



Estimation of Genetic Parameters and Trends for Weaning-to-first Service Interval and Litter Traits in a Commercial Landrace-Large White Swine Population in Northern Thailand*

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ABSTRACT : The objectives of this research were the estimation of genetic parameters and trends for weaning-to-first service interval (WSI), and litter traits in a commercial swine population composed of Landrace (L), Large White (T), LT, and TL animals in Chiang Mai, Northern Thailand. The dataset contained 4,399 records of WSI, number of piglets born alive (NBA), litter weight of live piglets at birth (LBW), number of piglets at weaning (NPW), and litter weight at weaning (LWW). Variance and covariance components were estimated with REML using 2-trait analyses. An animal model was used for WSI and a sire-dam model for litter traits. Fixed effects were farrowing year-season, breed group of sow, breed group of boar (litter traits), parity, heterosis (litter traits), sow age, and lactation length (NPW and LWW). Random effects were boar (litter traits), sow, permanent environment, and residual. Heritabilities for direct genetic effects were low for WSI (0.04 ± 0.02) and litter traits (0.05 ± 0.02 to 0.06 ± 0.02). Most heritabilities for maternal litter trait effects were 20% to 50% lower than their direct counterparts. Repeatability for WSI was similar to its heritability. Repeatabilities for litter traits ranged from 0.15 ± 0.02 to 0.18 ± 0.02 . Direct genetic, permanent environment, and phenotypic correlations between WSI and litter traits were near zero. Direct genetic correlations among litter traits ranged from 0.56 ± 0.20 to 0.95 ± 0.05 , except for near zero estimates between NBA and LWW, and LBW and LWW. Maternal, permanent environment, and phenotypic correlations among litter traits had similar patterns of values to direct genetic correlations. Boar genetic trends were small and significant only for NBA (-0.015 ± 0.005 piglets/yr, $p < 0.004$). Sow genetic trends were small, negative, and significant (-0.036 ± 0.013 d/yr, $p < 0.01$ for WSI; -0.017 ± 0.005 piglets/yr, $p < 0.007$, for NBA; -0.015 ± 0.005 kg/yr, $p < 0.01$, for LBW; -0.019 ± 0.008 piglets/yr, $p < 0.02$, for NPW; and -0.022 ± 0.006 kg/yr, $p < 0.003$, for LWW). Permanent environmental correlations were small, negative, and significant only for WSI (-0.028 ± 0.011 d/yr, $p < 0.02$). Environmental trends were positive and significant only for litter traits ($p < 0.01$ to $p < 0.0003$). Selection based on predicted genetic values rather than phenotypes could be advantageous in this population. A single trait analysis could be used for WSI and a multiple trait analysis could be implemented for litter traits. (**Key Words :** Genetic Parameters, Litter Traits, Service Interval, Swine, Trends, Tropical)

INTRODUCTION

Commercial swine producers in Thailand consider both production and reproduction traits in their genetic

improvement programs. Litter traits such as number born alive (NBA), number of piglets at weaning (NPW), litter weight of live piglets at birth (LBW), and litter weaning weight (LWW) are normally used in sow selection programs. In recent years, commercial producers have begun to use weaning-to-first service interval (WSI) to cull and select sows in commercial swine operations. This trait is economically relevant for the efficiency of commercial operations because it represents a non-productive period for sows. Thus, commercial swine producers need reliable estimates of genetic variability for WSI and litter traits, as well as genetic associations between WSI and litter traits to carry out effective genetic improvement programs for these traits in Thailand.

Reported estimates of heritability in the hot and humid

* This research was part of the Ph.D. Dissertation of the first author, and it was funded by Rajamangala University of Technology Suvarnabhumi, Thailand. Authors express their appreciation to KURDI for its financial support and to the Four T Co., Ltd. for providing relevant information on the swine population.

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Received July 10, 2009; Accepted October 9, 2009

environmental conditions of Thailand were few and low for WSI and for litter traits (0.17 ± 0.03 for WSI with logarithmically transformed data, Imboonta et al., 2007; 0.11 ± 0.04 for NBA and 0.08 ± 0.03 for LBW, Pholsing et al., 2009; and 0.01 ± 0.02 for NPW and 0.08 ± 0.03 for LWW, Suwanasopee, 2006). The only available estimates of genetic correlations between WSI and litter traits in Thailand were the near zero values between WSI and total number of piglets born in a purebred Landrace population (-0.07 ± 0.34 to 0.05 ± 0.23 ; Imboonta et al., 2007). In addition to genetic parameters, estimation of genetic and phenotypic trends for WSI and litter traits would give information to Thai swine producers on the effectiveness of their genetic improvement and management programs. The only estimates of genetic trends for swine in Thailand are for WSI (0.01 ± 0.01 d/yr) and for total number of piglets born (-0.02 ± 0.02 piglets/yr) in a purebred Landrace commercial population (Imboonta et al., 2007). Estimations of genetic and phenotypic correlations between WSI and litter traits, and genetic trends for these traits have not been done in Thai swine populations composed of purebred and crossbred animals. Thus, the objectives of this study were to estimate genetic parameters and trends for WSI and litter traits in an open-house commercial swine population composed of purebred Landrace, Large White, and crossbred Landrace \times Large White in the province of Chiang Mai, Northern Thailand.

MATERIALS AND METHODS

Animals, dataset, and traits

A commercial Landrace-Large White swine population composed of purebred and crossbred animals located in the northern part of Thailand (Chiang Mai province) provided data for this study. Data were collected from 1989 to 2008. The original dataset of 12,974 records was edited for erroneous and incomplete information. All identified cross-fostered records were eliminated. The edited dataset contained 4,399 records of each of the five traits of interest: weaning-to-first-service interval (WSI, d; time from weaning to date of first insemination), number of piglets born alive (NBA, piglets), litter weight of live piglets at birth (LBW, kg), number of piglets at weaning (NPW,

piglets), and litter weight at weaning (LWW, kg). Two breeds were represented in the dataset, Landrace (L) and Large White (T). Breed groups of sows were L, T, and reciprocal crossbred groups LT and TL. Breed groups of boars were L and T. There were 356 boars and 1,852 sows represented in the dataset. The pedigree file contained 3,081 animals (660 boars and 2,421 sows).

Table 1 shows the numbers of boars, sows, and records for all traits by breed group of boar and breed group of sow. Numbers of records by breed group of boar were similar for the two boar groups (L = 46.8% and T = 53.2%), whereas the majority of sow records were from L sows (61.2%) followed by T sows (29.5%), TL sows (5.7%), and LT sows (3.6%). Numbers of records for litter traits (NBA, LBW, NPW, and LWW) by type of mating were 1,162 (26.4%) for purebred matings (L \times L and T \times T), 2,827 (64.3%) for crossbred matings (L \times T and T \times L), and 410 (9.3%) for backcrosses of purebred boars and crossbred sows (L \times LT, L \times TL, T \times LT, and T \times TL). Parity of sows was classified into 7 groups: 1, 2, 3, 4, 5, 6, and ≥ 7 . Numbers of records for parity groups 1 to 7 were 954 (21.7%), 794 (18.0%), 681 (15.5%), 594 (13.5%), 516 (11.7%), 400 (9.1%), and 462 (10.5%), respectively. Age at farrowing of sows ranged from 10 mo (parity group 1) to 76 mo (parity group 7). Lactation length ranged from 12 d to 37 d (mean = 25.14 d, SD = 2.85 d). All records had complete information for all traits. Means, SD, minimum, and maximum values for each trait (WSI, NBA, LBW, NPW, and LWW) are presented in Table 2.

Climate, nutrition, and management

The average temperature in Northern Thailand from 1989 to 2008 was 26.2°C (12.4°C to 38.4°C) and the average humidity was 71.6% (44.0% to 90.0%; Thai Meteorological Department, 2009). Seasons were classified as winter (November to February), summer (March to June), and rainy (July to October). Average temperature by season was 23.2°C (3.8°C to 37.7°C) in winter, 28.3°C (13.8°C to 42.4°C) in summer, and 27.1°C (14.0°C to 39.0°C) in the rainy season. Average humidity by season was 68.7% (49.0% to 83.0%) in winter, 65.0% (44.0% to 84.0%) in summer, and 81.2% (74.0% to 90.0%) in the rainy season.

