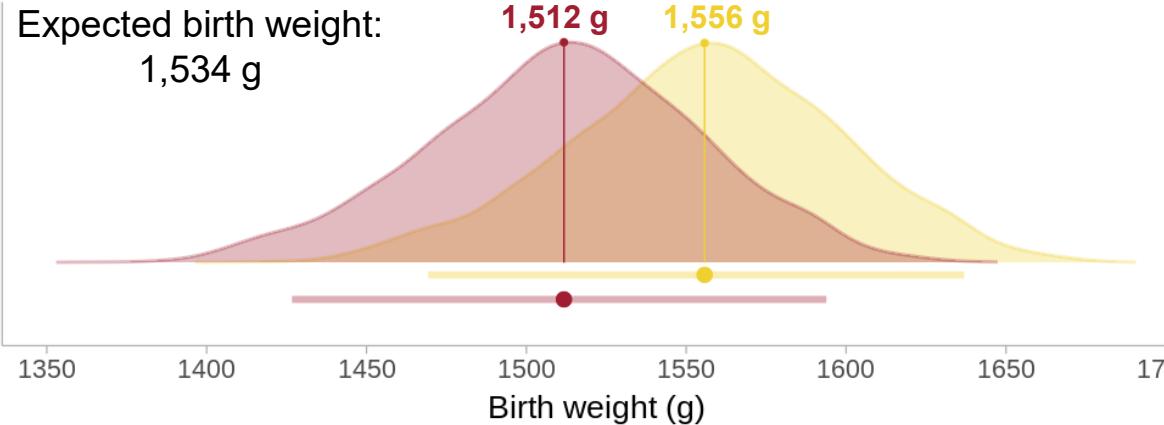
# Genetic parameters



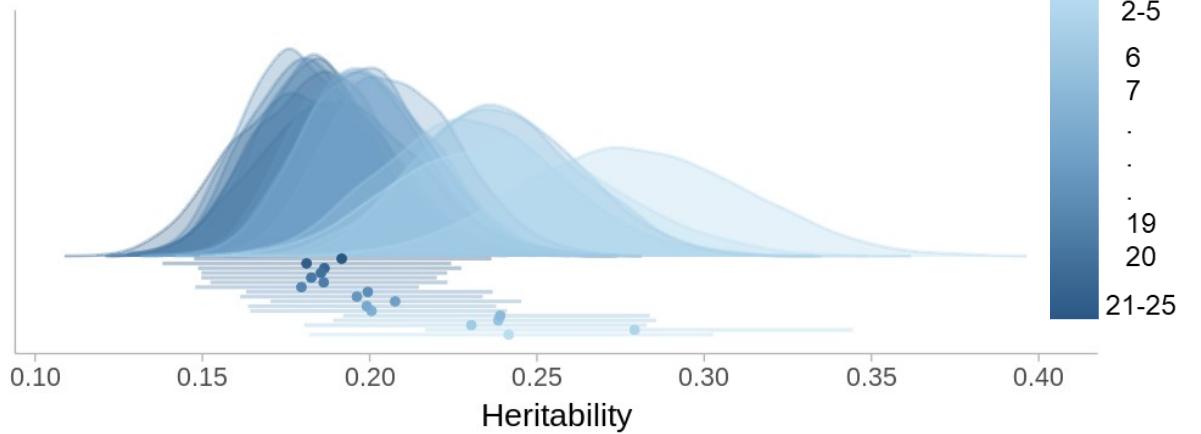
	$\sigma_{a^*}^2$	$\rho$	GCV
<b>Pigs</b> 95% Crl	0.036 (0.018, 0.057)	0.398 (0.166, 0.622)	0.187 (0.135, 0.240)
<b>Mice</b> Clau Gene 95% Crl	0.040 (0.028, 0.052)	0.364 (0.144, 0.576)	0.199 (0.167, 0.229)

