

**Title:** Genetic improvement of farrowing rate and non-productive days in swine by selection for litters per sow per year - **NPB #09-204**

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### Industry Summary

The first purpose of this study was to determine the genetic and phenotypic correlations between maternal and post-weaning traits from a seedstock swine breeding system. The post-weaning traits examined included backfat (BF), percent lean (PCL) and days to market (D100), all adjusted to 100kg live weight. The strongest phenotypic correlation was between PCL and BF at  $-0.72$  ( $P < 0.05$ ). The genetic correlations between LSY and each of the post-weaning traits (BF, PCL, and D100) were  $0.02$ ,  $-0.16$ , and  $0.26$  ( $P > 0.05$ ), respectively. The correlations between litters per sow per year and post-weaning traits suggest that selecting based on litters per sow per year should not negatively impact the post-weaning traits in the herd. The direction of the correlation between number born alive and post-weaning traits was non-significant from this study. The second purpose of this study was to determine the genetic control of LSY and the relationship between individual sires breeding values (BV) for litters/sow/year (LSY) and progeny farrowing rate means. The heritability of LSY from this study was found to be low ( $< 0.15$ ). This suggests that BLUP based breeding value estimation must be used to make genetic progress in LSY. The correlation between the LSY BV and the sire progeny mean farrowing rate was  $0.21$  for those sires who had 10 or more daughters. The correlation between LSY BV and sire progeny mean for farrowing rate suggests that selecting for LSY could positively impact farrowing rate, and thereby reduce non-productive sow days.

### Keywords

Swine, reproduction, selection, litters/sow/year, farrowing rate

### Scientific Abstract

The first purpose of this study was to determine the genetic and phenotypic relationships between litters per sow per year (LSY) and other economically important reproductive and post-weaning traits from a commercial swine breeding company. Determining the genetic and phenotypic correlations among traits can help breeders evaluate the expected impacts their selection decisions have on other economically important production traits that may or may not be included in the selection criteria. This is particularly important when considering reproductive and post-weaning traits because of the undesirable genetic relationships that typically exist between reproductive and post-weaning traits. There were 32,602 litter records from 7,674 sows used in this study. The sows were born between the years 1992 and 2009. Post-weaning traits were recorded on male and female pigs. This data set has 44,040 growth records. Starting in 2003, post-weaning traits were measured on gilts before they entered the breeding herd. Data was collected from 4 herds with a single production system. The traits collected included number born alive (NBA), wean to estrus (W2E), adjusted back fat (BF), percent lean (PCL), and days to 100 kg (D100). Litters per sow per year (LSY) were calculated based on recorded information. Number born alive and wean to estrus were recorded for every litter produced in the herd. Genetic parameter estimates were calculated in ASREML. The model used for the reproductive traits contained fixed effects of parity, contemporary group, and breed. Age at first successful mating was fitted as a quadratic covariate,

and animal and a permanent environment were fitted as random effects. The model used for the post-weaning growth traits contained fixed effects of contemporary group, sex, feeder type, and breed. Animal and a common litter effect were fitted as random effects. The heritability estimates were as follows: 0.15 for NBA, 0.03 for LSY, 0.03 for W2E, 0.52 for BF, 0.33 for D100, and 0.36 for PCL. The genetic correlation between LSY and W2E is large and favorable. The genetic correlations between LSY and the three post-weaning traits (BF, D100, and PCL) have large standard errors and are unclear in direction. Some economically important traits can be favorably changed indirectly with selection on LSY; however, a selection index will be needed to ensure that post-weaning growth traits are not adversely affected by selection on LSY.