Table 1. Number of boars and sows and number of records by breed group

Breed group ¹	Number of boars	Number of sows	Number of records	
			Breed group of boar	Breed group of sow
L	190	1,094	2,059	2,691
T	166	571	2,340	1,298
LT	-	81	-	160
TL	-	106	-	250
Total	356	1,852	4,399	4,399

¹ L = Landrace, T = Large White, LT = Landrace \times Large White, and TL = Large White \times Landrace.

Table 2. Descriptive statistics for weaning-to-first service interval and litter traits

Trait ¹	Number of records	Number of Boars	Number of Sows	Mean	SD	Min	Max
WSI (d)	4,399	356	1,852	6.52	5.15	1.00	60.00
NBA (piglets)	4,399	356	1,852	10.49	2.76	1.00	21.00
LBW (kg)	4,399	356	1,852	16.05	4.66	0.60	39.70
NPW (piglets)	4,399	356	1,852	8.57	2.46	1.00	16.00
LWW (kg)	4,399	356	1,852	59.39	19.12	3.50	138.60

¹ WSI = Weaning-to-first service interval; NBA = Number of piglets born alive; LBW = Litter weight of live piglets at birth; NPW = Number of piglets at weaning; LWW = Litter weight at weaning.

All gilts and sows were managed in an open-house system with foggers (gilts and non-lactating sows) or dippers (nursing sows) that were activated when the ambient temperature rose above 33°C. Breeder boars were kept in a close-house system with evaporative cooling. Boars, non-lactating sows, and gilts received 2.5 kg of concentrate twice a day (16% crude protein and 3,200 to 3,500 kcal/kg). Nursing sows were fed 5 to 6 kg of concentrate (17 to 18% crude protein and 4,060 kcal/kg) 4 times a day.

Replacement gilts were inseminated for the first time at 8 to 9 months of age or 140 kg of body weight. Pregnant sows were kept in a breeder cage until approximately 7 days before parturition, and then taken to a farrowing barn with dippers. Piglets were weaned at roughly 7 kg (26 to 30 d of age). Estrus of gilts and weaned sows was detected by boar exposure every day. Gilts and sows were inseminated twice with the same boar (12 h after detection of estrus and 12 h after the first insemination).

Estimation of variance and covariance components

Variance and covariance components were estimated using restricted maximum likelihood procedures (Harville, 1977) using an average information algorithm (Gilmour et al., 1995). Computations were performed with the ASREML program (Gilmour et al., 2006).

The dataset allowed estimation of variance components with at most two traits (ASREML failed to converge when 3 or more traits were analyzed simultaneously). Ten pairwise analyses were conducted: WSI-NBA, WSI-LBW, WSI-NPW, WSI-LWW, NBA-LBW, NBA-NPW, NBA-LWW, LBW-NPW, LBW-LWW, and NPW-LWW. An animal model (Quaas and Pollak, 1980) was used for WSI, and a sire-dam model (Henderson, 1984) was used for litter traits (NBA, LBW, NPW, and LWW). The model for WSI had farrowing year-season (FYS; 49 year-season combinations), parity of sow (7 parity groups) as fixed subclass effects, age of sow, and lactation length of sow as fixed covariates, breed group of sow (4 groups: L, T, LT, and TL) as fixed genetic group effects, and sow genetic effect, direct permanent environment of sow, and residual as random effects. The model for litter traits contained FYS

(49 year-season combinations), parity of sow (7 parity groups) as fixed subclass effects, breed group of boar (2 groups: L and T), breed group of sow (4 groups: L, T, LT, and TL), and heterosis of the litter (as a function of heterozygosity = probability of alleles of different breeds in one locus of piglets in a litter) as fixed genetic group effects, age of sow, and lactation length of sow (for NPW and LWW only) as fixed covariates, and boar genetic effect, sow genetic effect, maternal permanent environment of sow, and residual as random effects. Thus, the model for these bivariate analyses, in matrix notation, was as follows:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{g1} & 0 \\ 0 & Z_{g2} \end{bmatrix} \begin{bmatrix} g_1 \\ g_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} p_1 \\ p_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where, y_i = vector of records for trait i , $i = 1, 2$, where traits 1 and 2 were the 10 pairwise analyses (i.e., WSI-NBA, WSI-LBW, WSI-NPW, WSI-LWW, NBA-LBW, NBA-NPW, NBA-LWW, LBW-NPW, LBW-LWW, and NPW-LWW);

b_i = vector of fixed environmental effects for trait i , $i = 1, 2$. Fixed environmental effects were the same for all traits, i.e., farrowing year-season, parity of sow, age of sow, and lactation length of sow, except for NPW and LWW that had no lactation length of sow in their models;

g_i = vector of fixed genetic group effects for trait i , $i = 1, 2$. Genetic group effects were breed group of sow effects for WSI, and breed group of boar, breed group of sow, and heterosis effects for litter traits;

u_i = vector of random genetic effects for trait i , $i = 1, 2$. Random genetic effects were sow genetic effects for WSI, and boar and sow genetic effects for litter traits;

p_i = vector of random permanent environmental effects for trait i , $i = 1, 2$. Random permanent environmental effects were direct permanent environmental effects of the sow for WSI, and maternal permanent environmental effects of the sow for litter traits;

e_i = vector of random residuals for trait i , $i = 1, 2$;

X_i = incidence matrix of 1's and 0's relating records in

y_i to environmental fixed effects in vector b_i for trait i , $i = 1, 2$;

Z_{gi} = incidence matrix of 1's, 0's, and h's relating records in y_i to breed groups and heterosis effects in vector g_i for trait i , $i = 1, 2$. Records are related to breed groups of sows and boars through 1's and 0's, and through h's to heterosis effects of the litter, where h = probability (breed j boar) × probability (breed k sow) + probability (breed k boar) × probability (breed j sow), and j and k represent different breeds (Elzo, 1990; Elzo and Wakeman, 1994);

Z_i = incidence matrix of 1's and 0's relating records in y_i to random genetic effects in vector u_i for trait i , $i = 1, 2$; and

W_i = incidence matrix of 1's and 0's relating records in y_i to permanent environmental effects in vector p_i for trait i , $i = 1, 2$.

The variance of the random genetic effects for the pair-wise analyses involving WSI and litter traits (WSI-NBA, WSI-LBW, WSI-NPW, and WSI-LWW) was equal to $A \times V_{d,sd}$ where A = additive relationship matrix among animals in the pedigree file (boars and sows) and $V_{d,sd}$ = 3×3 matrix of variances and covariances among additive direct sow effects for trait 1, 1/2 additive direct genetic boar effects for trait 2, and 1/2 additive direct+maternal sow genetic effects for trait 2, where trait 1 = WSI, and trait 2 = NBA, LBW, NPW, or LWW. The $V_{d,sd}$ matrix for traits 1 and 2 was as follows:

$$V_{d,sd} = \begin{bmatrix} \text{var}(sow_1) & \text{cov}(sow_1, boar_2) & \text{cov}(sow_1, sow_2) \\ \text{cov}(boar_2, sow_1) & \text{var}(boar_2) & \text{cov}(boar_2, sow_2) \\ \text{cov}(sow_2, sow_1) & \text{cov}(sow_2, boar_2) & \text{var}(sow_2) \end{bmatrix}$$

In terms of additive direct (AD) and additive maternal (AM) genetic variances and covariances, matrix $V_{d,sd}$ was equal to:

$$V_{d,sd} = \begin{bmatrix} \sigma_{AD_1}^2 & \frac{1}{2}\sigma_{AD_1,AD_2} & \frac{1}{2}\sigma_{AD_1,AD_2} + \sigma_{AD_1,AM_2} \\ \frac{1}{2}\sigma_{AD_2,AD_1} & \frac{1}{4}\sigma_{AD_1,AD_2} & \frac{1}{4}\sigma_{AD_2}^2 + \frac{1}{2}\sigma_{AD_2,AM_2} \\ \frac{1}{2}\sigma_{AD_2,AD_1} + \frac{1}{2}\sigma_{AM_2,AD_1} & \frac{1}{4}\sigma_{AD_2}^2 + \frac{1}{2}\sigma_{AM_2,AD_2} & \frac{1}{4}\sigma_{AD_2}^2 + \sigma_{AD_2,AM_2} + \sigma_{AM_2}^2 \end{bmatrix}$$

