Approaches to increase piglet survival through breeding

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Introduction

Litter size is one of the most important traits in sow productivity, but selection for litter size increases piglet mortality (Högberg and Rydhmer, 2000). Although there might be no genetic relationship between the number of live born and stillborn piglets (Holm et al., 2004; Arango et al., 2005) or even a positive one (Su et al., 2007), unfavourable correlations between number of piglets born alive and those dying before weaning are reported (Hermesch, 2001; Serenius et al., 2004).

Most studies on piglet survival are based on a repeatability model when accounting for different parities (e.g., Wolf et al., 2008) or on first parity only (e.g., Holm et al., 2004). The objectives of this study were to estimate genetic parameters from birth to weaning in first and second parity on a litter level, and also for individual piglet survival in the first parity.

Material

Data on 20 531 1st and 7 332 2nd parity purebred Norwegian Landrace litters collected from January 2001 until September 2008 by the national recording system were used. The traits analysed (Table 1) were no. piglets born alive (**LB**), no. stillborn piglets (**SB**), no. of piglets dying during suckling period (**DS**), total number of piglets dead until weaning (**TD**), no. of weaned piglets (**W**), within litter SD at 3 wk (**SDLW3**), and litter weight at 3 wk (**LW3**).

Table 1. Unadjusted means and SD for litter traits in 1st and 2nd parities.

Trait	1st parity		2nd parity	
	Mean	**SD**	**Mean**	**SD**
No. of piglets born alive (LB)[1]	11,9	2,8	12,8	3,0
No. of stillborn piglets (SB)[1]	1,2	1,2	1,3	1,5
No. of piglets dying until weaning (DS)[1]	2,0	2,0	2,3	2,2
No. all piglets dead until weaning (TD)[1]	3,2	2,5	3,6	2,7
No. of piglets weaned (W)[1]	9,9	2,5	10,5	2,5
SD litter weight at 3wk, kg (SDLW3)[2]	1,04	0,40	1,28	0,47
Litter weight at 3 wk, kg (LW3)[2]	64,2	18,9	76,0	20,4

[1]1st parity: N=20 531; 2nd parity: N=7 332; [2]1st parity: N=20,335; 2nd parity: N=7 276; (N=number of litters)

Individual piglet survival was studied on piglets born by 1st parity sows. The traits were survival at birth (**SVB**), after birth to 3 wk (**SV0-3**) and overall survival until 3wk (**SV3**). The traits were scored 0 for dead, and 1 for alive (Table 2).

Table 2. Number of records (piglets), unadjusted means, and SD for individual piglet survival in 1st parity.

Trait	N^1	Mean	SD
Individual piglet survival at birth, % (SVB)	229 651	91,0	28,6
Individual piglet survival after birth to 3 wk, % (SV0-3)	208 996	84,4	36,3
Individual piglet survival until 3 wk, % (SV3)	229 651	76,8	42,2

Statistical models

Litter traits across parity were analysed in 2-trait models, the relationship among LB, and survival traits in 2 3-trait models (LB-SB-TD and LB-DS-TD). 5-trait models were used to analyze the interrelationship of all litter traits (LB-TD-LW3-SDLW3-LW3) within parity. The statistical model was:

$$y = Xb + Za + e$$

where y = a vector of observations; and b = a vector of fixed effects including herd-year and month of farrowing in both parities, and age at 1st farrowing additionally in the 1st parity as a linear covariable; a = a vector of additive genetic effects of the sow; e = a vector of residual effects; X and Z = appropriate incidence matrices.

Individual piglet survival was analyzed using the model:

$$y = Xb + Wl + Z_a a + Z_m m + e$$

The fixed effects were herd-year and month at birth as well as no. piglets born as a linear covariate; a and m = vectors of direct and maternal additive effects of the piglet and sow, respectively; l = a vector of litter effects; W, Z_a, and Z_m = appropriate incidence matrices. The analyses were carried out using DMU-AI, version 4.7 (Madsen and Jensen, 2008). Total heritability was defined as $h^2_t = (\sigma^2_a + 0,5\sigma^2_m + 1,5\sigma_{am}) / \sigma^2_p$.

Results and discussion

Heritablitity estimates for LB in 1st and 2nd parity was 0,11±0,01 and 0,10±0,02, respectively. While heritability estimates for SB (1st parity: 0,08±0,01; 2nd parity: 0,09±0,02) and DS (1st parity: 0,07±0,01; 2nd parity: 0,05±0,01) were lower, the estimates for TD (1st parity: 0,11±0,01; 2nd parity: 0,11±0,01) were on the same level as for LB. Estimates for W and SDLW3 ranged from 0,08 to 0,12 and were slightly higher in the 2nd parity, while the highest estimates were for LW3 in 1st (0,15±0,01) and 2nd parity (0,16±0,02). These estimates are within the range of heritability estimates in the literature (e.g., Damgaard et al., 2003; Serenius et al., 2004; Wolf et al., 2008). The genetic correlations between 1st and 2nd parity for LB

and mortality traits varied from 0,93 for LB to 0,99 for DS (results not shown) and corresponded to the estimates by Arango et al. (2005). For these traits a repeatability model accounting for the increase of variances across parities could be used.

