Genetic correlations between gestation length

and litter traits of sows

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Abstract

The aim of this study was to estimate genetic correlations between gestation length (GL) total number of piglets born (TB), number of piglets born alive (BA) and number of stillborn piglets (SB). Data of Landrace (LR), Large White (LW) and Duroc (DR) sows from one nucleus farm were analyzed. Data used in this study were 28,809 records of sows farrowing during 2006 to 2019. The factors effecting traits were examined by using GLM procedure in SAS program. Variance and covariance components were estimated using AIREMLF90 program. The model was applied with fixed effects for contemporary group, breed and parity, and random effects for animal, permanent environmental effect and residual effect. Heritabilities ranged from 0.26 to 0.32, 0.05 to 0.13, 0.07 to 0.12 and 0.01 to 0.03 for GL, TB, BA and SB, respectively. Genetic correlations between TB and BA were high (0.99) in all breeds. Genetic correlations of GL with TB and BA were negative. Genetic correlations between TB, BA and SB were positive. All the results suggest that selection for larger TB will increase BA and SB in LR and DR as well as decrease GL in DR. However, in LR and LW, selection for larger TB would probably result in a correlated decrease in GL. In regards to the positive genetic correlation between TB and SB, piglet mortality should be considered as a selection criterion to improve piglet survival. This study presents breed-specific estimates of genetic parameters for GL and litter traits in Thailand. It provides information to apply in breeding program for specific breed.

Introduction

Gestation length (GL) in sows is an important trait for farm management. In general, GL in sows is 114 to 116 days, with only 10% of sows farrowing before 114 days (Decaluwe et al., 2012). Factors that affect to GL in sows consist of breed, parity, season, genetic of piglets and total number of piglets born (Sasaki and Koketsu, 2007; Rydhmer et al., 2008). Studies have shown relationships between GL and litter traits which include total number of piglets born, number of piglets born alive, and number of stillborn piglets (Rydhmer et al., 2008; Vanderhaeghe et al., 2011; Imboonta and Kuhaaudomlarp, 2012). These studies indicated that sows with GL shorter than 114 days had significantly more stillborn piglets and a larger litter size compared to sows with a normal GL (114 to 117 days). According to the genetic studies of GL, genetic correlation between GL and total number of piglets born was negative (Rydhmer et al., 2008; Imboonta and Kuhaaudomlarp, 2012). It was suggested that selection for increase total number of piglets born leads to short GL. Nowadays, a major focus of Thai pig producers is to increase number of litters per sow per year. This selection objective might have effect on GL of sows. On the contrary, natural gestation length has risen as the total number of piglets born has risen. This is confirmed by a gradual increase in GL, on average 115.5 to 116.9 days that was reported in previous studies (Rydhmer et al., 2008; Imboonta and Kuhaaudomlarp, 2012; Udomchanya et al., 2019). However, there have been few reports on genetic parameters of and genetic correlations between GL and litter traits, especially in Thailand. Imboonta and Kuhaaudomlarp (2012) studied the genetic association between GL and litter traits over six maternal breed groups (Landrace, Large White and their 50% as well as 75% crossbreds). Genetic parameters for specific breed in maternal lines and paternal lines, especially for Duroc that was a popular paternal breed in Thailand have not been investigated. It is, therefore, important to know the degree of genetic determination of GL, litter traits and their relationships to guide the effectiveness of selection on them. The aim of this study was to estimate genetic correlation among gestation length, total number of piglets born, number of piglets born alive and number of stillborn piglets. The result from this study may provide benefits for swine producer in selection plan and breeding.

Materials and Methods

Data: All animals in this study were raised in accordance with guidelines of the Department of Livestock Development, Ministry of agriculture and Cooperatives, Thailand. Data used in this study were collected from one nucleus herd located in the east part of Thailand and taken from sows that farrowed during the period from January 2006 to June 2019. The data contained 28,809 farrowing records collected from Landrace (LR), Large White (LW) and Duroc (DR) sows. As the parity of sows at the moment of data collection varied between 1 and 6. The studied traits included GL, number of piglets born alive (BA), number of stillborn piglets (SB) and total number of piglets born (TB) which included BA and SB.