The variance of the genetic random effects for the pair-wise analyses involving litter traits (NBA-LBW, NBA-NPW, NBA-LWW, LBW-NPW, LBW-LWW, and NPW-LWW) was equal to $A \times V_{sd,sd}$ where A = additive relationship matrix among animals in the pedigree file (boars and sows) and $V_{sd,sd}$ = 4×4 matrix of variances and covariances among 1/2 additive direct genetic boar effects for trait 1, 1/2 additive direct genetic boar effects for trait 2, 1/2 additive direct+maternal sow genetic effects for trait 1, and 1/2 additive direct+maternal sow genetic effects for trait 2. The matrix $V_{sd,sd}$ for traits 1 and 2 was as follows:

$$V_{sd,sd} = \begin{bmatrix} \text{var}(boar_1) & \text{cov}(boar_1, boar_2) & \text{cov}(boar_1, sow_1) & \text{cov}(boar_1, sow_2) \\ \text{cov}(boar_2, boar_1) & \text{var}(boar_2) & \text{cov}(boar_2, sow_1) & \text{cov}(boar_2, sow_2) \\ \text{cov}(sow_1, boar_1) & \text{cov}(sow_1, boar_2) & \text{var}(sow_1) & \text{cov}(sow_1, sow_2) \\ \text{cov}(sow_2, boar_1) & \text{cov}(sow_2, boar_2) & \text{cov}(sow_2, sow_1) & \text{var}(sow_2) \end{bmatrix}$$

In terms of additive direct (AD) and additive maternal (AM) genetic variances and covariances, matrix $V_{sd,sd}$ was equal to:

$$V_{sd,sd} = \begin{bmatrix} \frac{1}{4}\sigma_{AD}^2 & \frac{1}{4}\sigma_{ADAD} & \frac{1}{4}\sigma_{AD}^2 + \frac{1}{2}\sigma_{ADAM} & \frac{1}{4}\sigma_{ADAD} + \frac{1}{2}\sigma_{ADAM} \\ \frac{1}{4}\sigma_{ADAD} & \frac{1}{4}\sigma_{AD}^2 & \frac{1}{4}\sigma_{ADAD} + \frac{1}{2}\sigma_{ADAM} & \frac{1}{4}\sigma_{AD}^2 + \frac{1}{2}\sigma_{ADAM} \\ \frac{1}{4}\sigma_{AD}^2 + \frac{1}{2}\sigma_{ADAM} & \frac{1}{4}\sigma_{ADAD} + \frac{1}{2}\sigma_{ADAM} & \frac{1}{4}\sigma_{AD}^2 + \sigma_{ADAM} + \sigma_{AM}^2 & \frac{1}{4}\sigma_{ADAD} + \frac{1}{2}\sigma_{ADAM} + \frac{1}{2}\sigma_{AMAD} + \sigma_{AMAM} \\ \frac{1}{4}\sigma_{ADAD} + \frac{1}{2}\sigma_{ADAM} & \frac{1}{4}\sigma_{AD}^2 + \frac{1}{2}\sigma_{ADAM} & \frac{1}{4}\sigma_{ADAD} + \frac{1}{2}\sigma_{ADAM} + \sigma_{AMAD} & \frac{1}{4}\sigma_{AD}^2 + \sigma_{ADAM} + \sigma_{AM}^2 \end{bmatrix}$$

Unfortunately, the dataset did not permit the computation of covariances between boar and sow effects (pair-wise analyses failed to converge with ASREML). Thus, all covariances between boar and sow effects were assumed to be zero. This assumption rendered $V_{sd,sd}$ block diagonal with two 2×2 blocks. The first block contained variances and covariances between 1/2 additive direct genetic boar effects for traits 1 and 2. The second block contained the variances and covariances between 1/2 additive direct+maternal sow genetic effects for traits 1 and 2. Thus, matrix $V_{sd,sd}$ with these assumptions was equal to:

$$V_{sd,sd} = \begin{bmatrix} \text{var}(boar_1) & \text{cov}(boar_1, boar_2) & 0 & 0 \\ \text{cov}(boar_2, boar_1) & \text{var}(boar_2) & 0 & 0 \\ 0 & 0 & \text{var}(sow_1) & \text{cov}(sow_1, sow_2) \\ 0 & 0 & \text{cov}(sow_2, sow_1) & \text{var}(sow_2) \end{bmatrix}$$

and in terms of additive direct (AD) and additive maternal (AM) genetic variances and covariances, the approximate matrix $V_{sd,sd}$ was equal to:

$$V_{sd,sd} = \begin{bmatrix} \frac{1}{4}\sigma_{AD}^2 & \frac{1}{4}\sigma_{ADAD} & 0 & 0 \\ \frac{1}{4}\sigma_{ADAD} & \frac{1}{4}\sigma_{AD}^2 & 0 & 0 \\ 0 & 0 & \frac{1}{4}\sigma_{AD}^2 + \sigma_{ADAM} + \sigma_{AM}^2 & \frac{1}{4}\sigma_{ADAD} + \frac{1}{2}\sigma_{ADAM} + \frac{1}{2}\sigma_{AMAD} + \sigma_{AMAM} \\ 0 & 0 & \frac{1}{4}\sigma_{ADAD} + \frac{1}{2}\sigma_{ADAM} + \frac{1}{2}\sigma_{AMAD} + \sigma_{AMAM} & \frac{1}{4}\sigma_{AD}^2 + \sigma_{ADAM} + \sigma_{AM}^2 \end{bmatrix}$$

The permanent environmental matrix of variances and covariances for all pairwise analyses was equal to $I \times V_p$, where I = identity matrix, and V_p = matrix of variances and covariance between permanent environmental effects of the sow for traits 1 and 2. Thus, $V_p = \begin{bmatrix} \sigma_{p_1}^2 & \sigma_{p_1 p_2} \\ \sigma_{p_2 p_1} & \sigma_{p_2}^2 \end{bmatrix}$. Notice that permanent environmental effects of the sow are direct for WSI and maternal for litter traits.

The residual variance matrix for all pair-wise analyses was equal to $I * V_e$, where I = identity matrix, and V_e =

matrix of variances and covariance between residual effects for traits 1 and 2. Thus,

$$V_e = \begin{bmatrix} \sigma_{e_1}^2 & \sigma_{e_1e_2} \\ \sigma_{e_2e_1} & \sigma_{e_2}^2 \end{bmatrix}.$$

Estimation of genetic parameters

Estimates of heritabilities for direct genetic effects for WSI, NBA, LBW, NPW, and LWW were computed as the ratio of their respective additive direct genetic to phenotypic variances. Estimates of additive direct genetic variances were equal to the sow variance for WSI, and equal to twice the boar variance for litter traits. Phenotypic variances were computed as the sum of sow genetic, sow direct permanent environment, and residual variances for WSI. Phenotypic variances for litter traits were equal to the sum of boar genetic, sow genetic, sow maternal permanent environment, and residual variances for litter traits.

Estimates of heritabilities for maternal effects for NBA, LBW, NPW, and LWW were computed as the ratio of their respective additive maternal to phenotypic variances. Estimates of maternal variances were equal to the sow variance minus the boar variance for each trait. Estimates of repeatabilities were equal to the ratio of the sum of additive plus maternal permanent environmental variances over phenotypic variances.

Estimates of additive direct genetic correlations were equal to the ratio of additive direct genetic covariances between two traits over the square root of the product of the additive direct genetic variances of these traits. Additive direct genetic correlations between WSI and litter traits were estimated as the ratio of 2 times covariance (sow WSI, boar litter trait *i*) over the square root of (1/4 sow variance for WSI times boar variance for litter trait *i*), where litter trait *i* = NBA, LBW, NPW, and LWW. Estimates of additive direct genetic correlations for litter traits were equal to the ratio of the boar covariance between traits 1 and 2 divided by the square root of the product of the boar variances for traits 1 and 2.

Estimates of maternal correlations for litter traits were equal to the ratio of maternal covariances between two traits divided by the square root of the product of the maternal variances for these traits. As with maternal variances, maternal covariances were estimated as the difference between sow covariances and boar covariances.

