Piglet Survival Genetically Correlated with Longevity in Sows

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Introduction

One of the goals in pig breeding is to genetically improve sow productivity, i.e. increase litter size, piglet survival, farrowing index, and longevity. Litter size has been very effectively improved over the last 10 years at the cost of a decline in piglet survival due to a negative relationship with litter size (Knol 2001). Improved litter size also has a negative effect on gestation length. Large litters are born earlier but are less mature which negatively affects piglet survival (Rydhmer *et al.* 2008). Because selection for increased litter size resulted in a decrease in piglet survival (van der Lende *et al.* 2002) it triggered selection for piglet survival. Genetically piglet survival is determined by the genes of the piglet, the biological dam and the foster dam. However, it is difficult to disentangle the genetics of piglet survival and so far knowledge is lacking on how the disentanglement of piglet survival is related to the ability of a sow to efficiently produce piglets during her life. Particularly longevity has attained limited attention and consequences of selection for piglet survival on sow longevity are not known. The reproductive performance of a breeding sow strongly influences longevity as reproductive failure is the number one reason for sows that are voluntarily culled (Stalder *et al.* 2004). The objective of this research therefore was to estimate genetic correlations between piglet survival, gestation length, and sow longevity.

Material and methods

Data description and definition of traits. Data were obtained at the experimental farm Beilen owned by the Institute for Pig Genetics (IPG) with approximately 200 commercial crossbred sows. Gilts were bought from other farms and all piglets were fattened. Data consisted of 35,985 records and a full pedigree file was available (50,241 records). Survival was measured on piglets while gestation length and longevity were measured on sows Gestation length (GL; 2,632 records) was measured in full days and was the difference between date of farrowing and date of first insemination in the last estrus. Longevity (Long; 533 records) was the apparent survival on the farm to start a 2nd cycle, i.e. 0 if there is no 2nd parity and 1 if there was a 2nd parity. Survival had a value of 100 or 0 when a piglet did or did not survive until weaning (33,006 records). Gestation length, longevity and piglet survival were all analyzed as continuous traits.

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Based on Knol (2001) survival was described by vitality (VIT; direct piglet effect), uterus quality (UQ; effect of the biological dam), and mothering ability (MA; effect of foster dam). Vitality is defined as the piglet's will to survive and is the combined effect of farrowing survival and survival till weaning. Uterus quality is the ability of the biological mother to provide an environment for growing embryos and to deliver her piglets alive. Mothering ability is the ability of the sow to nurse her piglets and give offspring a good chance to survive till weaning. Mandatory cross-fostering of 25% of the piglets was based on birth weight.

Statistical analyses. (Co)variance components and genetic parameters for univariate models were analyzed using ASReml. Univariate models in matrix notation were:

Gestation length model: $\boldsymbol{y} = \mathbf{X}_1\boldsymbol{b} + \mathbf{Z}_1\boldsymbol{a} + \mathbf{Z}_2\boldsymbol{s} + \mathbf{Z}_3\boldsymbol{pe} + \boldsymbol{e}$
Longevity model: $\boldsymbol{y} = \mathbf{X}_2\boldsymbol{b} + \mathbf{Z}_1\boldsymbol{a} + \boldsymbol{e}$
Survival model: $\boldsymbol{y} = \mathbf{X}_3\boldsymbol{b} + \mathbf{Z}_1\boldsymbol{a} + \mathbf{Z}_4\boldsymbol{m} + \mathbf{Z}_5\boldsymbol{f} + \mathbf{Z}_6\boldsymbol{lit} + \boldsymbol{e}$

where $\boldsymbol{a}$ is a vector of direct genetic effects, $\boldsymbol{s}$ of service sire effects, $\boldsymbol{pe}$ of permanent environment effects, $\boldsymbol{m}$ of maternal genetic effects, $\boldsymbol{f}$ of foster dam genetic effects, $\boldsymbol{lit}$ of common environmental effects and $\boldsymbol{e}$ of residual effects. $\mathbf{Z}_i$ are incidence matrices relating observations to random effects. Fixed effects were year/season$^{(\mathbf{X}_1,\mathbf{X}_2,\mathbf{X}_3)}$, cross$^{(\mathbf{X}_1,\mathbf{X}_2,\mathbf{X}_3)}$, parity$^{(\mathbf{X}_1,\mathbf{X}_2)}$, litter size$^{(\mathbf{X}_1)}$, birth weight$^{(\mathbf{X}_1)}$, sex$^{(\mathbf{X}_1)}$, re-insemination yes/no$^{(\mathbf{X}_2)}$. Models on GL, a repeatability model, and Long were straightforward as covariance's among random effects were assumed zero. The covariance structure for the random effects of the survival model was as follows:

$$\mathbf{G} = \begin{bmatrix} \mathbf{A}\sigma_a^2 & \mathbf{A}\sigma_{am} & \mathbf{A}\sigma_{af} & \mathbf{0} \\ \mathbf{A}\sigma_{am} & \mathbf{A}\sigma_m^2 & \mathbf{A}\sigma_{mf} & \mathbf{0} \\ \mathbf{A}\sigma_{af} & \mathbf{A}\sigma_{mf} & \mathbf{A}\sigma_f^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_{lit}^2 \end{bmatrix}$$

where σ_a^2 is the direct genetic variance (VIT), σ_m^2 the maternal genetic variance of the biological dam (UQ), σ_f^2 the maternal genetic variance of the foster dam (MA), σ_{lit}^2 the part of the common environmental effects explained by the 'litter at birth effect', **A** was built using relationships between all animals in the pedigree, and **I** was an identity matrix. The estimated covariance's were used to determine the genetic correlations (r_g) between VIT, UQ, and MA. Bivariate models were used to determine r_g's between survival and GL and Long respectively. In case bivariate models showed no convergence over iterations, the method described by Calo *et al.* (1973) was used to estimate r_g's. This method correlates estimated breeding values (EBV's) from univariate models adjusted for the reliability of those EBV's. Only EBV's of sows with a record on GL were used (660 records) because none of the piglets had an own performance record on GL which causes the EBV's of sibs within a litter to be the same. Standard errors (s.e.) of the r_g's were calculated using the formula given by Robertson (1959).

