Breeding for uniformity in piglet birth weight to improve survival

Claudia Kasper[1], Alfredo Lepori[2], Juan Pablo Gutiérrez[3], Nora Formoso-Rafferty[4], Ewa Sell-Kubiak[5] and Isabel Cervantes[3]

[1]Agroscope, Animal GenoPhenomics, Switzerland, [2]Suisag, Switzerland, [3]Departamento de Producción Animal, Facultad de Veterinaria, Universidad Complutense de Madrid, Spain, [4]Departamento de Producción Agraria, ETSIAAB, Universidad Politécnica de Madrid, Spain, [5]Department of Genetics and Animal Breeding, Poznan University of Life Sciences, Poland

Contact: claudia.kasper@agroscope.admin.ch

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
Pedigree data: 45,737 individuals
Traits: birth weight (**BW**) and the probability of stillborn (**SB**)

★ Homoscedastic model (BW and SB)

$$y_i = x_i b + z_i a + n_i m + w_i c + e_i$$

Fixed effects (b):
- Sex (2 levels: male or female)
- Month-year (75 levels)
- Litter size (18 levels: 2-5, 6, 7… 20 or >20)
- Parity number (10 levels)

Random effects:
- Litter (**c**)
- Additive genetic effect individual (**a**)
- Maternal genetic effect (**m**)

★ Heteroscedastic model (BW and its variability)

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

** parameters associated with environmental variability* $\varepsilon_i \sim N(0,1)$

Fixed effects (b, b*):
- Sex (2 levels: male or female)
- Month-year (75 levels)
- Litter size (18 levels: 2-5, 6, 7… 20 or >20)
- Parity number (10 levels)

Random effects:
- Litter (**c**, **c***)
- Additive genetic effect mother (**u**, **u***)

Software: GSEVM (Ibáñez-Escriche et al., 2010)
TM (Legarra, 2008)

Results

Genetic parameters - Homoscedastic model
in TM (multitrait BW and SB)

	a (BW)	a (SB)	m (BW)	m (SB)
a (BW)	**0.040 ± 0.012**	0.100 ± 0.385	-0.240 ± 0.176	-0.074 ± 0.213
a (SB)		**0.004 ± 0.002**	0.198 ± 0.331	-0.188 ± 0.298
m (BW)			**0.229 ± 0.025**	-0.012 ± 0.110
m (SB)				**0.049 ± 0.010**

Posterior means and standard deviations of individual (a) and maternal (m) heritabilities on the diagonal and genetic correlations across traits and genetic effects above diagonal.

Genetic parameters - Heteroscedastic model
in GSEVM (BW and its variability)

σ^2_u	σ^2_{u*}	ρ	GCV
add. genet. var. BW	**add. genet. var. BW variability**	**gen. corr. BW and BW variability**	**genetic coefficient of variation**
28192 (± 2022)	0.084 (± 0.016)	**0.238 (± 0.089)**	0.290

Posterior means and standard deviations

Correlation between predicted breeding values

	û*	a (BW)	m (BW)	a (SB)	m (SB)
û (maternal)	0.360	0.116	0.967	0.793	-0.160
û*		-0.010	0.340	0.144	-0.036
a (SB)			-0.061	0.431	-0.184
m (BW)				0.746	-0.166
a (SB)					-0.320

Pearson correlations. *û* and *û** from heteroscedastic model and *a* and *m* from homoscedastic model.

Conclusion

- There is **potential for selection** to reduce environmental birth weight variability due to additive genetic variance at sow level.
- The positive genetic correlation between mean birth weight and its variability might be unfavourable.
- However, the correlation between maternal breeding values indicates that **survival will not be negatively affected.**

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