Farm management: Sows were raised in evaporative cooling system building and were vaccinated according to the veterinarian's recommendations which were vaccines for swine fever, pseudorabies and foot and mouth disease. Sows were fed with sufficient amounts to meet their nutritional requirement (National, Research Council 1998; National, Research Council 2012). Water was available ad libitum via drinking nipple system. Gilts received boar stimulation at approximately 26 weeks of age and were mated on the second observed estrus, or later, at a minimum age of 32 weeks and at a minimum weight of 120 kilograms. Estrus detection was performed with presence of boars twice daily, in the morning and evening. Females were artificially inseminated with same boar semen, totaling three and two times per estrus for gilts and sows, respectively. Sows were moved to farrowing house one week before the expected farrowing date. Sows were accommodated day and night during parturition by farrowing house workers and were interfered with as little as possible. In case of dystocia, manual assistance was administered to sows but it was not recorded. GL was calculated as the number of days between first insemination administered and farrowing.

In this population, breeding programs are specialized between sire and dam lines, with different selection objectives. Sire line was mainly selected for production traits, while dam lines were selected for reproduction traits. Replacement gilts, in this study, were selected according to the selection indexes. For sire line (DR), selection index comprised of estimated breeding value of average daily gain and backfat thickness, accounting for 50% and 50% of the total selection effect, respectively. For dam lines (LR and LW), the selection index comprised of estimated breeding value of average daily gain, backfat thickness and TB, accounting for 20%, 20%, and 60% of the total selection effect, respectively. In addition, sows were culled based on poor performance, such as low TB, leg problems, disease and old age, with more than 6 parities.

Statistical analyses: Statistical analyses were performed using SAS software package, version 9.4 (SAS, 2013). Descriptive statistics were carried out using MEANS and FREQ procedures for continuous and categorical data, respectively. Based on raw data, frequency of GL together with the mean number of TB, BA and SB were used to plot in Figure 1 in order to reveal the relationship between them. Fixed effects were examined for their significance ($P<0.05$), using the generalized linear model (GLM) procedure. Year-month at mating (YMM) and year-month at farrowing (YMF) were considered as the contemporary groups. Parity number was classified into 6 groups including 1, 2, 3, 4, 5, and 6. The following model was used for GL: $y_{ijkl} = YMM_i + breed_j + parity_k + error_{ijkl}$, while the following model was used for TB, BA and SB: $y_{ijkl} = YMF_i + breed_j + parity_k + error_{ijkl}$. The effect of YMM_i (162 herd-year-months at mating), YMF_i (162 herd-year-months at farrowing), $breed_j$ (LR, LW or DR) and $parity_k$ (6 classes) were fixed.

For analysis of genetic parameters, farrowing records of each breed were analyzed separately. A

statistical model was fitted using AIREMLF90 (Misztal *et al.*, 2018). The statistical model, in matrix notation, was

$$y = Xb + Za + Wpe + e$$

where y is the observation vector of studied traits (four traits simultaneously, i.e. GL, TB, BA and SB); b is the vector of fixed effects; a is the vector of random additive genetic effects of animals, which was assumed to be distributed $N(0, A\sigma_a^2)$, where A is the numerator relationship matrix among animals; pe is a vector of permanent environmental effects, assumed to be distributed $N(0, I\sigma_{pe}^2)$, uncorrelated with other random effects and where I is the identity matrix; and e is a vector of residual effects, which was assumed to be distributed $N(0, I\sigma_e^2)$. Incidence matrix X related records to fixed effects, incidence matrix Z related

records to additive genetic random effects and incidence matrix W related records to permanent environmental random effects.

