



Bayesian inference of genetic parameters on litter size and gestation length in Hungarian Landrace and Hungarian Large White pigs

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ABSTRACT - Genetic parameters of number of piglets born alive (NBA) and gestation length (GL) were analyzed for 39798 Hungarian Landrace (HLA, 141397 records) and 70356 Hungarian Large White (HLW, 246961 records) sows. Bivariate repeatability animal models were used, applying a Bayesian statistics. Estimated and heritability repeatabilities (within brackets), were low for NBA, 0.07 (0.14) for HLA and 0.08 (0.17) for HLW, but somewhat higher for GL, 0.18 (0.27) for HLA and 0.26 (0.35) for HLW. Estimated genetic correlations between NBA and GL were low, -0.08 for HLA and -0.05 for HLW.

Key words: Genetic parameters, Litter size, Gestation length, Pigs, Gibbs sampling.

Introduction - Although traits most closely connected with reproductive fitness have the lowest heritability (Falconer and Mackay, 1996), genetic variability exists for several reproductive measures and suggests that genetic improvement in reproduction is possible (Rothschild, 1996). The efficiency of this selection is mainly determined by the genetic parameters of the chosen reproductive traits. The objective of this study was therefore to estimate genetic parameters of the fitness traits (number of piglets born alive, NBA and gestation length, GL) recorded for Hungarian Landrace (HLA) and Hungarian Large White (HLW) pigs. A Bayesian approach taking into account also the effects of inbreeding was applied.

Material and methods - *Data information.* Reproductive performance of purebred HLA and HLW sows was collected by the National Institute for Agricultural Quality Control of Hungary in the course of a field test performed from 1979 to 2004. The analyzed traits were NBA and GL. Aspect of data editing was described by a previous study (Farkas *et al.*, 2007)

using the same dataset. After data editing the numbers of herd and herd-year-season classes of these pig breeds were 120, 164 and 2187, 2065, respectively. Records of 39798 HLA and 70356 HLW sows were considered in the analysis. Descriptive statistics are presented in Table 1. *Statistical models.* NBA and GL were analyzed with bivariate repeatability animal model. Litter inbreeding coefficients, dam inbreeding coefficient and complete generation equivalents for sows and litters were defined as covariates.

Furthermore, herd-year-season, parity (1-8), additive genetic, permanent and residual environmental effects were also considered.

Table 1. Descriptive statistics for the number of piglets born alive and gestation length (in days) in Hungarian Landrace (HLA) and Hungarian Large White (HLW) pig populations.

Trait	Number of records	Mean	Standard deviation
Number of piglets born alive			
- HLA	141,047	9.793	2.312
- HLW	246,150	10.051	2.575
Gestation length			
- HLA	141,397	115.983	2.007
- HLW	246,961	115.281	1.832

For NBA and GL the model was:

$$(y \mid b, a, pe, R_0) \sim N(Xb + Za + Wpe, R_0 \otimes I_n)$$

X, Z and W are known incidence matrices, I_n is an identity matrix and R_0 is a 2x2 residual (co)variance matrix. The vectors b, a, and pe contain the environmental, genetic and permanent environmental effects. A bounded uniform distribution was assigned to represent vague previous knowledge for the vector b. The genetic effects a were assumed to be Gaussian:

$$a \sim N(0, G_0 \otimes A)$$

Where A is an additive genetic relationship matrix and G_0 is a 2x2 additive genetic (co)variance matrix. The permanent environmental effects pe were assumed to be independent and Gaussian:

$$pe \sim N(0, C_0 \otimes I_s)$$

Where 0 is a vector of zeroes and C_0 is a 2x2 additive permanent environment (co)variance matrix between traits, I_s is an identity matrix with the same order of permanent environmental effects. Bounded uniform priors were assumed for non-zero elements of matrices R_0 , G_0 and C_0 . The applied procedure was described in detail by Farkas *et al.* (2007). Contrary to the previous study (Farkas *et al.*, 2007) every chain element was taken into account for both breeds (2 merged chains with 220.000 elements per chain), according to Bohmanova *et al.*, (2008).

Results and conclusions - Features of the marginal posterior distributions of the heritabilities (narrow and broad) are shown in Table 2. Means, medians and modes of these distributions were practically the same. Narrow and broad sense heritability estimates of NBA

Table 2. Heritability and repeatability (in brackets) estimates of the number of piglets born alive and gestation length (in days) in Hungarian Landrace (HLA) and Hungarian Large White (HLW) pig populations.

Trait	Mean	Median	Mode	HPD _{99%}	MCse (10 ⁻⁵)
Number of piglets born alive					
- HLA	0.07 (0.14)	0.07 (0.14)	0.07 (0.14)	0.06-0.09 (0.13-0.16)	8.0 (2.7)
- HLW	0.08 (0.17)	0.08 (0.17)	0.08 (0.17)	0.06-0.09 (0.16-0.18)	6.4 (1.9)
Gestation length					
- HLA	0.18 (0.27)	0.18 (0.27)	0.18 (0.27)	0.15-0.20 (0.26-0.29)	8.7 (2.4)
- HLW	0.26 (0.35)	0.26 (0.35)	0.25 (0.35)	0.24-0.28 (0.34-0.36)	7.0 (1.7)

Mean=mean of the marginal posterior density; Median=median of the marginal posterior density; Mode=mode of the marginal posterior density; HPD_{99%}=Symmetric 99% posterior density region; MCse=Monte Carlo Standard error.

were low for both breeds and are in accordance with Alfonso *et al.* (1997). Substantially higher heritability and repeatability estimates were found for GL, especially for HLW. Similar results were found by Hanenberg *et al.* (2001). Hanenberg *et al.* (2001) noted that the GL had a favourable positive genetic correlation with maternal ability. Thus, inclusion of GL as a selection criterion will also improve maternal ability. The considerable heritability of GL obtained is also in favour of including GL in selection. Means of the correlation coefficient estimates between NBA and GL were -0.08 (HPD_{99%}: -0.19, +0.04) and -0.05 (HPD_{99%}: -0.14, +0.03) for HLA and HLW, respectively. These results were also in accordance with Hanenberg *et al.* (2001). The magnitude of estimated genetic parameters indicated that reproductive performance in HLA and HLW can be improved by selection. The low genetic correlation between GL and NBA is favourable and hinders the adverse effect of GL on NBA, particularly if GL is used as selection criteria to improve reproductive performance.

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