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When to farrow?
Genetic correlation between gestation length and piglet survival

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Abstract

The study is based on 18913 sows from nucleus herds and 1037 sows from an experimental herd. All sows were primiparous Swedish Yorkshire sows with purebred litters. Gestation length was analysed together with no. born alive, no. stillborn and no. dead before weaning. A sire-dam model was used to estimate direct and maternal genetic effects. Gestation length had a mean of 115.5-115.8 days (SD 1.5). The direct heritability for gestation length was estimated at 0.33 and 0.24 in the two data sets. The maternal heritability was estimated at 0.18 and 0.40. The genetic correlations estimated between gestation length and no. stillborn were low. The direct genetic correlation between gestation length and no. dead before weaning was positive (0.19; longer gestation - higher mortality) and the corresponding maternal correlation was negative (-0.37; longer gestation - lower mortality). We conclude that gestation length is influenced by the genotype of the litter as well as the genotype of the sow, and that gestation length could be an important trait when breeding for improved piglet survival.

Introduction

The sow is unique with regard to litter size. No other animal of the same size gives birth to such a large litter. Even though so many piglets are born in a litter, the piglets are relatively well developed at birth. A large part of this development takes place during the last days of gestation. During this short period, the piglet's brain and liver are developed at a high rate, and a vital deposition of energy reserves takes place (Hakkarainen, 1975). It seems plausible that a longer gestation could improve piglet maturation at birth and thus piglet survival.

Due to the unfavourable genetic correlation between litter size at birth and piglet survival, selection for large litters at birth needs to be complemented with selection for increased survival (Knol, 2001; Lund et al., 2002). To record piglet mortality seems simple, but cross fostering and lack of individual records on each piglets' survival complicates the recording. In most data bases, a large part of the piglets are missing. The dates of mating and farrowing needed to calculate gestation length are, however, included in all data bases. Hanenberg et al. (2001) and Knol (2001) used these data, and found positive genetic correlations between gestation length and piglet survival.

Farrowing is preceded by large hormonal changes in the sow. When the corpora lutea are degenerated during the final part of gestation, plasma concentration of progesterone decreases.

At the same time, oestrogen level increases. These hormonal changes are prerequisites for a normal farrowing. It is, however, the foetuses that initiate the endocrine sequence of events that ends with the farrowing. The hypothalamus of the foetus responds to an increased physiological stress during late gestation, by stimulating the anterior pituitary gland to release ACTH. High ACTH level leads to an increased secretion of corticosteroids from the piglet's adrenal cortex, which triggers farrowing (Hunter, 1980). Since both sow and piglets thus play active roles in the control of farrowing time, we wanted to estimate the genetic effects of the piglets and the sow on gestation length.

Material and methods

The analyses were based on two data sets, one from Swedish nucleus herds and one from SLU's experimental herd. The data set from the experimental herd was small. The reason why we used both data sets is that piglet survival after birth is not yet recorded in the Swedish litter recording scheme. Both data sets included primiparous Swedish Yorkshire sows with purebred litters. The pedigree files included 1534 animals for the experimental herd and 16334 animals for the nucleus herds. Gestation length was recorded in full days, as farrowing date minus mating date. In Sweden, farrowings are not induced by hormonal treatments on a routine basis.

On data from the nucleus herds, gestation length was analysed together with number born alive and number stillborn piglets. The random effect of herd-year (271 herd-years) and the fixed effects of farrowing month (12 classes) and mating (AI or natural) were included, together with the random genetic effects. In data from the experimental herd, gestation length was analysed together with number born alive and number of pigs that were born alive but dead before weaning (5 weeks). The fixed effect of farrowing batch (39 batches) was included in the model, together with the random genetic effects.