The model used for GL included parities and year-month at mating as fixed effects, while the model used for TB, BA and SB included parities and year- month at farrowing as fixed effects. Heritabilities $[h^2 = \sigma_a^2/(\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2)]$, permanent environmental variance in proportion to total variance $[c^2 = \sigma_{pe}^2/(\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2)]$ and repeatability $[r = \sigma_a^2 + \sigma_{pe}^2/(\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2)]$ were calculated from variance components of additive genetic animal effect (σ_a^2), permanent environmental effects (σ_{pe}^2) and residual (σ_e^2) (Falconer and Mackay, 1996).
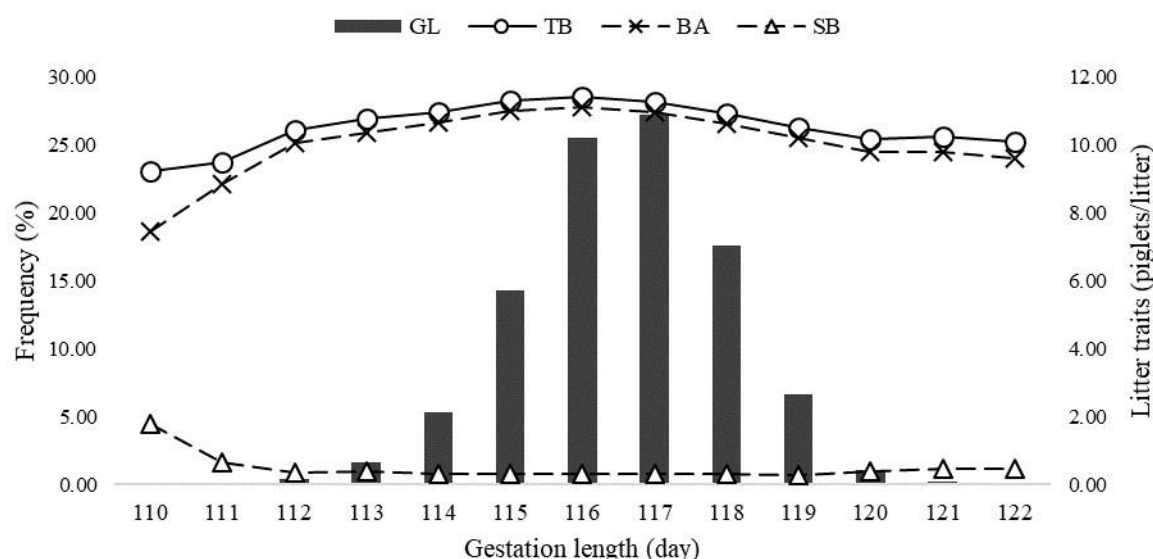

Figure 1   Distribution of gestation length (GL), average number of piglet born in total (TB), average number of piglets born alive (BA) and average number of stillborn piglets (SB), in relation to gestation length. N = 28,809 records.

Results

Descriptive statistics: Number of records, number of sows, means and standard deviations for GL, TB, BA, and SB classified by breeds are given in Table 1. Data used in this study was collected from 7,905 sows. The average parity of studied sows was 2.98. The distribution of individual GL in relation to means of litter traits is presented in Figure 1. This result shows that 84.60% of all 28,809 farrowing records took place between 115 and 118 days after service. In addition, the mean number of TB and BA for this GL group were higher than those from GL<115 days and GL>118 days. The corresponding average TB and BA for the sows with GL between 115 and 118 days were 11.23 and 10.92 piglets/litter, respectively. Whereas TB and BA for the sows with GL<115 were 10.17 and 9.48 piglets/litter, respectively and sows with GL>118 days were 10.39 and 10.01 piglets/litter, respectively. Furthermore, sows with GL in range of 115 to 118 days had the lowest SB (0.30 piglets/litter) while sows with GL<115 days and GL>118 days had high SB, on average 0.70 and 0.40 piglets/litter, respectively.

Breed effect: Least square means and standard errors of studied traits are shown in Table 2. The results showed that LR sows had a significantly longest GL and also had the highest TB and BA compared to LW and DR sows (*P*<0.001). On the other hand, LW sows had significantly lower SB than LR and DR sows (*P*<0.001).

Parity effect: Least square means and standard errors of GL, TB, BA and SB classified by parity are presented in Table 3. From the present data, sows in each parity had similar value of GL. However, GL in the first and second parity were significantly longer than those in the following parities (*P* < 0.001). The results showed that the best reproductive performance in terms of high TB and BA as well as low SB was found in 3rd to 5th parity sows.