Results of the genetic relationship among mortality traits and LB are shown in Table 3. Genetic correlations between LB and SB were around 0 in the 1st parity, and slightly positive in the 2nd, while the correlations between LB and DS in 1st and 2nd parity were rather high. Similar results were reported by Hermesch (2001) sustaining that selection for LB leads to an increase in preweaning piglet mortality. As expected, SB, and in particular DS, were highly correlated with TD, of which they constitute components.

Table 3. Genetic correlations (SE) among piglet mortality traits and number of live born piglets in 1st and 2nd parities. (Traits see Table 1).

Trait[1]	1st parity	2nd parity
LB – SB	-0,04 (0,10)	0,29 (0,17)
LB – DS	0,66 (0,06)	0,47 (0,12)
SB – TD	0,75 (0,05)	0,79 (0,08)
DS – TD	0,90 (0,02)	0,92 (0,03)

Table 4 shows genetic correlations among the economically most important reproductive traits and piglet mortality. The genetic correlations between LB and W were high in both parities, those between LB and LW3 intermediate. The relationship between TD and LB was similar to that between DS and LB shown above. However, the correlations of TD with W and LW3 were low and not significant. SDLW3 is a measure of evenness of the litter. The genetic correlation of SDLW3 with TD was slightly positive, and with W slightly negative. At the age of 3wk most piglets with low birth weight will have died. Thus, SDLW3 cannot reflect piglet survival as well as within litter variation of piglet weight at birth would do. Estimates of Damgaard et al. (2003) for relationships between within litter variation both, at birth and 3 wk, and piglet survival were not significant.

Table 4. Genetic correlations (SE) among litter traits in 1st litter (above diagonal) and 2nd litter (below diagonal). (Traits see Table 1).

Trait[1]	LB	TD	W	SDLW3	LW3
LB		0,44 (0,07)	0,78 (0,04)	-0,12 (0,10)	0,41 (0,06)
TD	0,49 (0,12)		-0,14 (0,09)	0,19 (0,09)	-0,12 (0,08)
W	0,80 (0,06)	-0,08 (0,15)		-0,28 (0,10)	0,13 (0,05)
SDLW3	-0,12 (0,16)	0,29 (0,15)	-0,24 (0,15)		0,29 (0,08)
LW3	0,54 (0,09)	-0,13 (0,13)	0,12 (0,06)	0,14 (0,13)	

Results of genetic parameters for individual piglet survival are presented in Table 5. Animal (direct) and maternal genetic variances were similar for SV0-3 and SV3,

while for SVB the maternal genetic component was about twice as high as the animal component. Estimates of heritability for total liability were about double of those for direct heritability. Genetic correlations between animal and maternal genetic effects were low, but positive, while in other studies negative relationships were reported (e.g., Su et al., 2008; Arango et al., 2006; Knol et al., 2002).

Table 5. Estimates of animal additive genetic (V_a), maternal genetic (V_m), and litter variances (V_l), direct (h^2_d) and maternal heritability (h^2_m), and genetic correlations between direct and maternal genetic effects ($r_{(a,m)}$) for liabilities of individual piglet survival at different stages in 1st litters[1]. (Ve =1, SE in parenthesis; traits see Table 2).

Trait	V_a	V_m	V_l	h^2_d	h^2_m	h^2_t	$r_{(a,m)}$
SVB	0.010	0.023	0.083	0.009	0.021	0.021	0.063
	(0.003)	(0.005)	(0.005)	(0.002)	(0.004)	(0.005)	(0.181)
SV0-3	0.014	0.016	0.072	0.013	0.014	0.027	0.326
	(0.003)	(0.003)	(0.004)	(0.003)	(0.003)	(0.005)	(0.154)
SV3	0.013	0.015	0.056	0.012	0.014	0.021	0.101
	(0.002)	(0.003)	(0.003)	(0.002)	(0.003)	(0,004)	(0,141)

Based on the present results, selection for LB would be efficient to increase W, but at the cost of an increase in mortality (TD and DS). Selection for piglet survival on litter level would not have a negative impact on the direct component of survival of the individual piglet. However, considering both, the maternal and the individual, components on the piglet level would be most efficient as the genetic correlation between them is rather low.

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