Results and discussion

The estimated heritability for survival was 0.024±0.0091 and compares well with the estimate found by Knol (2001) of 0.06. Although the heritability is low we estimated that genetic progress in piglet survival of 0.54% per year is possible when selecting for improved vitality. The heritability of GL was estimated at 0.35±0.074 and is in agreement with the heritability's found by Hanenberg *et al.* (2001) and Knol (2001) of 0.29 and 0.34 respectively. The high heritability of GL is also confirmed by Rydhmer *et al.* (2008) who estimated a heritability for GL of 0.30. The heritability of Long was 0.18±0.136 and in literature estimated heritability's for Long ranged from 0.07 till 0.27 based on different methods for analysis, on different sow lines and on different definitions of sow longevity (longevity, stayability or lifetime prolificacy) (Stalder *et al.* 2004).

Table 1: Genetic correlations among traits with heritability's on the diagonal [α]

Traits		Survival			GL	Long
		VIT	UQ	MA		
Survival						
Vitality	(VIT)	**0.024**				
Uterus Quality	(UQ)	- 0.38±0.59	**0.033**			
Mothering Ability	(MA)	0.58±0.79	- 0.23±0.29	**0.035**		
Gestation Length	(GL)	*0.72*±0.07	*0.26*±0.16	*0.42*±0.07	**0.35**	
Longevity	(Long)	*0.93*±0.04	- *0.58*±0.02	*0.56*±0.11	0.27±0.19	**0.18**

[α] Correlations shown in italics were based on correlations among EBV's of 660 sows according to Calo *et al.* (1973)

All estimated r_g's with s.e. are shown in Table 1. Genetic correlations between VIT and UQ and MA respectively resulted from the univariate survival model. The r_g between VIT and UQ was negative (-0.38). This negative r_g means that vital piglets will have a poor UQ when they become breeding sows later in life. The r_g between VIT and MA was positive (+0.58) and indicates that strong vital piglets have a better MA when they become breeding sows later in life. Vital piglets have a strong will to survive and likely stimulate their mother to care for them, e.g. produce more milk. In this way the vital piglets stimulate their mother to have good mothering abilities. This could have caused confounding between VIT and MA, but mandatory cross-fostering allowed us to break this link and to get unbiased estimates.

Estimated genetic correlations of GL with VIT, UQ, MA, and Long were all positive (0.72, 0.26, 0.42, and 0.27 respectively). Hanenberg *et al.* (2001) found r_g's between GL and MA per parity ranging from 0.36 to 0.50. The estimated r_g found in this research (0.42) is well within that range. That all r_g's with GL are positive is not surprising as a prolonged GL gives a piglet more time to fully develop which likely has a carry over effect for the rest of a piglet's life. An important part of development takes place during the last few days of gestation (Rydhmer *et al.* 2008).

The strong positive r_g between Long and VIT (+0.93) indicates that stronger (female) piglets have a better chance to produce more litters. A vital piglet is well developed and is slightly fatter (Knol 2001) which might therefore come in heat easily and have less leg problems as a breeding sow (i.e. Long is 1).

The negative genetic correlations of uterus quality with vitality, mothering ability, and longevity are problematic from a breeding point of view. Uterus quality is the quality of the biological mother as an environment for growing embryos. To separate uterus quality from mothering ability cross-fostering is required. Mandatory cross-fostering was applied on the farm this research was based on. Although cross-fostering was mandatory, a possible limitation is that it was not applied randomly but based on weight of piglets and on the quality of a mother, e.g. number of working teats.

Some other limitations of this research are: the size of the dataset, which was relatively small and resulted in large standard errors, and treating binary traits as continuous variables. ASReml, however, allows for only one binary variable and in most breeding value estimation procedures binary traits are treated as continuous variables.

Sow longevity is a problem which is illustrated by the annual report from Danish Pig Production in 2008 showing a sow mortality rate that is reaching 15% (Walling 2009). The positive genetic correlation of vitality with longevity is favorable and very interesting for pig breeding companies. It suggests that selection on vitality will increase sow longevity. Longevity is important because a good longevity increases the opportunity of a sow to be sufficiently productive (piglets weaned and sold per lifetime) to achieve a return on the replacement gilt investment cost (Stalder *et al.* 2004). The high genetic correlation between vitality and longevity found in this research probably is an overestimation because of the small dataset. However, if further research shows that the genetic correlation between vitality and longevity is indeed positive it will be beneficial to pig breeding programs.

Conclusion

Uterus quality was negatively correlated with vitality, mothering ability, and longevity and therefore the genetic ability of the dam to develop piglets in utero and deliver piglets that can be weaned will deteriorate if a population is selected for piglet survival and longevity in sows. However, selection for piglet survival will improve piglet vitality, mothering ability, and the ability to produce more litters (i.e. longevity).

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