Genetic parameters: Heritability (h²), permanent environmental variance in proportion to total variance (c²) and repeatability (r) of GL, TB, BA, and SB in LR, LW and DR sows are shown in Table 4. Heritability estimates for GL varied from 0.26 to 0.32. Heritabilities of TB and BA ranged between 0.11 and 0.13 in LR and LW sows, whereas lower heritabilities were obtained

for DR sows (0.05 and 0.07 for TB and BA, respectively). Low heritabilities were estimated for SB.

The permanent environmental variances in proportion to total variances for GL and SB were low. Moderate proportions of permanent environmental variance were found for TB (0.18 to 0.30) and BA (0.19 to 0.29). Repeatability estimates for GL, TB and BA were low (ranging from 0.31 to 0.40), whereas the repeatability estimates for SB were negligible.

Genetic and phenotypic correlations among the studied traits in LR, LW, and DR are presented in Table 5. Gestation length had low genetic correlations with TB and BA for all breeds, varying from 0.00 to -0.16. However, significant negative genetic correlations (*P*<0.05) were observed between GL and TB in DR as well as between GL and BA in both LR and DR. Strong positive genetic correlations were obtained between TB and BA (0.99) in all breeds. Genetic correlations of SB with other traits showed a notable difference between breeds. For LR, SB was positively and significantly correlated with GL (0.41), TB (0.48) and BA (0.42). In contrast, SB of LW exhibited only non-significant genetic correlations with GL, TB and BA. The significant genetic correlations appeared between GL and SB (-0.24), TB and SB (0.79) together with BA and SB (0.84) in DR.

Phenotypic correlations between GL and litter traits (TB, BA and SB) were very low (-0.09 to 0.00) in all breeds (Table 5). However, low positive phenotypic correlations (0.30 to 0.36) were found between TB and BA.

Table 1   Number of records and sows as well as means ± SD (Min - Max) of the studied traits classified by breed

Variable[1]	Landrace	Large White	Duroc	All breeds
No. of records	14,112	9,655	5,042	28,809
No. of sows	3,782	2,665	1,458	7,905
GL (days)	116.81 ± 1.34	116.67 ± 1.38	115.63 ± 1.49	116.56 ± 1.45
	(110 - 122)	(110 - 122)	(110 - 122)	(110 - 122)
TB (piglets/litter)	11.70 ± 3.02	11.32 ± 2.96	9.30 ± 2.60	11.15 ± 3.06
	(1 - 25)	(1 - 25)	(1 - 24)	(1 - 25)
BA (piglets/litter)	11.37 ± 3.02	11.05 ± 2.98	8.98 ± 2.64	10.85 ± 3.07
	(1 - 20)	(1 - 20)	(1 - 20)	(1 - 20)
SB (piglets/litter)	0.33 ± 0.65	0.27 ± 0.58	0.32 ± 0.62	0.30 ± 0.62
	(0 - 10)	(0 - 12)	(0 - 8)	(0 - 12)
Parity	3.06 ± 1.66	2.96 ± 1.63	2.84 ± 1.58	2.98 ± 1.64
	(1 - 6)	(1 - 6)	(1 - 6)	(1 - 6)

[1] GL = gestation length, TB = total number of piglets born, BA = number of piglets born alive,
   SB = number of stillborn piglets

Table 2   Least square means ± standard errors of gestation length (GL), total number of piglets born, (TB) number of piglets born alive (BA) and number of stillborn piglets (SB) classified by breed

Breed	No. of records	GL (days)	TB (piglets/litter)	BA (piglets/litter)	SB (piglets/litter)
Landrace	14,112	116.73 ± 0.01[a]	11.93 ± 0.03[a]	11.58 ± 0.03[a]	0.35 ± 0.01[a]
Large white	9,655	116.65 ± 0.01[b]	11.44 ± 0.03[b]	11.15 ± 0.03[b]	0.29 ± 0.01[b]
Duroc	5,042	115.61 ± 0.02[c]	9.40 ± 0.04[c]	9.06 ± 0.04[c]	0.34 ± 0.01[a]

[a-c] Least square means in the same column with different superscript differ (*P*<0.001)