Since each individual piglet's influence on the initiation of farrowing is impossible to measure, we did not use an animal model for piglets. Instead, we regarded the whole litter as one biological unit and used the following model with random genetic effects of the sire and the dam of the litter: *y* = herd-year + month + mating + sire + dam + error, where *y* is gestation length, number born alive and number stillborn or number dead. These three traits were analysed simultaneously. The (co)variance components were estimated using the average information restricted maximum likelihood (AI-REML) procedure (Jensen et al., 1997) in the DMU package (Madsen and Jensen, 2000).

In the sire-dam model, the sire effect ($_{\mathrm{s}}$) constitutes half the sire's direct genetic effect ($_{\mathrm{a}}$) and the dam effect ($_{\mathrm{d}}$) constitutes half the dam's direct genetic effect plus the maternal genetic effect ($_{\mathrm{m}}$). As a result, the variances and covariances estimated will be a mixture of direct and maternal effects. Within a trait the relationships are:
$\sigma_{\mathrm{d}}^2 = \sigma_{\mathrm{m}}^2 + \sigma_{\mathrm{a,m}} + 1/4\,\sigma_{\mathrm{a}}^2$, $\sigma_{\mathrm{s}}^2 = 1/4\,\sigma_{\mathrm{a}}^2$ and $\sigma_{\mathrm{s,d}} = 1/2\,\sigma_{\mathrm{a,m}} + 1/4\,\sigma_{\mathrm{a}}^2$.
Covariances between traits are:
$\sigma_{d1,d2} = \sigma_{m1,m2} + 1/2\sigma_{a1,m2} + 1/2\sigma_{a2,m1} + 1/4\sigma_{a1,a2}$, $\sigma_{\mathrm{s1,s2}} = 1/4\,\sigma_{\mathrm{a1,a2}}$, and $\sigma_{\mathrm{s1,d2}} = 1/2\,\sigma_{\mathrm{a1,m2}} + 1/4\,\sigma_{\mathrm{a1,a2}}$.
These relationships were used to transform results from the analyses into a variance covariance matrix between direct and maternal effects. The phenotypic variance was calculated as:
$\sigma_p^2 = \sigma_a^2 + \sigma_m^2 + \sigma_{am} + \sigma_e^2$. For the nucleus data, the herd-year variance was also included in the phenotypic variance.

Results

Both data sets showed a similar distribution of gestation length, with a low standard deviation (figure 1).

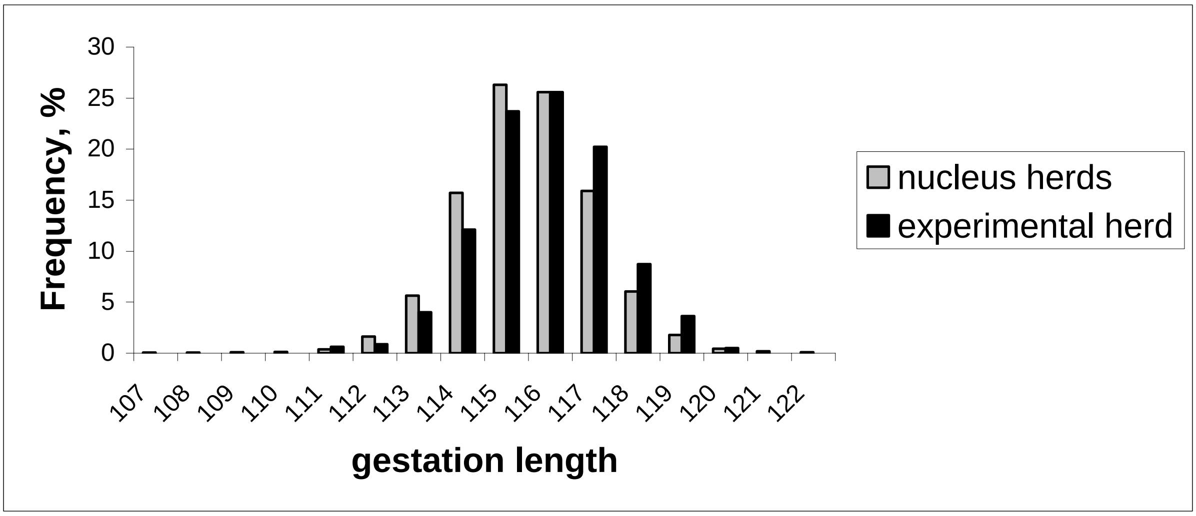

Figure 1. Gestation length of 801 sows in an experimental herd and 18913 sows in nucleus herds.