Permanent environmental correlations and phenotypic correlations for all traits were estimated as the ratio of their respective covariances divided by the square root of their variances.

Computations of heritabilities, correlations (genetic, permanent environmental), and their standard errors were carried out using the ASREML program (Gilmour et al.,

2006).

Genetic and phenotypic trends

Weighted means of expected progeny differences (EPD) by farrowing year (FY) were computed for boar and sow EPD for WSI, boar EPD for litter traits, and sow EPD for litter traits. Boar and sow EPD were computed as the sum of a breed group effect plus a random genetic deviation. Boar breed groups (L and T) and sow breed groups (L, T, LT, and TL) were deviated from L. Random genetic deviations were the random boar and sow genetic effects. In addition, weighted means of sow permanent environmental deviations (PED) by FY were also computed for WSI and litter traits. Weighted means of EPD and PED were plotted against FY numbers. A linear regression was fitted to the set of means of boar EPD, sow EPD, and sow PED for each trait and regression coefficients computed to assess trends over time using the regression procedure of SAS (SAS, 2008).

Environmental changes over time were visualized by plotting FY least squares solutions for each trait against FY. Regression coefficients of FY solutions on FY were used to evaluate environmental trends. Computations were carried out with the regression procedure of SAS (SAS, 2008).

RESULTS AND DISCUSSION

Environmental fixed effects

Farrowing year-season was an important effect ($p < 0.0001$) for all traits. Estimates ranged from 2.7 ± 3.9 d ($p < 0.48$) to 10.8 ± 1.7 d ($p < 0.0001$) for WSI, from 7.5 ± 1.6 piglets ($p < 0.0001$) to 12.9 ± 0.7 piglets ($p < 0.0001$) for NBA, from 10.4 ± 1.2 kg ($p < 0.0001$) to 19.5 ± 1.1 kg ($p < 0.0001$) for LBW, from 5.9 ± 1.6 piglets ($p < 0.0001$) to 11.3 ± 1.5 piglets ($p < 0.0001$) for NPW, and from 23.9 ± 11.4 kg ($p < 0.0001$) to 59.1 ± 5.7 kg ($p < 0.0001$) for LWW. Estimates fluctuated more across FYS for WSI than for litter traits, and all of them tended to increase from 1989 to 2008.

Ranges of estimates for FYS found in this study were similar to those obtained in other Thai swine populations for WSI (Tantasuparuk et al., 2001; Suriyasomboon et al., 2006; Imboonta et al., 2007), NBA (Suwanosopee et al., 2005; Pholsing et al., 2009), LBW (Pholsing et al., 2009), and NPW and LWW (Suwanosopee, 2006). Variation among estimates of FYS for WSI and litter traits was the result of the combined effects of climate (seasonal fluctuations in temperature and humidity), nutrition (composition and nutritional content of diets), and management during the years of the study. Lack of adaptation of sows that were progeny of imported boars from temperate countries may have been a contributing factor for low FYS means.

Parity was also an important factor ($p < 0.0001$) for all

traits. First parity sows had: i) longer WSI than parity groups 2 to 6 (from 2.2 ± 0.3 d, $p < 0.0001$, longer than parity 2 sows to 2.8 ± 0.8 d, $p < 0.01$, longer than parity 6 sows); ii) smaller NBA than parities 2 to 6 (from -0.9 ± 0.1 piglets, $p < 0.0001$, less than parity 2 sows to -1.7 ± 0.2 piglets, $p < 0.0001$, less than parity 3 sows); iii) lighter LBW than parities 2 to 6 (from -2.2 ± 0.6 kg, $p < 0.005$, lighter than parity 6 sows to -3.4 ± 0.3 kg, $p < 0.0001$, lighter than parity 3 sows); iv) smaller NPW than any other parity group (from -1.3 ± 0.1 piglets, $p < 0.0001$, less than parity 2 sows to -1.8 ± 0.3 piglets, $p < 0.0001$, less than parity 5 sows); and vi) lighter LWW than all other parity groups (from -11.7 ± 1.0 kg, $p < 0.0001$, less than parity 2 sows to -15.8 ± 1.3 kg, $p < 0.0001$, less than parity 3 sows). Second and later parity sows had similar WSI values. However, sows from parity 2 had smaller NBA than sows from parities 3 (-0.7 ± 0.1 piglets, $p < 0.0001$) and 4 (-0.7 ± 0.2 piglets, $p < 0.009$), lighter LBW than parity 3 sows (-0.8 ± 0.2 kg, $p < 0.002$), smaller NPW than parity 3 sows (-0.5 ± 0.1 piglets, $p < 0.20$), and lighter LWW than parity 3 sows (-4.1 ± 1.0 kg, $p < 0.0008$).

Parity estimates for WSI and litter traits here had a similar pattern to those reported for other Thai swine populations (Suriyasomboon et al., 2006; Imboonta et al., 2007). Primiparous sows had larger parity values for WSI and smaller ones for litter traits than multiparous sows, likely because of their need to allocate a fraction of the energy and protein from ingested nutrients to body growth in addition to allocating nutrients for gestation, lactation, and maintenance (Reese et al., 1982; Whittemore, 1996; Pluske et al., 1998).

Age of sow was unimportant for all traits. This means that the range of ages within parity had no major effect in this dataset. Lactation length was relevant for LWW (0.7 ± 0.1 kg/d, $p < 0.0001$) indicating that longer lactations resulted in heavier LWW, but not for either WSI or NPW. Conversely, Tantasuparuk et al. (2000b, 2001) found lactation length to be non-significant for WSI, NPW, and LWW in purebred and crossbred L and T swine herds in central Thailand. Lactation length effects on WSI were mixed in temperate regions. Longer lactation lengths increased WSI in a Landrace-Hampshire-Yorkshire population ($p < 0.05$; Ehlers et al., 2005), but decreased WSI in commercial United States swine populations ($p < 0.05$; Koketsu and Dial, 1997) and in Swedish Landrace and Yorkshire ($p < 0.0001$; Tummaruk et al., 2000). Extended lactations increased LWW in commercial swine farms in the United States ($p < 0.05$; Koketsu and Dial, 1997) and in Large White and Hybrid populations in Canada, but had no influence on NPW ($p < 0.0001$; Willis et al., 2003).

Genetic fixed effects

Breed group of boar was non-significant for all litter

traits suggesting that L and T sires used in this population were of similar genetic value for NBA, LBW, NPW, and LWW. This suggests that boars in this population were chosen using similar criteria regardless of breed (L and T) throughout the length of the study. On the other hand, breed group of sow was significant for WSI ($p < 0.003$), NBA ($p < 0.007$), LBW ($p < 0.0002$), NPW ($p < 0.03$), and LWW ($p < 0.04$). Crossbred TL sows had longer WSI than purebred L (1.3 ± 0.4 d, $p < 0.01$) and T (1.6 ± 0.4 d, $p < 0.01$), larger NBA than L (0.8 ± 0.2 piglets, $p < 0.001$) and T (0.9 ± 0.2 piglets, $p < 0.0003$), heavier LBW than L (1.1 ± 0.3 kg, $p < 0.002$), T (1.4 ± 0.3 kg, $p < 0.0001$), and LT (1.1 ± 0.4 kg, $p < 0.05$), larger NPW than L (0.6 ± 0.2 piglets, $p < 0.02$) and T (0.5 ± 0.2 piglets, $p < 0.03$), and heavier LWW than L (3.5 ± 1.4 kg, $p < 0.08$) and T (3.9 ± 1.4 kg, $p < 0.04$). Sows from breed groups L, T, and LT had similar WSI, NBA, LBW, NPW, and LWW. These results indicate that, as with boars, the same phenotypic culling and selection criteria were applied to all sows regardless of their breed composition. The outcome was a group of purebred L and T sows of similar mean additive genetic performance for WSI and litter traits, and TL crossbred sows that were superior to both LT crossbred and purebred L and T sows.