Table 3   Least square means ± standard errors of gestation length (GL), total number of piglets born (TB), number of piglets born alive (BA) and number of stillborn piglets (SB) classified by parity

Parity	No. of records	GL (days)	TB (piglets/litter)	BA (piglets/litter)	SB (piglets/litter)
1	7,086	116.37 ± 0.02[a]	10.75 ± 0.03[b]	10.41 ± 0.04[b]	0.33 ± 0.01[b]
2	5,850	116.39 ± 0.02[a]	10.48 ± 0.04[c]	10.20 ± 0.04[c]	0.28 ± 0.01[c]
3	5,156	116.32 ± 0.02[b]	11.13 ± 0.04[a]	10.82 ± 0.04[a]	0.31 ± 0.01[b]
4	4,437	116.32 ± 0.02[b]	11.17 ± 0.04[a]	10.85 ± 0.04[a]	0.33 ± 0.01[b]
5	3,631	116.30 ± 0.02[b]	11.13 ± 0.05[a]	10.79 ± 0.05[a]	0.34 ± 0.01[b]
6	2,649	116.29 ± 0.03[b]	10.87 ± 0.06[b]	10.50 ± 0.06[b]	0.37 ± 0.01[a]

[a-c] Least square mean in the same column with different superscript differ (*P*<0.001)

Table 4   Estimates of variance component, heritability (h^2), permanent environmental variance in proportion to total variance (c^2), repeatability (r) and standard error (SE) of the studied traits

Breed[1]	Trait[2]	σ_a^2	σ_{pe}^2	σ_e^2	h² ± SE	c² ± SE	r ± SE
LR	GL	0.481	0.061	1.029	0.31 ± 0.02	0.04 ± 0.01	0.34 ± 0.01
	TB	1.074	1.580	6.022	0.12 ± 0.02	0.18 ± 0.01	0.31 ± 0.01
	BA	1.004	1.665	6.130	0.11 ± 0.02	0.19 ± 0.01	0.30 ± 0.01
	SB	0.001	0.002	0.049	0.02 ± 0.01	0.03 ± 0.01	0.05 ± 0.01
LW	GL	0.428	0.112	1.091	0.26 ± 0.02	0.07 ± 0.02	0.33 ± 0.01
	TB	1.063	1.730	5.524	0.13 ± 0.02	0.21 ± 0.02	0.34 ± 0.01
	BA	1.024	1.779	5.658	0.12 ± 0.02	0.21 ± 0.02	0.33 ± 0.01
	SB	0.001	0.001	0.042	0.01 ± 0.01	0.03 ± 0.01	0.04 ± 0.01
DR	GL	0.616	0.153	1.135	0.32 ± 0.01	0.08 ± 0.00	0.40 ± 0.01
	TB	0.347	2.064	4.374	0.05 ± 0.00	0.30 ± 0.01	0.36 ± 0.01
	BA	0.459	2.046	4.503	0.07 ± 0.00	0.29 ± 0.01	0.36 ± 0.01
	SB	0.002	0.0001	0.049	0.03 ± 0.00	0.002 ± 0.00	0.03 ± 0.00

[1] LR = Landrace, LW = Large white, DR = Duroc
[2] GL = gestation length, TB = total number of piglets born, BA = number of piglets born alive, SB = number of stillborn piglets

Table 5   Genetic correlations ±SE (above the diagonal) and phenotypic correlations ± SE (below the diagonal) among the studied traits

Breed[1]	Trait[2]	GL	TB	BA	SB
LR	GL	-	-0.12 ± 0.07	-0.16 ± 0.07	0.41 ± 0.18
	TB	-0.07 ± 0.01	-	0.99 ± 0.00	0.48 ± 0.20
	BA	-0.08 ± 0.01	0.30 ± 0.01	-	0.42 ± 0.21
	SB	0.03 ± 0.01	0.00 ± 0.01	-0.01 ± 0.01	-
LW	GL	-	-0.01 ± 0.09	0.00 ± 0.09	-0.12 ± 0.22
	TB	-0.05 ± 0.01	-	0.99 ± 0.00	0.31 ± 0.31
	BA	-0.04 ± 0.01	0.33 ± 0.01	-	0.25 ± 0.33
	SB	-0.01 ± 0.01	0.00 ± 0.01	-0.01 ± 0.01	-
DR	GL	-	-0.16 ± 0.02	-0.10 ± 0.02	-0.24 ± 0.00
	TB	-0.09 ± 0.01	-	0.99 ± 0.00	0.79 ± 0.01
	BA	-0.08 ± 0.01	0.36 ± 0.01	-	0.84 ± 0.01
	SB	-0.02 ± 0.00	-0.03 ± 0.00	-0.04 ± 0.00	-