The second purpose of this study was to determine the relationship between individual sires' breeding values (BV) for litters/sow/year (LSY) and progeny farrowing rate means. Breeding values for LSY were estimated using ASREML and the heritability for this dataset was found to be 0.11 ( $P < 0.01$ ). A data set from a production system consisting of records for 48,662 sows from 9 herds was used for this analysis. Landrace, Large White, and  $F_1$  ( $Y \times L$  or  $L \times Y$ ) crossbred females were included in the analyses. Breed, contemporary group of last litter, and parity of last litter were fitted as fixed effects. Age at first service was included as a quadratic covariate. Animal was fitted as a random effect. The heritability estimate of LSY was 0.11. Sire progeny farrowing rate means were calculated as total number of services of the sire's daughters divided by the total litters farrowed from the sire's daughters. The Spearman rank correlation between the LSY BV and the farrowing rate of the sires was calculated using SAS software. When all sires were included in the analysis (4,115 sires), the correlation between the sire's LSY BV and mean for farrowing rate was 0.38 ( $P < 0.01$ ). When sires with 5 or more daughters were included (980 sires), the correlation was 0.45 ( $P < 0.01$ ). When sires with 10 or more daughters were included (733 sires), the correlation was 0.49 ( $P < 0.01$ ). When all sires were ranked based on their breeding values, the sire progeny mean farrowing rate of those sires in the top 25% of LSY BVS was 89.0%. The sire progeny mean farrowing rate for the bottom 25% was 74.3%. This suggests that improving LSY could result in indirect improvement of farrowing rate.

## Introduction

In our current times of high feed prices and increasing expense of inputs, the cost of maintaining the sow herd has risen greatly over the past few years. If a sow is not gestating a successful litter, or nursing a litter, she is not generating income for the pork producer. 'Non-productive sow days' is the term used for these instances. The major traits impacting non-productive sow days (NPD) are farrowing rate, and the intervals of entry to first service, weaning to service, and weaning to removal. Weaning to service and/or weaning to estrus interval are measurable traits, and have been shown to have a genetic base that will respond to selection. However, the number of NPD gained from successful selection on these two traits is rather minimal. The trait with the most potential to reduce NPD is farrowing rate. When a sow is bred, but does not have a litter, the number of NPD generated is 21 at a minimum, and can be much greater depending on the management of the sow herd. The problem is it is virtually impossible to directly select for farrowing rate. When a sow is bred, but does not farrow, the cause is not clear due to the possibility of several factors. Was the sow infertile? Was the semen bad? Did the inseminator do a poor job? Was the weather too hot? When a situation such as this exists, with no clear cause of the litter being lost, direct selection will not work. However, indirect selection may be possible if there is another trait that is closely associated with farrowing rate, and is routinely measured at the farm. One trait that is routinely measured on the sow farm, that should be closely associated with farrowing rate, is litters per sow per year (LSY). Litters per sow per year is objectively measured as the proportion of breeding female days attributed to successful gestation days and expressed on an annualized basis. However, genetic improvement in reproductive efficiency by directly selecting for LSY has not yet been studied in depth. It may be possible to make a permanent genetic improvement in LSY (and indirectly improve farrowing rate) if LSY is found to have appropriate characteristics for making genetic improvement. To accomplish genetic improvement through selection, several areas must be considered about the trait of LSY. First, accurate data must be collected of adequate size from representative swine herds. Secondly, the distribution of the trait must be normal. Thirdly, the traits must have an adequate genetic control, or heritability to respond to selection. And fourthly, the genetic correlation between LSY and other economically important traits should not be unfavorable.

## Objectives

Indirect selection for increasing farrowing rate by selection for LSY has not yet been studied in depth. It may be possible to make a permanent genetic improvement in LSY (and indirectly improve farrowing rate and reduce non-productive sow days) if LSY is found to have characteristics appropriate for making genetic improvement. These characteristics include having a normal distribution, having adequate genetic control to respond to selection, and not being genetic correlated in an undesirable manner to other economically important traits. In order to determine if the trait of LSY has these characteristics, the first step will be to secure access to datasets from multiple swine farms where the traits that influence NPD are accurately measured, and the pedigree structure of the sows in the herd are accurately maintained. From these datasets the distribution of the traits can be examined as to their normality. If LSY expresses a normal distribution, then the variance components of LSY can be examined, and broken down into genetic versus non-genetic causes. This will tell us if LSY has an adequate heritability or genetic control to respond to selection. The estimation of variance components would then be expanded to a multiple trait procedure, to examine if any genetic correlations exist between LSY and other reproductive traits of interest.

## Materials and Methods

The data for the first part of this study was obtained from a commercial swine breeding company in Europe. The data were from nucleus and multiplication herds, and was collected on purebred individuals. The dataset contained 32,602 litter records from Landrace and Large White sows from November 1992 to December 2010. A total of 7,674 sows from 4 herds were used in the analysis. There were 4,149 Landrace and 2,505 Large White sows with 21,162 and 11,440 litters, respectively. Litter weaning age for these herds was  $27 \pm 8$  days. Number born alive (NBA) and wean to estrus (W2E) were collected on every litter. Litter per sow per year (LSY) were calculated based on the records for each sow. The post-weaning traits in the data set were adjusted backfat (adjusted to 100 kg) (BF), days to 100 kg (D100), percent lean (PCL). The post-weaning traits were collected beginning in 1999 resulting in 44,040 records. Table 1 shows the means and standard deviations for each trait.