Tantasuparuk et al. (2000a) found L to have longer ($p < 0.0001$) WSI and larger ($p < 0.0001$) NBA than T in central Thailand. In addition, Suwanasopee (2006) found weaning-to-estrous interval to be longer in L than in T ($p < 0.05$), and in crossbred LT and TL than in purebred L and T ($p < 0.05$). On the other hand, Suwanasopee (2006) also found no differences between L and T for NPW and LWW; however, crossbred TL and LT groups had larger NPW and LWW than purebred L and T. It should be mentioned that the model in Suwanasopee (2006) did not separate additive and non-additive effects for crossbred groups, thus comparisons of crossbred and purebred groups include both additive and non-additive effects, not only additive effects as in the models for litter traits used here.

Heterosis had positive effects on all traits, thus they were disadvantageous for WSI, but advantageous for litter traits. Heterosis effects tended to increase WSI (0.9 ± 0.3 d; $p < 0.007$), NBA (0.2 ± 0.1 piglets, $p < 0.054$), LBW (0.4 ± 0.2 kg, $p < 0.008$), NPW (0.03 ± 0.02 piglets, $p < 0.06$), and LWW (1.5 ± 0.1 kg, $p < 0.0001$) between 1989 and 2008. The estimate of heterosis for WSI was computed as the difference between the mean of the solutions for crossbred groups (TL and LT) minus the mean of the solutions for the parental breeds (T and L), whereas estimates of heterosis for litter traits were equal to the solutions for heterosis as functions of heterozygosities. Positive heterosis estimates were also found for weaning-to-first estrous interval (0.4 ± 0.1 d for TL and 0.4 ± 0.1 d for LT), NPW (1.5 ± 0.2 piglets for TL and 1.6 ± 0.2 piglets for LT), and LWW (15.3 ± 1.2 kg

Table 3. Direct heritabilities (upper diagonals), direct genetic variances (lower diagonals), direct genetic correlations (above diagonal) and direct genetic covariances (below diagonal) for weaning-to-first service interval and litter traits

Trait	Trait ¹				
	WSI	NBA	LBW	NPW	LWW
WSI	0.04±0.02 ² 0.92±0.51	0.05±0.71	0.09±0.00 ⁴	0.29±0.00 ⁴	0.05±0.00 ⁴
NBA	0.03±0.39	0.05±0.02 ³ 0.33±0.15	0.73±0.13	0.85±0.11	0.08±0.02
LBW	0.08±0.00 ⁴	0.38±0.20	0.06±0.02 0.82±0.33	0.56±0.20	0.06±0.02
NPW	0.13±0.00 ⁴	0.29±0.13	0.29±0.18	0.06±0.03 0.30±0.14	0.95±0.05
LWW	0.18±0.00 ⁴	0.19±0.09	0.21±0.12	1.98±0.94	0.05±0.02 14.50±7.00

¹ WSI = Weaning-to-first service interval; NBA = Number of piglets born alive; LBW = Litter weight of live piglets at birth; NPW = number of piglets at weaning; LWW = Litter weight at weaning.

² Heritability and direct genetic variance from WSI-NBA analysis.

³ Minimum heritability value of three pairwise estimates (upper element) and corresponding average for direct genetic variance (lower element).

⁴ Constrained estimate; ASREML provided no standard error.

for TL and 15.6±1.0 for LT) in a Landrace-Large White Thai population (Suwanasopee, 2006). These values were estimated as differences between crossbred and purebred least squares means, thus they accounted for intra-locus and inter-loci interactions, whereas heterosis estimates here only include intra-locus interactions.

Genetic parameters for additive direct genetic effects

Variances and heritabilities for additive direct genetic effects for WSI and litter traits were all low (Table 3). Upper diagonal elements in Table 3 show estimates of heritabilities and lower diagonal elements are estimates of additive direct genetic variances. The direct heritability (0.04±0.02) and genetic variance (0.90±0.51 d²) for WSI were from the WSI-NBA analysis (this was the only 2-trait analysis involving WSI that converged without constraints in ASREML). Estimates of direct heritabilities for litter traits were equal for the three 2-trait analyses for NPW (0.06±0.03), LWW (0.05±0.02), and LBW (0.06±0.02). The estimate of direct heritability for NBA ranged from 0.05±0.02 to 0.06±0.02.

Imboonta et al. (2007) estimated substantially higher values of heritability for WSI (0.16±0.03 to 0.18±0.04 for the first three parities) in a purebred Landrace population using logarithmically transformed WSI data (ten Napel et al., 1995). Estimates of similar magnitude were also obtained by Ehlers et al. (2005) in a Landrace-Hampshire-Yorkshire population in the United States (0.20) and by Hanenberg et al. (2001) for first parity sows in Dutch Landrace (0.14±0.01) using similarly transformed WSI data. Contrarily, Suwanasopee et al. (2005) estimated a heritability of 0.03±0.01 for weaning-to-estrous interval in Landrace-Yorkshire population in central Thailand similar

to the northern Thai population used here. Similarly, Hanenberg et al. (2001) estimated a much lower heritability for WSI in parities 2 to 6 (0.07±0.01). These last two estimates are similar to the estimate obtained in this population (0.04±0.02) using WSI data from all parities.

Heritabilities reported for litter traits in Thailand were low and comparable to estimates here. Pholsing et al. (2009) estimated heritabilities of 0.11±0.04 for NBA and 0.08±0.03 for LBW in a Pietrain-Large White population. Suwanasopee et al. (2005) estimated a heritability of 0.07 for NBA, and Suwanasopee (2006) computed heritabilities of 0.01±0.02 for NPW and 0.08±0.03 for LWW in a Large White, Landrace and Duroc population. Imboonta et al. (2007) estimated a heritability of 0.03±0.02 for total number of piglets born. Heritability values for litter traits in temperate regions were also low, ranging from 0.08 to 0.15 for NBA, 0.05 to 0.07 for NPW, and 0.08 to 0.09 for LWW in populations of Landrace, Yorkshire, Duroc, and Hampshire pigs in the United States and The Netherlands (Hanenberg et al., 2001; Chen et al., 2003; Ehlers et al., 2005).

Additive direct genetic covariances and direct genetic correlations between WSI and litter traits were all close to zero (Table 3). Only the direct genetic covariance and correlation between WSI and NBA converged without constraints, and had a large standard error. Additive direct genetic correlations among litter traits were all positive (Table 3). The near zero direct genetic correlations between WSI and litter traits indicate that using a multiple trait analysis involving WSI and litter traits would yield no increase in accuracy of prediction over a single-trait analysis for WSI. Thus, animals in this population could be evaluated for WSI using single trait genetic evaluation

procedures without detrimental impact on the accuracy of their genetic predictions for WSI.

As expected, high and positive estimates of additive direct genetic correlations were obtained between NBA and LBW (0.73 ± 0.13) and NPW and LWW (0.95 ± 0.05) indicating a close positive association between the number of live piglets per litter at birth and at weaning and the weight of the litter at these times. There was also a high positive association between direct genetic effects for number of live piglets at birth and at weaning (0.85 ± 0.11) and a moderate association between direct genetic effects for litter weight at birth and number of live piglets at weaning (0.56 ± 0.20). Correlations between NBA and LWW, and between LBW and LWW were near zero. These genetic correlation estimates among litter traits suggest that a multiple trait analysis for litter traits would be advantageous to increase accuracies of prediction in this population.

Direct genetic correlations between WSI and litter traits here were unavailable in other Thai studies. However, Imboonta et al. (2007) estimated a genetic correlation between WSI and total number of piglets born of 0.07 ± 0.27 in a Landrace population in eastern Thailand that was similar to the correlation between WSI and NBA estimated here. Similarly, low values of correlations were estimated between WEI and NBA (-0.01), WEI and NPW (0.51 ± 0.47), and WEI and LWW (0.01 ± 0.24) in Large White and Landrace populations in central Thailand (Suwanasopee et al., 2005; Suwanasopee, 2006). There was general agreement between correlation estimates here and those from swine populations in temperate regions. Genetic correlations between WSI and NBA were similar to values here in Norwegian Landrace (first parity = 0.05 ± 0.04 ; later parities = 0.03 ± 0.07 ; Holm et al., 2005), and somewhat higher in a Landrace-Hampshire-Yorkshire population in the United States (0.15 to 0.16; Ehlers et al., 2005). Genetic correlations were also found to be low between WSI and NPW (0.13) and between WSI and LWW (0.16) in a

Landrace-Large White population in the Czech Republic (Adamec and Johnson, 1997). Genetic correlations between NBA and litter traits at weaning were lower than the estimate obtained here between NBA and NPW (0.14 to 0.19), but comparable between NBA and LWW (0.14 to 0.15), and NPW and LWW (0.75) in a Landrace-Yorkshire population in the United States (Chen et al., 2003).