# Effect of sex and litter size...

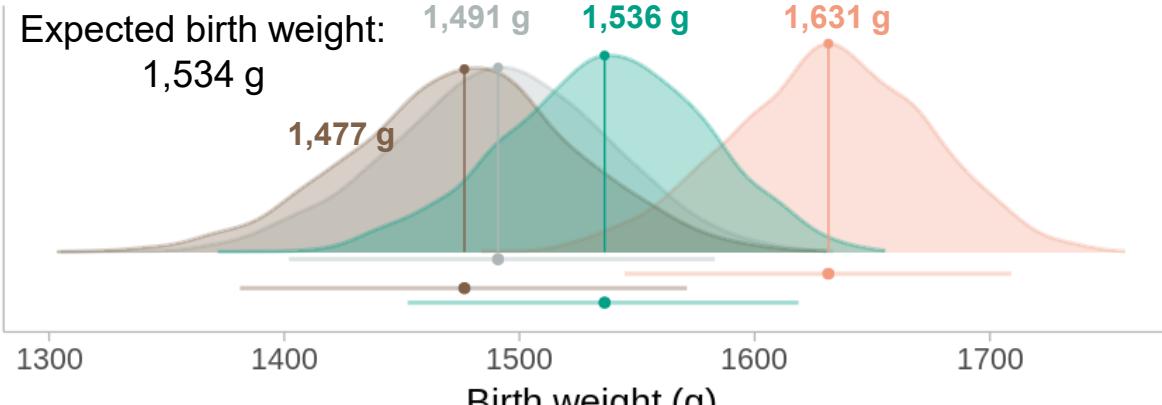
*...on birth weight*



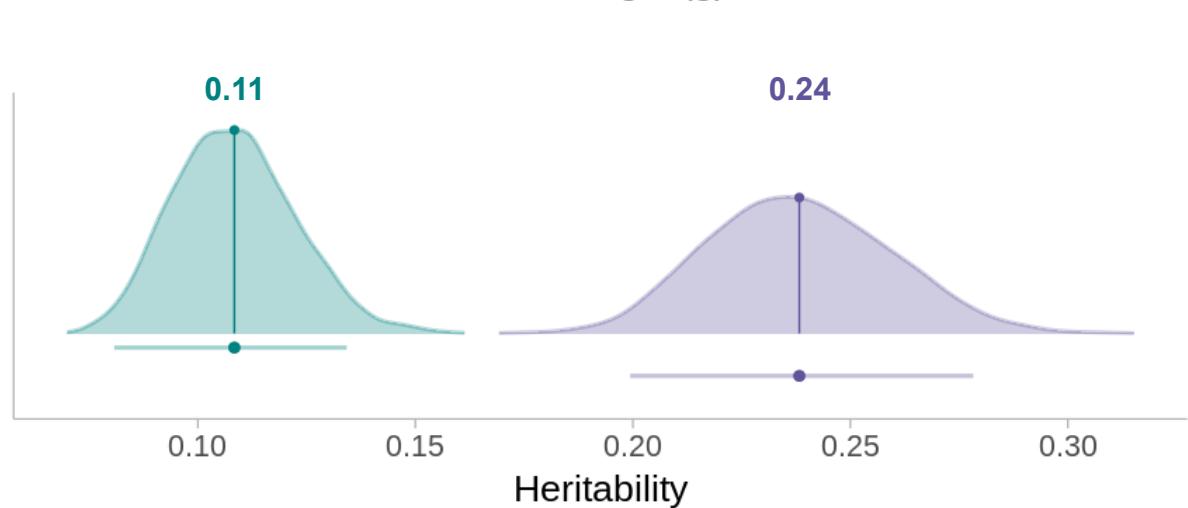