LSY was calculated using the formula:

$$\frac{(\text{number of days gestating})/115}{(\text{number of days in the breeding herd})/365}$$

where the number of days in the breeding herd was defined as the number of days from the first successful mating of the sow to the weaning date of the last litter of the sow. Number of days gestating was defined as the sum of each gestation length of the sow.

The heritability of each of the traits was estimated. The following model was used for the reproductive and lifetime production traits:

$$y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_k + X_l\tau_1 + X_l^2\tau_2 + \delta_l + \varphi_l + \varepsilon$$

where  $y_{ijkl}$  is the response for sow  $l$  that is breed  $i$ , parity  $j$ , and in contemporary group  $k$ ,

$\mu$  is the overall mean,  $\alpha_i$  is the effect of breed  $i$ ,  $\beta_j$  is the effect of parity  $j$ ,  $\gamma_k$  is the effect of contemporary group  $k$ ,  $X_l\tau_1 + X_l^2\tau_2$  is the effect of age at first successful mating ( $X$ ) for sow  $l$ ,  $\delta_l$  is the random effect of sow  $l$ ,  $\varphi_l$  is the permanent environmental effect fitted as an uncorrelated random, and  $\varepsilon$  is the residual.

Contemporary group was defined as the herd, year, and month of farrowing for NBA, and W2E. The contemporary group for the lifetime traits was defined as herd, year, and season (three month period) for the last farrowing of the sow. Age at first successful mating was evaluated for all reproductive and lifetime production traits. Results of these analyses

found that age at first successful mating should be included as a quadratic covariate. Interactions were assumed to be small and insignificant. The permanent environmental effect was assumed to be distributed  $N(0, I\sigma_p^2)$ .

The following model was used for the post-weaning traits:

$$y_{ijkmnl} = \mu + \alpha_i + \beta_j + \gamma_k + \tau_m + \delta_n + \varphi_l + \varepsilon$$

where  $y_{ijkmnl}$  is the response for animal  $n$  that is breed  $i$ , sex  $j$ , contemporary  $k$ , feeder type  $m$  and litter  $l$ ,

$\mu$  is the overall mean,

$\alpha_i$  is the effect of breed  $i$ ,

$\beta_j$  is the effect of sex  $j$ ,

$\gamma_k$  is the effect of contemporary group  $k$ ,

$\delta_n$  is the random effect of animal  $n$ ,

$\varphi_l$  is the common litter effect fitted as an uncorrelated random, and

$\varepsilon$  is the residual.

Heritabilities were calculated as sow variance divided by the total variance. Variance components were estimated using ASREML (Gilmour et al., 2006). Correlations were calculated using the covariance between the two traits and the variances of the two traits. The standard errors for the heritabilities and correlations were calculated appropriately for the quotient of two random variables (Lynch and Walsh, 1998).

The data used in the second part of this study was obtained from 9 herds in a single production system in Asia. Data was collected from October 1993 to June 2009. A total of 231,858 records from 48,622 sows were used in the analysis. Sows were either Landrace (17,834 sows), Large White (13,836 sows), or  $F_1$  (Y×L or L×Y) crossbred (16,992 sows) females. In the dataset, 80,806 records were from the Landrace sows, 68,499 records were from the Large White sows, and 82,553 records were from the crossbred sows. Number born alive was recorded for each litter. Lifetime born alive (LTBA) was calculated by the number born alive for each litter of the sow. Litters per sow per year was extracted for PigCHAMP™ herd management software. Table 1 shows the simple means and standard deviations of each trait.