Genetic parameters for maternal genetic effects

Estimates of maternal heritabilities for litter traits (Table 4) were from 20% to 50% lower than heritabilities for additive direct heritabilities for NBA (0.04 ± 0.02), LBW (0.03 ± 0.02), and NPW (0.03 ± 0.02). Only the maternal heritability for LWW (0.06 ± 0.02) was 20% higher than its direct counterpart. Estimates of maternal heritabilities were the same for the three 2-trait analyses for NBA and LWW, whereas estimates ranged from 0.03 ± 0.02 to 0.04 ± 0.02 for LBW and NPW.

Estimates of maternal heritabilities for litter traits in Thailand were unavailable. However, estimates of maternal heritabilities obtained in this population were within the range of estimates from swine populations in temperate regions. Maternal heritabilities for NBA, NPW, and LWW were found to be either zero or near zero (0.00 to 0.02) in a Landrace-Yorkshire swine population in the United States (Chen et al., 2003) and for NBA and NPW in Czech Landrace and Large White (Adamec and Johnson, 1997). Somewhat higher estimates of maternal heritability were computed for NBA and NPW in Polish Large White (0.03 to 0.10; Kaplon et al., 1991) and Canadian Landrace and Yorkshire (0.04 ± 0.04 to 0.08 ± 0.04 ; Southwood and Kennedy, 1990), and for LWW in Czech Landrace and Large White (0.05; Adamec and Johnson, 1997).

Lower values of maternal than direct heritabilities for litter traits indicate that more genetic progress could be achieved by selecting for direct than for maternal effects in this population. However, selection for maternal effects

Table 4. Maternal heritabilities (upper diagonals), maternal variances (lower diagonals), maternal correlations (above diagonal) and maternal covariances (below diagonal) for litter traits

Trait	Trait ¹			
	NBA	LBW	NPW	LWW
NBA	0.04 ± 0.02 0.22 ± 0.14	0.78 ± 0.15	0.54 ± 0.29	0.03 ± 0.03
LBW	0.26 ± 0.18	0.03 ± 0.02^2 0.46 ± 0.29	0.50 ± 0.31	0.04 ± 0.03
NPW	0.11 ± 0.11	0.15 ± 0.16	0.03 ± 0.02^2 0.18 ± 0.12	0.94 ± 0.06
LWW	0.06 ± 0.08	0.13 ± 0.12	1.68 ± 0.87	0.06 ± 0.02 17.77 ± 6.92

¹ NBA = Number of piglets born alive; LBW = Litter weight of live piglets at birth; NPW = Number of piglets at weaning; LWW = Litter weight at weaning.

² Minimum heritability value of three pairwise estimates (upper element) and corresponding maternal genetic variance (lower element).

should also be considered as an integral part of a selection program because of its impact on both birth and weaning litter traits. Thus, selection of boars and sows with high EPD for direct and maternal effects would likely produce the most desirable changes in direct and maternal genetic values in the population. Because of the larger selection intensity that can be applied to boars, their impact on genetic progress could be substantially larger than that of sows. In addition, because Thai swine farmers frequently import L and T boars, it would be advantageous to choose these boars using direct and maternal genetic information to speed up genetic progress for WSI and litter traits in Thailand.

Estimates of maternal correlations among litter traits were all positive and had the same pattern as additive direct genetic correlations. The highest estimates of maternal correlations occurred between NBA and LBW (0.78 ± 0.15) and NPW and LWW (0.94 ± 0.06), whereas moderate maternal correlations existed between NBA and NPW (0.54 ± 0.29) and LBW and NPW (0.50 ± 0.31), and near zero maternal correlations between NBA and LWW, and between LBW and LWW. These correlations suggest that the relationship between the maternal ability of sows at birth and at weaning is primarily associated with the survival of piglets from birth to weaning, but not with the weight of the litter at weaning. This result seems reasonable because maternal ability for birth traits is primarily determined by the ability of the sow to provide an appropriate intrauterine environment, whereas maternal ability for weaning traits is largely associated with a milk production and nursing behavior.

Maternal correlations among litter traits in Thailand were unavailable. Kaplon et al. (1991) estimated correlations between sow genetic effects of 0.91 between NBA and NPW, 0.68 between NBA and LWW, and 0.80 between NPW and LWW in Polish Large White. In addition, contrary to the positive medium size correlation between NBA and NPW here, estimates in temperate regions ranged from negative to positive for Landrace and Yorkshire. Lund et al. (2002) estimated maternal correlations between % NBA and % NPW of 0.25 ± 0.09 in Landrace and -0.48 ± 0.31 in Yorkshire, whereas Su et al. (2008) estimated maternal correlations of -0.14 ± 0.18 for Landrace and -0.03 ± 0.21 for Yorkshire. Factors that likely contributed to differences in correlation estimates in these studies include differences in statistical methodology and genetic characteristics of each swine population.

Repeatabilities, permanent environmental correlations, and phenotypic correlations

The estimate of repeatability for WSI (0.04 ± 0.02) was equal to the estimate of heritability suggesting that

permanent environment was irrelevant for this trait. On the other hand, repeatability estimates for all litter traits were from 60% to 100% larger than the combined direct genetic and maternal to phenotypic ratios suggesting that permanent maternal environmental effects were important for litter traits in this population. Repeatability estimates from the three 2-trait analyses were equal for NBA (0.18 ± 0.02), LBW (0.18 ± 0.02), and NPW (0.15 ± 0.02), and ranged from 0.15 ± 0.02 to 0.16 ± 0.02 for LWW. These low repeatability estimates emphasize the importance of obtaining several records per sow for WSI and litter traits to improve the accuracy of prediction of future records of sows as well as to increase the accuracy of prediction of sow EPD, boar EPD, and progeny EPD in Thai swine populations.

Suwanasopee et al. (2005) found repeatability estimates for weaning-to-estrous interval (0.06) and for NBA (0.15) in a swine population in central Thailand that were similar to the repeatabilities estimated here for WSI and NBA. No other repeatability estimates for WSI or litter traits were available in Thailand. However, in the humid subtropics of southern Brazil, Siewerdt and Cardellino (1995) estimated repeatabilities in swine populations of Landrace and Large White for NBA (0.16 ± 0.01 for L and 0.14 ± 0.01 for T), LBW (0.19 ± 0.02 for L and 0.15 ± 0.01 for T), NPW (0.15 ± 0.02 for L and 0.12 ± 0.01 for T), and LWW (0.15 ± 0.02 for L and 0.13 ± 0.01 for T) that were very close to the ones estimated here. Somewhat lower estimates of repeatability were estimated in temperate regions by Adamec and Johnson (1997) in Czech Landrace and Large White (0.11 for NBA, 0.10 for NPW, and 0.11 for LWW), and by Chen et al. (2003) in U.S. Landrace and Yorkshire pigs (0.14 to 0.17 for NBA, 0.08 to 0.11 for NPW, and 0.12 to 0.14 for LWW).