[1] LR = Landrace, LW = Large white, DR = Duroc
[2] GL = gestation length, TB = total number of piglets born, BA = number of piglets born alive, SB = number of stillborn piglets

Discussion

Breed effect: Numerous studies have shown the effect of breed on both litter traits and gestation length in pigs (Serenius *et al.*, 2004; Imboonta and Kuhaaudomlarp, 2012; Lewis and Hermesch, 2013). Breed differences were also found in the current study, that is, LR had the largest litters and the longest GL, whereas DR sows had the smallest litters and the shortest GL. Similar to the finding of Lewis and Hermesch (2013) who reported that LR had the longest GL (115.5 days) followed, respectively, by LW (115.1 days) and DR (114.7 days). Serenius *et al.* (2004), on the contrary, reported that LW (117.0 days) had longer GL than LR (116.5 days). It should be mention that, nowadays, natural gestation length has risen as the number of total born piglets has risen. Our results were similar, in that the least square means of GL ranged from 115.61 in Duroc to 116.73 in Landrace sows. Pietruszka *et al.* (2020) reported the average gestation length of 117.6 day in crossbred sows and Nowak *et al.* (2020) reported

the average gestation length of 118.4 day in Berkshire sows.

For litter traits in this study, LR had the largest TB and BA. This result is inconsistent with some previous studies, which reported that LW sows had more TB and BA than LR sows (Serenius *et al.*, 2004; Lewis and Hermesch, 2013). This difference could be due to genetic background of those sows or because of selection emphasized different targets. The SB differences between breed of sows were that SB of LW (0.29 piglets/litter) was smaller than those of LR and DR (0.35 and 0.34 piglets/litter, respectively). However, the number of SB in the current study was smaller than earlier studies of Serenius *et al.* (2004) who reported that SB in LR and LW sows were 0.8 and 0.9 piglets/litter, respectively as well as Lewis and Hermesch (2013) who reported that SB in LR, LW and DR sows were 0.90, 1.01 and 1.31 piglets/litter, respectively. One of the reasons that our SB was low might be due to the fact that all animals were

supervised around parturition. Such human interventions in the peripartum period have been shown to reduce mortality by as much as 44% (White *et al.*, 1996).

Parity effect: Sows in the first and second parities had longer GL than sows in older parities. The current result agrees with the study of Imboonta and Kuhaaudomlarp (2012) who reported that first- and second-parity sows had longer GL than sows of third or greater parity. However, variation in GL between parities was very low. The variation coefficient, in the current study, was only 1.24 % that confirms the finding of Rydhmer *et al.* (2008) who reported the variation coefficient of 1%.

Results from the current study showed a significant influence of parity on litter traits with TB and BA reaching maximum between the third and fifth parity. This is in line with earlier studies that showed significant effect of parity on reproductive traits, with performance increasing as parity increasing but decreasing after forth parity (Hoving *et al.*, 2011; Imboonta and Kuhaaudomlarp, 2012; Zhang *et al.*, 2016). According to Zhang *et al.* (2016), higher litter size in older parity sows might due to the fact that gilts and young sows have low ovulation rates compared to mature sows. As sows advance in age, more eggs are released during ovulation and uterus capacity is increased resulting in higher number of piglets born.

Sixth-parity sows in this study had the highest SB, and this result is in accordance with the study of Vanderhaeghe *et al.* (2011) who reported that sows with more than 6 parities had higher SB than younger parity sows. That more SB in litters of older parity sows than in those of younger ones may be causatively linked with the excessive fatness of old sows and with poor uterine muscle tone leading to less efficient expulsion and prolonged farrowing (Vanderhaeghe *et al.*, 2013).