The heritability of each of the traits was estimated. The following model was used for the estimation of the heritabilities:

$$y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_k + X_l\tau_1 + X_l^2\tau_2 + \delta_l + \varphi_l + \varepsilon$$

where  $y_{ijkl}$  is the response for sow  $l$  that is breed  $i$ , parity  $j$ , and in contemporary group  $k$ ,

$\mu$  is the overall mean,

$\alpha_i$  is the effect of breed  $i$ ,

$\beta_j$  is the effect of parity  $j$ ,

$\gamma_k$  is the effect of contemporary group  $k$ ,

$X_l\tau_1 + X_l^2\tau_2$  is the effect of age at first service mating ( $X$ ) for sow  $l$ ,

$\delta_l$  is the random effect of sow  $l$ ,

$\varphi_i$  is the permanent environmental effect fitted as an uncorrelated random, and

$\varepsilon$  is the residual.

Contemporary group was defined as the herd, year, and month of the farrowing for NBA. For LTBA and LSY, contemporary group was defined as the herd, year, and season (4 month period) for the last litter of the sow. Permanent environment was only fitted for NBA. The permanent environmental effects were assumed to be independent and identically normally distributed with the variance  $\sigma_p^2$ . The software used to estimate the heritabilities and correlations between the traits was ASREML (Gilmour et al., 2006). The correlations and standard errors are calculated as described in Lynch and Walsh (1998). This model was also used to estimate the LSY breeding values of the sires.

A total of 251,992 service records were collected on 47,898 sows. Sire progeny mean farrowing rates were calculated by the total number of litters from all daughters divided by the total number of services on all daughters. The average number of daughters per sire was 10. The mean farrowing rate for the sires was  $82.9\% \pm 16\%$ . The maximum was 100%, and the minimum was 5.3%. The correlation between sire progeny means and LSY BV was estimated using the PROC CORR procedure in SAS (SAS Inst., Inc., Cary, NC). Both the Pearson and Spearman Rank correlations were estimated. PROC UNIVARIATE was used to determine range for each percentile of the LSY BVs. The average farrowing rate was calculated for each 5% percentile of the breeding values using the PROC MEANS procedure.

## Results and Discussion

From the first part of the study, the additive genetic variances along with the residual variances are shown for each of the traits analyzed. The additive genetic variance was 0.003, 0.64, 1.39, 46.05, 1.83, and 1.42 for LSY, W2E, NBA, D100, PCL, and BF, respectively. The variance explained by the permanent environment is shown in Table 1 for NBA and W2E. The variation due to permanent environment was 0.81 and 0.73 for NBA and W2E, respectively. The proportion of the total variation in NBA explained by the permanent environment was 0.09, and for W2E, the proportion was 0.04. The variance due to the common litter effect is also shown in Table 1 for D100, BF, and PCL. The variation due to a common litter effect was 20.01, 0.22, and 0.16 for D100, PCL, and BF, respectively. The proportion of the total variation in D100, PCL, and BF due to a common litter effect was 0.12, 0.04, and 0.05, respectively.

The heritabilities for BF, D100, and PCL were 0.41, 0.33, and 0.36, respectively. The heritabilities for LSY, NBA and W2E are 0.03, 0.15, and 0.03, respectively. These heritabilities are shown in Table 3. The genetic and phenotypic correlations among the reproductive and post-weaning growth traits are shown in Table 2. The genetic correlation between LSY and W2E is -0.96 which is favorable. The genetic correlations ( $\pm$ SE) between LSY and the three post-weaning traits are 0.26 ( $\pm$ 0.19) D100, -0.16 ( $\pm$ 0.14) for PCL, and -0.02 ( $\pm$ 0.14) for BF. The genetic correlations between LSY and the post-weaning growth traits have large standard errors resulting in the direction of the correlation being unclear.

The results of this study show that LSY is lowly heritable and therefore, can be incorporated into a selection program and improved if a BLUP based breeding value estimation procedure is utilized. However, expected progress or improvement in LSY resulting from selection would be slow as is the case when genetically improving other reproductive performance traits through traditional selection methods.

Before including LSY in a selection program, its genetic correlations with other economically important traits must be considered. Selection for LSY would result in improvement for the trait as well as improvement for several other economically important traits; however, the impact of selection for LSY on some economically important traits, such as BF, D100, and PCL should be considered.

The genetic correlations between LSY and the three post-weaning traits (BF, PCL, and D100) were found to be unfavorable, but with large standard errors. The genetic correlations between the three post-weaning traits are similar to previously reported estimates in the scientific literature. This suggests that the genetic correlation estimations found in this study are within the range reported by other researchers. There have been few genetic correlation estimates

among lifetime reproductive traits and post-weaning growth traits. The estimations that have been reported have high standard errors. These high standard errors cause the correlation to be indistinguishable from zero.