Direct permanent environmental correlations as well as phenotypic correlations between WSI and litter traits were close to zero (Table 5). These correlations lend support to the statement above that WSI could be analyzed separately from litter traits without detriment to the accuracy of genetic predictions. Near zero phenotypic correlations also were found in Thailand between weaning-to-first estrous interval and NBA (Suwanasopee et al., 2005) and between WSI and litter traits in the United States (NBA, LBW; Ehlers et al., 2005). Maternal permanent environmental correlations and phenotypic correlations among litter traits (Table 5) followed the same pattern as direct genetic and maternal correlations. Higher estimates of maternal permanent environmental correlations existed between NBA and LBW (0.80 ± 0.05), NBA and NPW (0.82 ± 0.08), LBW and NPW (0.78 ± 0.09), and NPW and LWW (0.94 ± 0.04). Similarly, moderate to high phenotypic correlation estimates were computed between NBA and LBW (0.83 ± 0.01), NBA and NPW (0.63 ± 0.01), LBW and NPW ($0.55 \pm$

Table 5. Repeatabilities, permanent environmental correlations (above diagonal) and phenotypic correlations (below diagonal) for weaning-to-first service interval and litter traits

Trait	Trait ¹				
	WSI	NBA	LBW	NPW	LWW
WSI	0.04±0.02 ²	0.24±0.33	0.06±0.01	0.03±0.00	0.03±0.00
NBA	-0.00±0.03	0.18±0.02	0.80±0.05	0.82±0.08	0.08±0.01
LBW	0.01±0.01	0.83±0.01	0.18±0.02	0.78±0.09	0.09±0.01
NPW	-0.00±0.01	0.63±0.01	0.55±0.01	0.15±0.02	0.94±0.04
LWW	-0.00±0.02	0.05±0.00	0.05±0.00	0.88±0.00	0.15±0.02 ³

¹ WSI = Weaning-to-first service interval; NBA = Number of piglets born alive; LBW = Litter weight of live piglets at birth; NPW = Number of piglets at weaning; LWW = Litter weight at weaning.

² Repeatability from WSI-NBA analysis.

³ Minimum repeatability value of three pairwise estimates.

0.01), and NPW and LWW (0.88±0.00). Maternal permanent environment and phenotypic correlations between NBA and LWW, and between LBW and LWW were close to zero.

Similar estimates of phenotypic correlations to the ones computed here were obtained by Kaplon et al. (1991) between NBA and NPW (0.88) and NPW and LWW (0.86) in Polish Large White, and by Chen et al. (2003) between NBA and LWW (0.06 to 0.07) and between NPW and LWW (0.78 to 0.80). However, Kaplon et al. (1991) also reported a substantially higher phenotypic correlation between NBA and LWW (0.75), and Chen et al. (2003) obtained a much lower phenotypic correlation between NBA and NPW (0.05 to 0.06) than corresponding estimates here.

Genetic and environmental trends

Genetic trends for boar and sow EPD, and permanent

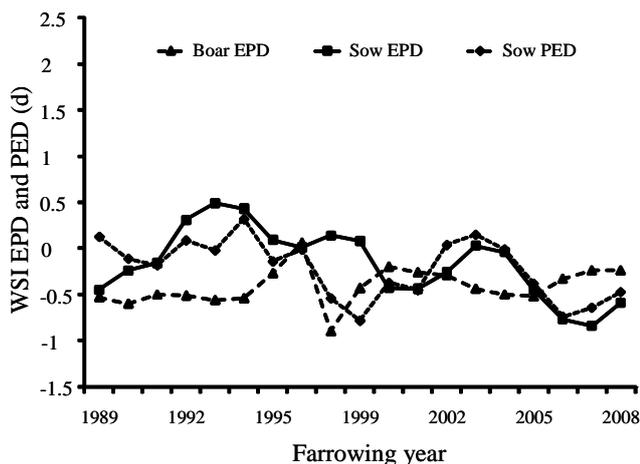


Figure 1. Mean weaning-to-first-service interval (WSI) boar and sow direct expected progeny differences (EPD) and sow direct permanent environmental differences (PED) by farrowing year (FY). Regression coefficients were 0.012±0.008 d/yr ($p<0.14$) for boar EPD on FY, -0.036±0.013 d/yr ($p<0.01$) for sow EPD on FY, and -0.028±0.011 d/yr ($p<0.02$) for sow PED on FY.

environmental trends for sows are shown in Figure 1 for WSI, Figure 2 for NBA, and Figure 3 for LBW. Figures of genetic trends for NPW and LWW (not shown) were similar to those for birth litter traits.

Boar genetic trend was significant for NBA ($p<0.004$), but not-significant for WSI and other litter traits. Regression coefficients for WSI and litter traits were 0.012±0.008 d/yr ($p<0.14$) for WSI, -0.015±0.005 piglets/yr ($p<0.004$) for NBA, 0.008±0.017 kg/yr ($p<0.64$) for LBW, -0.015±0.016 piglets/yr ($p<0.38$) for NPW, and -0.006±0.011 kg/yr ($p<0.55$) for LWW. Genetic trends for sows were negative and significant for all traits. Thus, sow genetic trends were favorable only for WSI and unfavorable for all litter traits. Regression coefficients were -0.036±0.013 d/yr ($p<0.01$) for WSI, -0.017±0.005 piglets/yr ($p<0.007$) for NBA, -0.015±0.005 kg/yr ($p<0.01$) for LBW, -0.019±0.008 piglets/yr ($p<0.02$) for NPW, and -0.022±

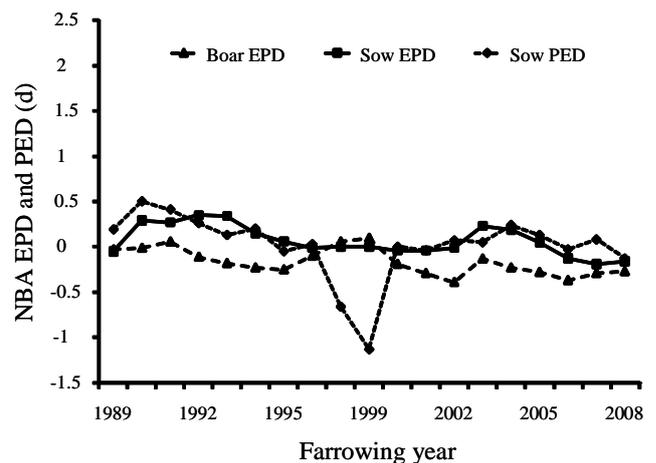


Figure 2. Mean number of piglets born alive (NBA) boar direct expected progeny differences (EPD), sow direct plus maternal EPD, and sow maternal permanent environmental differences (PED) by farrowing year (FY). Regression coefficients were -0.015±0.005 piglets/yr ($p<0.004$) for boar EPD on FY, -0.017±0.005 piglets/yr ($p<0.007$) for sow EPD on FY, and -0.015±0.014 piglets/yr ($p<0.29$) for sow PED on FY.

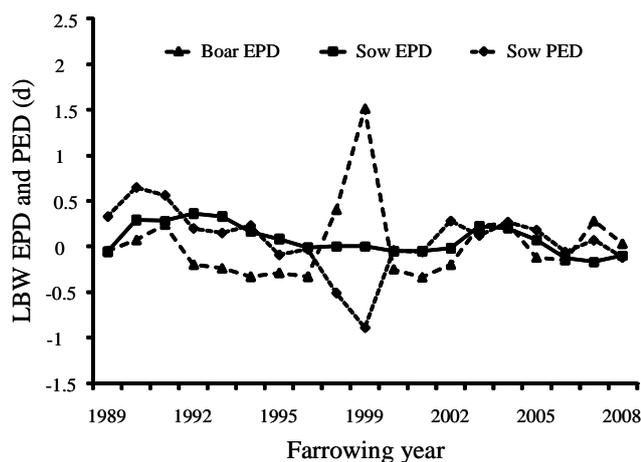


Figure 3. Mean litter weight of live piglets at birth (LBW) boar direct expected progeny differences (EPD), sow direct plus maternal EPD, and sow maternal permanent environmental differences (PED) by farrowing year (FY). Regression coefficients were 0.008 ± 0.017 kg/yr ($p < 0.64$) for boar EPD on FY, -0.015 ± 0.005 kg/yr ($p < 0.01$) for sow EPD on FY, and -0.019 ± 0.013 kg/yr ($p < 0.17$) for sow PED on FY.

0.006 kg/yr ($p < 0.003$) for LWV.

Boars and sows in this herd were selected based on phenotypic information for litter traits only (P. Cherdasatirakul, pers. comm., Four T Co. Ltd., Chiang Mai, Thailand). The low significant negative values for boar NBA genetic trend and for sow genetic trends for all litter traits suggest that the phenotypic information used was insufficient to successfully identify the best boars and sows for litter traits in this herd. The end result was low boar and sow genetic trends for all litter traits. Considering the low positive direct genetic correlations between WSI and litter traits estimated in this population, the favorable negative sow genetic trend for WSI may have been a correlated response to the negative selection pressure exerted on litter traits by the phenotypic selection used in this herd.