The present study showed that TB and BA were higher in 3rd to 5th parity sows compared with both younger sows and older sows. Nevertheless, SB was lower in 3rd to 5th parity sows compared with other parities. This result clearly shows that 3rd to 5th parity sows had the best reproductive performance considering TB, BA and SB.

Genetic parameters: The heritability estimates of GL in this study were moderate and quite similar to earlier reports (Rydhmer *et al.*, 2008; Lewis and Hermesch, 2013; Ogawa *et al.*, 2018). This indicated that GL was moderately heritable. Previous genetic studies on GL have shown that its heritability is higher compared to that of other reproductive traits (Serenius *et al.*, 2004; Rydhmer *et al.*, 2008; Lewis and Hermesch, 2013; Ogawa *et al.*, 2018). Heritability estimates for TB and BA were low in LR and LW sows (range between 0.11 and 0.13) and very low in DR (0.05 and 0.07, respectively). The low heritabilities of TB and BA were agreeable with Rydhmer *et al.* (2008) who reported heritability of 0.1 in both TB and BA of Swedish Yorkshire sows and Lewis and Hermesch (2013) who reported heritability of 0.13 in TB that estimated from LR, LW and DR. Although, TB and BA were lowly heritable, but these traits increased the total economic

value in commercial pig production. Lowly heritable traits of substantial economic value should be emphasized for improvement through better environmental conditions. However, faster gains, particularly for low heritability traits, could be made by selection on estimated breeding values calculated using more complete pedigree information in best linear unbiased prediction (BLUP) analysis. Heritability estimates of SB were relatively low (0.01 to 0.03) compare to other traits in this study. These results were in agreeance with those previously reported (Serenius *et al.*, 2004; Rydhmer *et al.*, 2008; Lewis and Hermesch, 2013).

The permanent environmental variance in proportion to total variances were low for GL and SB in this study. Imboonta and Kuhaaudomlarp (2012) reported the low proportion of permanent environmental variances for GL and SB (0.08 and 0.04, respectively) and Sevón-Aimonen and Uimari (2013) also reported low proportion of permanent environmental variance for SB (0.02), which were in agreement with our results. However, proportion of permanent environmental variances for TB and BA in this study were moderate and higher than their heritabilities. The estimates of permanent environmental effect represent environmental influences and non-additive genetic effect, which affects animals' performance for life. Thus knowing of permanent environmental effect of sows could assist the producer in addition to the breeding value in selecting sows for future performance in the same herd (Mrode, 2005)

The low repeatability estimates for GL, TB and BA indicated that correlations among parities are low, consequently, GL, TB and BA in later parities could somewhat be explained by those in the first parity. Our estimates (0.33-0.40) of repeatability in GL are in agreement with Ogawa *et al.* (2018) who reported that repeatability estimates for GL were 0.38 in LR and 0.40 in LW. However, our repeatability estimates for TB and BA seemed slightly higher than repeatability for TB (0.08) that estimated over six breed groups, including purebred and crossbred sows with parity ranged from 1 to 11 (Imboonta and Kuhaaudomlarp, 2012). Ogawa *et al.* (2018) reported the repeatability values of TB (0.21 in Landrace and 0.24 in Large White) and BA (0.19 in Landrace and 0.22 in Large White) which were estimated from the single-trait repeatability model for each breed. This apparent discrepancy may be explained by breed groups, parity number and model that were used in the analyses. Moreover, the high repeatability estimates may be due to low environmental variance acting on the sows.

In this study, TB was strongly genetically correlated with BA. Therefore, selection for TB is simultaneously indirect selection for BA in this population. Similar results were found by Serenius *et al.* (2004) and Ogawa *et al.* (2018), who found that the genetic correlations between TB and BA ranged from 0.91 to 0.95.