Litters per sow per year is favorably correlated with W2E. This indicates that W2E can be improved through selection on LSY. The correlation between LSY and W2E may indicate that improving LSY can reduce the non-productive days in the sow herd. The reduction in non-productive days may result in increased profitability for the swine operation if market prices are favorable.

From the second part of the study, the heritabilities and genetic and phenotypic correlations of NBA, LTBA, and LSY were estimated to be 0.02, 0.12, and 0.11, respectively, and are shown in Table 4. The genetic correlation between LSY and NBA is indistinguishable from zero. These correlations would indicate that selecting for LSY would not affect the genetic potential for NBA. The genetic correlation between LSY and LTBA is 0.25, suggesting that as the genetic potential for LSY increases, the genetic potential for LTBA will also increase. These genetic correlations would suggest that there is no adverse relationship between LSY and the other two traits, NBA and LTBA.

The Pearson correlation between the sire LSY BVs and their mean for farrowing rate was 0.28 for all sires, 0.41 for sires with 5 or more daughters, and 0.43 for sires with 10 or more daughters. The Spearman rank correlations for the three groups of sires were 0.38, 0.45, and 0.49, respectively. It is clear that farrowing rate tended to improve as the LSY BV ranking improved. The sires in the top 25% according to their LSY BVs had an average farrowing rate of 89.0%, while sires in the bottom 25% had an average farrowing rate of only 74.3%. There is a clear division between the mean farrowing rates at the 45<sup>th</sup> percentile. At this point, there is greater than a 3% increase in the mean farrowing rate between adjacent percentiles. When only sires with 10 or more daughters were included in the rankings, the top 25% had an average farrowing rate of 87.0% and the bottom 25% had an average of 75.0%. With this group of sires, the division occurs at the 50<sup>th</sup> percentile. These divisions suggest that independent culling levels for LSY could be incorporated to help improve the farrowing rate of the herd.

The results of this study across two data sets indicate that LSY can be incorporated into a selection program to improve the efficiency of the breeding herd. The heritability of LSY was estimated to be from 0.03 and 0.11; with a standard error less than 0.02. The estimate of the genetic correlation between LSY and LTBA was also different from zero. This positive association between LSY and LTBA may mean that selection for improved LSY can indirectly select for an increased number of pigs born during a sow's lifetime. This favorable relationship may improve the overall production efficiency of the herd if sows are able to produce more litters in a year and more piglets in a lifetime. There was not a significant genetic correlation between LSY and NBA suggesting that selecting for LSY would not adversely affect the NBA of each litter.

The average LSY for this dataset was 2.12 with a standard deviation of 0.40. Assuming an average gestation length of 115 days, a 21 day weaning management, and a 5 day weaning to estrus interval, 2.59 is the maximum LSY that could be achieved with a successful first service after weaning. The shortest farrowing interval possible would be 141 days. The maximum LSY is calculated by  $365 / 141$ . Since the average LSY of the herd is 0.47 away from the maximum possible, there is room for improvement and efficient, successful selection is possible. There is also sufficient variation for improvement to be made through selection.

From this study, there is strong evidence for a favorable relationship between LSY and FR. Selection for LSY could result in the indirect improving of the overall herd FR, since sires with higher LSY BVs tended to have higher FRs. Improving the farrowing rate in the herd can improve the profitability of the herd by reducing the number of non-productive days associated with unsuccessful services, and the labor costs associated with multiple services.

**Table 1:**

Estimated variance components (proportion of total variance) for reproductive and post-weaning traits from an Irish commercial swine breeding company<sup>a</sup>

Trait <sup>b</sup>	Additive Genetic	Permanent Environment	Common Litter	Residual
Number born alive	1.39	0.81 (0.09)	-	7.25
Litters per sow per year	0.0008	-	-	0.025
Wean to estrus (d)	0.64	0.73 (0.04)	-	18.22
Adjusted backfat (mm)	1.42	-	0.16 (0.05)	1.89
Days to 100 kg	46.05	-	20.01 (0.12)	96.77
Percent lean	1.83	-	0.22 (0.04)	2.98

<sup>a</sup>The dataset contained 32,602 litter records of Landrace, and Yorkshire sows from November 1992 to December 2010. A total of 7,674 sows from 4 herds were used in the analysis. There were 44,040 growth records in that data set. Heritabilities were calculated using ASREML and a model as described in the text.