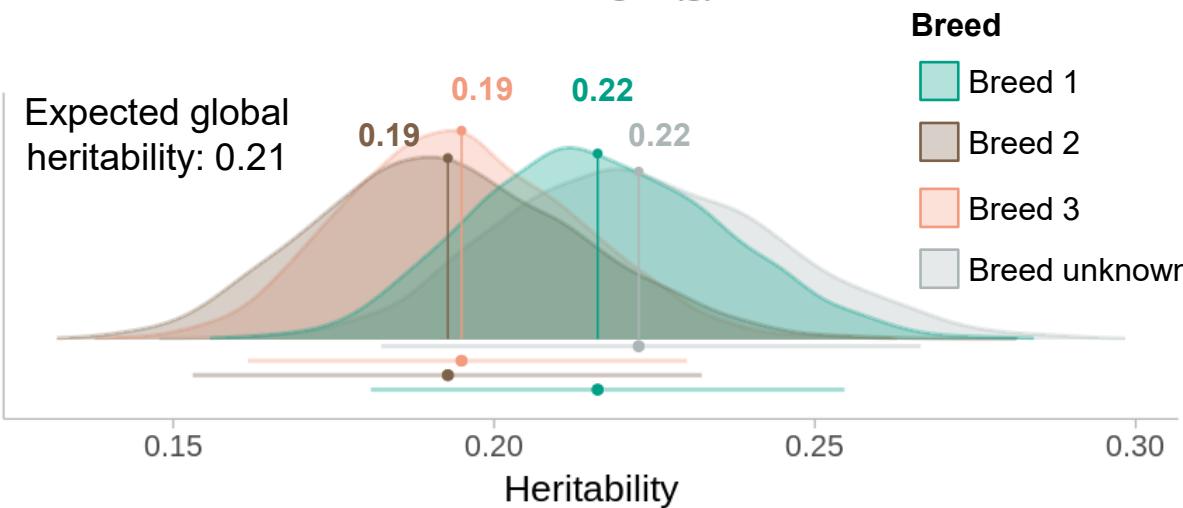
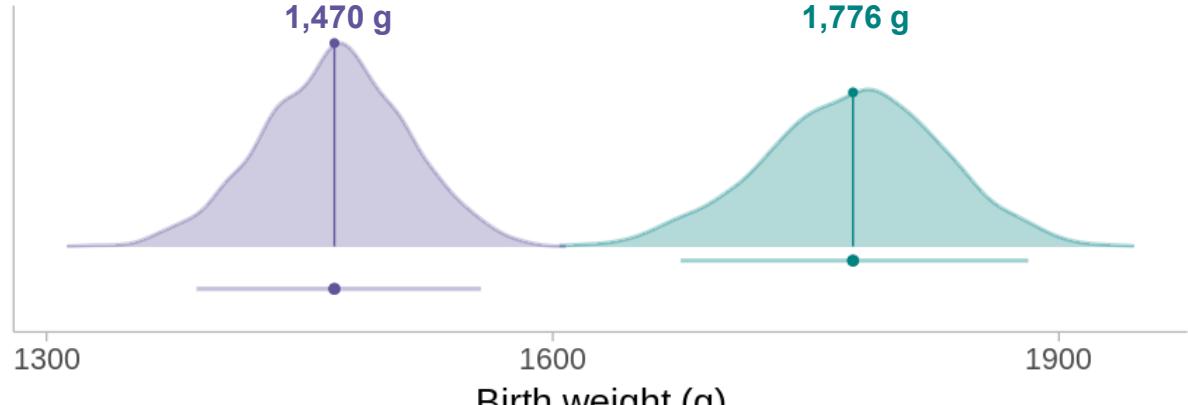
*...on its heritability*