Reports of genetic trends in Thailand were few. Imboonta et al. (2007) obtained a genetic trend of zero for WSI in a Thai Landrace herd in eastern Thailand, and Suwanasopee et al. (2005) estimated a negative genetic trend (-0.07 d/yr) for weaning-to-first estrous interval, and a positive genetic trend for NBA (0.026 piglets/yr) in a Landrace-Large White-Duroc population in central Thailand. When expressed as sow EPD per FY, the sow trend for weaning-to-first estrous interval of Suwanasopee et al. (2005) becomes -0.035 d/yr which is nearly identical to the sow trend found here. Contrarily, the NBA sow trend of Suwanasopee et al. (2005) becomes 0.013 piglets/yr, a value close to the opposite of the negative sow trend of -0.017 ± 0.005 piglets/yr found here for NBA.

Permanent environmental trends for sows were also negative for all traits, but significant only for WSI. The

favorable PED trend for WSI was -0.028 ± 0.011 d/yr ($p < 0.02$), and the unfavorable PED trends for litter traits were -0.015 ± 0.014 piglets/yr ($p < 0.29$) for NBA, -0.019 ± 0.013 kg/yr ($p < 0.17$) for LBW, -0.019 ± 0.022 piglets/yr ($p < 0.39$) for NPW, and -0.023 ± 0.013 kg/yr ($p < 0.09$) for LWV. Considering that several records per sow were likely used in the culling and selection process of multiparous sows, it is not surprising that sow permanent environmental effects showed the same pattern of trends as sow genetic effects.

Environmental trends expressed in terms of least squares solutions for FY over time were positive for all traits. Regression coefficients were 0.035 ± 0.060 d/yr ($p < 0.56$) for WSI, 0.165 ± 0.059 piglets/yr ($p < 0.01$) for NBA, 0.376 ± 0.084 kg/yr ($p < 0.0003$) for LBW, 0.086 ± 0.048 piglets/yr ($p < 0.08$) for NPW, and 1.121 ± 0.303 kg/yr ($p < 0.002$) for LWV. Trends of FY means over time are shown in Figure 4 for NBA and NPW, and Figure 5 for LBW and LWV. The lowest FY means for NBA and NPW in Figure 4 appear to have been due to lack of adaptation of daughters of imported boars to the hot and humid conditions in the farm at that time.

The positive environmental trends for litter trait means between 1989 and 2008 suggest that the level of nutrition, management, and health care of animals in this swine herd improved over time. The substantially larger regression estimates for environmental than for genetic trends suggest that sows chosen to remain in the herd based on superior phenotypic records for litter traits primarily reflected environmental rather than genetic effects. Thus, it would be advisable to implement a selection program based on predicted additive direct and maternal genetic values to improve the identification of superior replacement animals in this herd. If the selection goal continued to be the improvement of litter traits, then a multiple trait genetic evaluation involving all litter traits would be an appropriate alternative. A multiple trait system involving NBA, LBW, NPW, and LWV would increase the accuracy of prediction of all animals for all four traits simultaneously, thus increasing the accuracy of identification of superior animals for all traits and the likelihood of favorable genetic trends for all litter traits. If the selection program also included WSI, a single-trait analysis could be used. As indicated above, evaluation of WSI in a multiple trait system with litter traits would provide no advantage over a single trait analysis because of the low genetic correlations between WSI and litter traits estimated in this population. This new genetic evaluation system would require an accurate and timely data collection and data management system.

Although estimates of genetic parameters estimated here for WSI and litter traits were low, they were similar to values found in other swine populations in Thailand and in other countries. However, genetic trends were also low and mostly in the opposite direction to the goals of the selection

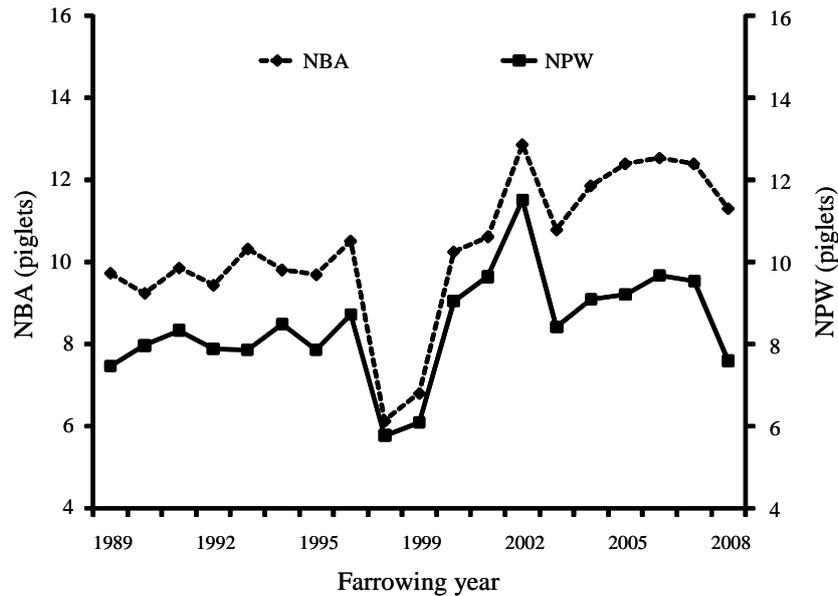


Figure 4. Least squares solutions for number of piglets born alive (NBA) and number of piglets at weaning (NPW) by farrowing year (FY). The regression coefficients of solutions on FY were 0.165 ± 0.059 piglets/yr ($p < 0.01$) for NBA, and 0.086 ± 0.048 piglets/yr ($p < 0.08$) for NPW.

program in the swine farm. Thus, the current phenotypic evaluation and selection program needs to be replaced with one based on multiple trait genetic predictions for litter traits and single trait genetic predictions for WSI. It would also be desirable if several farms joined efforts to create a larger breeding population in this region. This would increase the likelihood of identifying extraordinary animals, thus improving genetic trends in the extended population.

The proposed system could also serve as a model for future regional and national swine genetic improvement programs in Thailand.

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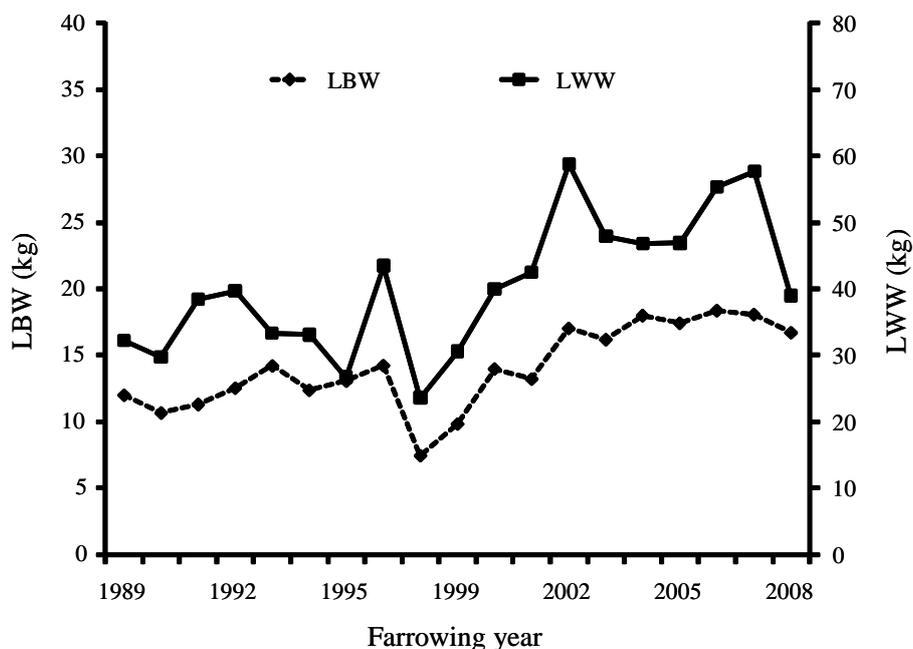


Figure 5. Least squares solutions for litter weight of live piglets at birth (LBW) and litter weight at weaning (LWW) by farrowing year (FY). The regression coefficients of solutions on FY were 0.376 ± 0.084 kg/yr ($p < 0.0003$) for LBW, and 1.121 ± 0.303 kg/yr ($p < 0.002$) for LWW.

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