<sup>b</sup>Number born alive and wean to estrus were collected on every litter. Litters per sow per year was calculated as described in the text. Adjusted backfat (adjusted to 100 kg), days to 100 kg, and percent lean were calculated post-weaning.

**Table 2:**

Genetic (above the diagonal) and phenotypic correlations (below the diagonal) ( $\pm$ SE) for reproductive and post-weaning traits estimated from an Irish commercial swine breeding company<sup>a</sup>

	LSY	D100	PCL	BF	NBA	W2E
<b>LSY<sup>b</sup></b>	-	0.26 (0.19)	-0.16 (0.14)	0.02 (0.14)	-0.21 (0.28)	-0.96 (0.04)
<b>D100</b>	-0.01 (0.03)	-	0.33 (0.03)	-0.03 (0.04)	0.33 (0.09)	-0.27 (0.63)
<b>PCL</b>	0.03 (0.03)	0.21 (0.01)	-	-0.94 (0.01)	-0.02 (0.09)	0.64 (1.79)
<b>BF</b>	-0.03 (0.03)	-0.01 (0.01)	-0.74 (0.00)	-	0.03 (0.09)	-0.31 (0.97)
<b>NBA</b>	0.00 (0.01)	-0.01 (0.01)	-0.02 (0.02)	-0.01 (0.01)	-	-0.64 (0.31)
<b>W2E</b>	-0.25 (0.01)	0.01 (0.01)	0.01 (0.01)	0.00 (0.01)	-0.04 (0.00)	-

<sup>a</sup>The dataset contained 32,602 litter records of Landrace, and Yorkshire sows from November 1992 to December 2010. A total of 7,674 sows from 4 herds were used in the analysis. There were 44,040 growth records in that data set. Correlations were calculated using ASREML and a model as described in the text.

<sup>b</sup>Number born alive (NBA) and wean to estrus (W2E) were collected on every litter. Litters per sow per year (LSY) was calculated as described in the text. Adjusted backfat (adjusted to 100 kg) (BF), days to 100 kg (D100), and percent lean (PCL) were calculated post-weaning.

**Table 3:**

Estimated heritability ( $\pm$ SE) for reproductive and post-weaning traits from an Irish commercial swine breeding company<sup>a</sup>

Trait <sup>b</sup>	Heritability ( $\pm$ SE)
Number born alive	0.15 ( $\pm$ 0.02)
Litters per sow per year	0.03 ( $\pm$ 0.02)
Wean to estrus (d)	0.03 ( $\pm$ 0.01)
Adjusted backfat (mm)	0.41 ( $\pm$ 0.01)
Days to 100 kg	0.28 ( $\pm$ 0.01)
Percent lean	0.36 ( $\pm$ 0.01)

<sup>a</sup>The dataset contained 32,602 litter records of Landrace, and Yorkshire sows from November 1992 to December 2010. A total of 7,674 sows from 4 herds were used in the analysis. There were 44,040 growth records in that data set. Heritabilities were calculated using ASREML and a model as described in the text.

<sup>b</sup>Number born alive and wean to estrus were collected on every litter. Litters per sow per year was calculated as described in the text. Adjusted backfat (adjusted to 100 kg), days to 100 kg, and percent lean were calculated post-weaning.

**Table 4:**

Heritabilities (on diagonal), genetic (above the diagonal) correlations, and phenotypic correlations (below the diagonal) ( $\pm$ SE) for reproductive traits estimated from a Thai swine production system<sup>a</sup>

	LSY	NBA	LTBA
LSY <sup>b</sup>	0.11 (0.01)	-0.03 (0.05)	0.16 (0.06)
NBA	-0.03 (0.05)	0.02 (0.002)	
LTBA	0.01 (0.01)		0.11 (0.01)

<sup>a</sup>The dataset contained 231,858 litter records of Landrace, Large White, and F1 cross sows from October 1993 to June 2009. A total of 48,662 sows from 9 herds were used in the analysis. There were 44,040 growth records in that data set.

<sup>b</sup>Number born alive (NBA) was collected on every litter. Lifetime born alive (LTBA) was calculated as the sum of each NBA record for the sow. Litters per sow per year (LSY) was extracted from PigCHAMP<sup>TM</sup>. Heritabilities and correlations were estimated using a model as described in the text.