# Effect of breed and age of sow...

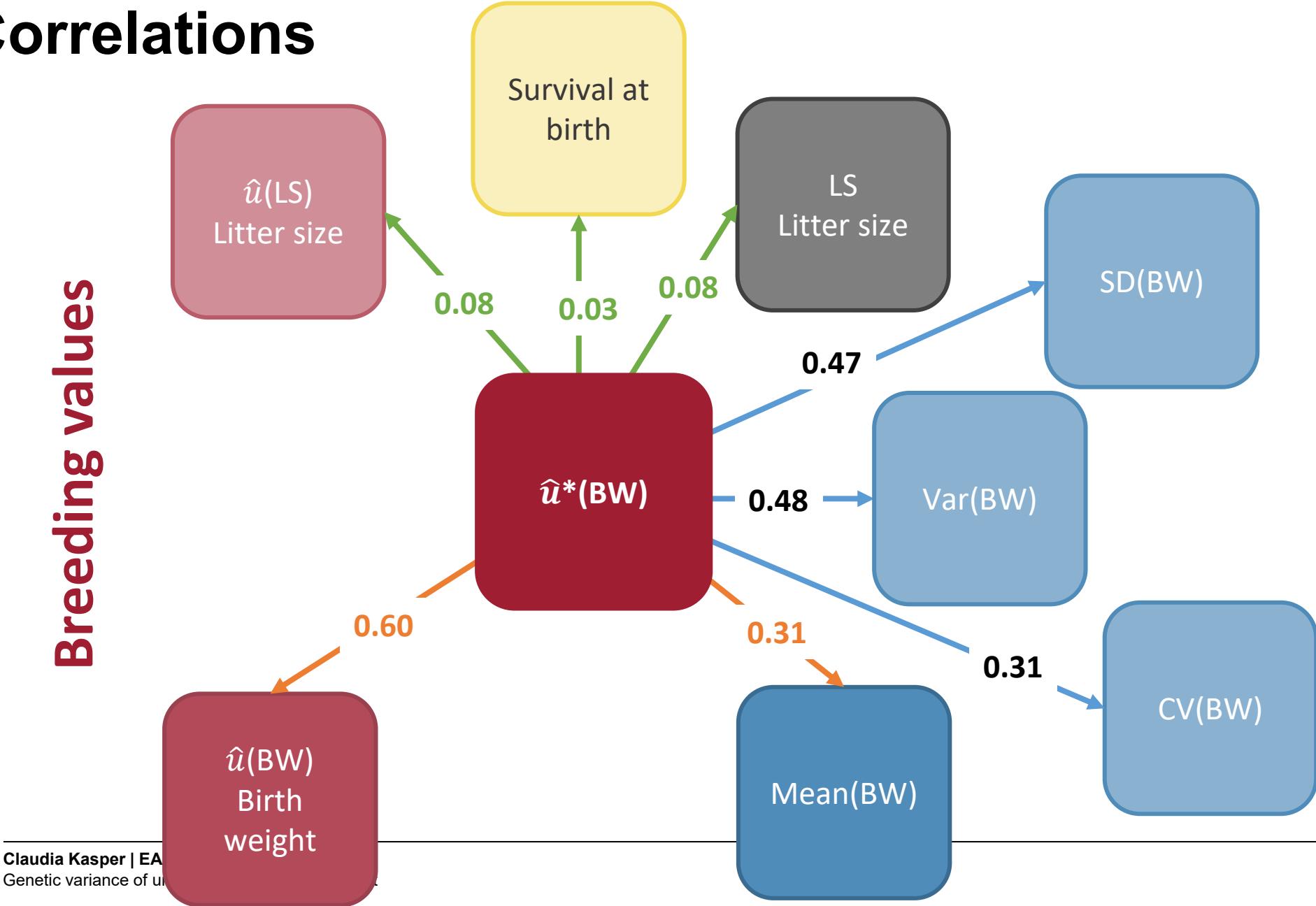


Young sow (< 1 year)      Older sow (> 5 years)



# Correlations

Breeding values



Phenotypes

# Conclusions

- **Potential for breeding**
- Similarity to mice, where breeding was successful
- Positive genetic **correlation of variability with mean**
  - unfavourable, but **survival not affected** (or even increased)
- «optimal birth weight» – «intermediate piglet»?

## Breeding for uniformity in piglet birth weight to improve survival

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### Background

Selection for **uniformity** in birth weight could lead to a more ethical and efficient livestock production because it results in more **robust animals**, which are easier to manage, more feed-efficient and are more likely to survive to weaning.

### Objective

Estimate the genetic component of residual variance for birth weight and its relationship with piglet survival in a Swiss experimental farm.

### Material and Methods

**Data set:** 43,135 records of BW from 3,163 litters of 986 sows



 Thank you!



Data collection and sharing



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# Thank you for your attention

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