Significant genetic correlations (-0.16) were observed between GL and TB that estimated from DR records, while, the genetic correlations estimated from LW and LR records were not different from zero. This indicated that DR sows with large litters farrowed

earlier than DR sows with small litters. In accordance with the study of Rydhmer *et al.* (2008) and Imboonta and Kuhaaudomlarp (2012) who reported that genetic correlations between GL and TB were -0.14 and -0.29, respectively. On the other hand, many studies reported that GL was not genetically correlated with TB (Serenius *et al.*, 2004; Zhang *et al.*, 2016; Ogawa *et al.*, 2018). Negative genetic correlations between GL and TB indicates that selection for TB will decrease GL. However, in practice, GL have been increasing steadily. This might be explained by the quantitative genetic theory of correlated response (Falconer and Mackay, 1996). The correlated response in GL will be effective if heritability of TB is higher than heritability of GL and genetic correlation between TB and GL is close to 1. In this study, heritability of TB was lower than heritability of GL and the genetic correlation between TB and GL was low. Thus, increasing in GL might depend on other traits in selection index. This phenomenon needs to be further explored.

However, genetic correlations between GL and BA were significant both in LR (-0.16) and DR (-0.10). Hormonal changes in sows and corticosteroids that produced by her piglets trigger the onset of parturition (Rydhmer *et al.*, 2008). Since both sow and piglets play active roles in the timing of parturition, then sows with high number of born alive piglets would have more trigger from cortisol hormone and farrow prior to sows with small BA. Interestingly, about non-significant genetic correlation between GL and BA that was observed in LW. It could be suggested that selection for increase BA will indirectly decrease GL in this population except LW.

Genetic correlation between GL and SB was moderate and positive in LR but low and negative in DR. Our results are in agreement with Rydhmer *et al.* (2008) who reported that genetic correlation between GL and SB was high and positive (0.76) in first-parity litters from the experimental herd, close to zero (0.04) in first-parity litters from nucleus herd and negative (-0.20) in second-parity litters from nucleus herd. It is therefore difficult to draw any conclusions regarding to the relationship between GL and SB. Possibly the inconsistent correlations might be caused by breed of sows and an emphasis on genetic selection that was different in our population. However, many studies reported that genetic correlation between GL and SB was not significant (Serenius *et al.*, 2004; Imboonta and Kuhaaudomlarp, 2012; Lewis and Hermesch, 2013; Ogawa *et al.*, 2018).

Genetic correlations between TB and SB were positive and stronger in DR than in LR. It was in line with the study of Imboonta and Kuhaaudomlarp (2012) and Lewis and Hermesch (2013) who reported that genetic correlations between TB and SB were 0.49 and 0.46, respectively. This indicated that selection for increased TB may cause the increase in SB. That could be described in biological aspect that larger litters tended to have a greater number of low-birth-weight piglets. Those piglets had low energy reserves in the body that brought to increased likelihood of stillborn (Leenhouwers *et al.*, 1999). Therefore, piglet mortality should be considered in the breeding programs to avoid further increase in SB as a result of selection for increased TB.

Unfavorable genetic correlations between BA and SB were estimated from LR and DR in the recent study. Ogawa *et al.* (2018) reported that genetic correlation between BA and SB were 0.20 and 0.33 in LR and LW, respectively. Serenius *et al.* (2004) reported the values of -0.11 and 0.17 as the genetic correlations in Finnish LR and LW populations, respectively. These indicate that the strength of genetic correlation between BA and SB depended on the population analyzed.

In conclusion, GL had moderate heritability in both sire (DR) and dam (LR, LW) lines. This indicates that genetic improvement could be made by direct selection on GL. Heritabilities for TB and BA were low (ranged between 0.11 and 0.13) in dam lines and was relatively lower (0.05 and 0.07) in sire line. This implies that the variations of TB and BA were due to environmental factors. Some genetic improvement could be made using selection; however, progress will be slow. Heritabilities for SB were near zero (ranged between 0.01 to 0.03) in all breeds. Genetic correlations among LR sows indicate that selection for larger TB will also increase BA and SB. It might, however, also result in shorter GL. Genetic correlations among DR sows indicate that selection for larger TB will increase BA and SB as well as decrease GL. In LW population, selection for larger TB will increase BA. Additional selection criteria should be considered when selecting for increased litter size to account for associated increase in SB.

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