Gestation length had a mean of 115 - 116 days (table 1). Litter size was slightly lower in the experimental herd than in the nucleus herds, but there was no difference in standard deviation.

Table 1. Characteristics of the studied Swedish Yorkshire sows and their litters

Trait	N	Mean	SD	Min	Max
Nucleus herds					
Gestation length, d	18913	115.5	1.5	107	122
No. born alive	18913	10.3	2.8	0	20
No. stillborn	18913	0.8	1.2	0	16
Experimental herd					
Gestation length, d	801	115.8	1.5	111	120
No. born alive	1037	9.9	2.8	0	18
No. dead	1037	1.4	1.7	0	13

Considerable direct and maternal genetic effects were found for all studied traits. Thus, gestation length regarded as a trait of the sow (when to farrow) and gestation length regarded as a trait of the litter (when to be born) are both heritable traits (table 2). The correlation between direct and maternal genetic effects on gestation length was low (r_{am}=-0.00 in the nucleus herds and r_{am}=0.11 in the experimental herd).

Table 2. REML estimates of direct (h^2_a) and maternal (h^2_m) heritabilities for gestation length, litter size and piglet mortality

Trait		Nucleus herds	Experimental herd
Gestation length	h^2_a	0.33	0.24
	h^2_m	0.18	0.40
No. born alive	h^2_a	0.07	0.12
	h^2_m	0.09	0.18
No. stillborn	h^2_a	0.03	
	h^2_m	0.06	
No. dead	h^2_a		0.05
	h^2_m		0.08

The estimated genetic correlations between gestation length and number of piglets born alive differed between the two data sets, but the environmental correlations were all negative and low (table 3). Both the direct and the maternal genetic correlations were negative when estimated on data from the experimental herd, which means that large litters are born earlier than small litters. The genetic correlations estimated on the larger data set from nucleus herds were much lower and here the direct correlation was positive.

Both genetic correlations between gestation length and number stillborn were very low. According to genetic correlations estimated on data from the experimental herd, sows carrying genes for a long gestation have a high genetic ability for piglet survival. On the other hand, piglets carrying genes for being born late have a low genetic ability for survival after birth.

Table 3. REML estimates of direct (r_a), maternal (r_m) and environmental ($r_{e)}$ correlations between gestation length, litter size and piglet mortality

Trait 1	Trait 2	Correlation	Nucleus herds	Experimental herd
Gestation length	No. born alive	r_a	0.06	-0.47
		r_m	-0.14	-0.35
		r_e	-0.14	-0.07
Gestation length	No. stillborn	r_a	-0.04	
		r_m	0.00	
		r_e	-0.05	
Gestation length	No. dead	r_a		0.19
		r_m		-0.37
		r_e		-0.12

Discussion

A sow is pregnant during three months, three weeks and three days, as learnt by anyone studying animal science. The variation between sows in gestation length is very low, with a variation coefficient of only 1 %, as compared to 2 % for cows (Hansen et al., 2004) and 3 %

for horses (Pérez et al., 2003). There was a small difference in average gestation length between the two data sets, 115.5 and 115.8 days. Hanenberg et al. (2001) reported a gestation length of 115.2 days (SD 1.5 d) in Dutch Landrace sows. Knol (2001) studied two dam lines and found a difference of 2 days in average gestation length between them.

Previous genetic studies of gestation length have shown that the heritability is rather high, as compared to other reproduction traits. Hanenberg et al. (2001) estimated the heritability at 0.25 and Knol (2001) at 0.35. In those studies, gestation length was analysed as a sow trait, without taking any genetic effect of the piglets into account. When we used such an animal model on our data from the nucleus herds, the heritability was estimated at 0.32, which is in good agreement with the Dutch estimates. Knol (2001) included a random effect of the litter father (with no relationship matrix) and found that the father explained 6 % of the total variation in gestation length. Since the boar can not influence the time of farrowing, the effect of the father must reflect the ability of the piglets to be born at a certain time. Although the whole chain of events during late gestation and farrowing is not fully understood, it is known that the piglets trigger the farrowing (Hunter, 1980). Thus, we estimated the genetic variation in gestation length not only as a sow trait, but also as a piglet trait.

Hansen et al. (2004) studied gestation length in primiparous dairy cows. They used a sire-maternal grandsire model and calculated direct (the calf) and maternal (the cow) genetic effects. We were inspired by their work, but a sire-maternal grandsire model does not fit pig data, since the daughter groups of most boars are rather small. An animal model with direct (the piglet) and maternal (the sow) genetic effects have previously been used for piglet survival (e.g. Van Arendonk et al., 1996). Therefore, it is known that piglets within a litter may have different breeding values for survival. It is possible that piglets within a litter also have different breeding values for corticosteroid secretion. But when the sow farrows, it is probably as a response to the accumulated amount of corticosteroids from the piglets, in addition to the change in secretion pattern of her own hormones (e.g. oestrogen and progesterone). Therefore we chose the sire-dam model, in which the whole litter is regarded as one biological unit. A sire-dam model has previously been used to estimate direct and maternal genetic effects on litter size and piglet survival (Lund et al., 2002).

Hansen et al. (2004) found that the direct heritability for gestation length was 6 times higher than the maternal heritability (0.42 vs 0.07). In our study, the heritabilities were between 0.18 and 0.40, but the direct was higher than the maternal in the data from nucleus herds and vice versa in the data from the experimental herd. Although semen from AI-boars born in the nucleus herds have been used in the experimental herd, many boars have also been selected within the herd and no animals have been introduced to the herd during the studied period. So the difference between the data sets might be partly genetic. The small size of the data set from the nucleus herd must, however, be kept in mind when comparing the estimates. The heritability estimates for litter size from this data are, for example, higher than most estimates in the literature (Lund et al., 2002; van Arendonk et al., 1996). Anyhow, both data sets show that gestation length is influenced by the genotype of the litter as well as the genotype of sow, and that the heritabilities are higher than for reproduction traits in general.

The maternal genetic correlations between gestation length and number born alive were negative in both data sets. Hanenberg et al. (2001) reported a negative genetic correlation between gestation length and total number born (r_g=-0.18). The maternal genetic correlation between gestation length and stillborn piglets was close to zero. This is in agreement with the genetic correlation of 0.04 between gestation length and stillborn found by Hanenberg et al. (2001). Hansen et al. (2004) estimated a low maternal genetic correlation between gestation length and stillbirth in dairy cattle (r_m=-0.04).

We found a negative maternal genetic correlation between gestation length and piglet mortality after birth (long gestation - low mortality, r_g=-0.4). Likewise, Hanenberg et al. (2001) estimated the genetic correlation between gestation length and percent weaned of piglets born alive at 0.41. Thus, selecting sows for later farrowing would probably increase piglet survival. There is, however, no reason to select piglets for being born late. On the contrary, piglets with a genetic capacity to be born early seem to have a higher capacity for survival after birth (born late - high mortality, r_g=0.2).

Knol (2001) found a positive genetic correlation between gestation length and average birth weight which seems logical, but the correlation was low (r_g=0.12). The next step in our work will be to estimate direct and maternal genetic correlations between gestation length and piglet growth. Furthermore, we will study later parities, to see if the correlations between gestation length and piglet survival change when the sow grows older. Sofar, we conclude that gestation length is genetically correlated with piglet survival and that gestation length could be changed by selection. But such a selection would be complicated, since the direct and maternal genetic correlations seem to work in opposite directions.

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