

210: Genetic Analysis of Production Traits in Different Parities using Multiple Trait Animal Models in a Thai Landrace-Yorkshire Swine Population

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ABSTRACT

Number of piglets born alive (**NBA**) and litter birth weight (**LTBW**) in different parities of 2,124 Landrace (**L**), 724 Yorkshire (**Y**), 2,650 Landrace × Yorkshire (**LY**) and 4,332 Yorkshire × Landrace (**YL**) sows were analyzed using multiple trait animal models (**MTM**). All sows farrowed from 1989 to 2013 in a commercial swine population, and all of them had four parities. The **MTM** contained the fixed effects of farrowing year-season, additive genetic group of the sow, heterosis of the sow, heterosis of the litter and age at first farrowing, and the random effects of sow, boar, and residual. A **MTM** that considered each trait in each parity as a separate trait (**MTM-PAR**) was compared with a **MTM** that considered each trait measured in the first, second and the sum from the third to the last parity (**MTM-SPAR**) as three separate traits. The estimates of heritability from **MTM-PAR** ranged from 0.04 ± 0.01 (second parity) to 0.09 ± 0.02 (fourth parity) for **NBA**, 0.07 ± 0.02 (second parity) to 0.16 ± 0.02 (third parity) for **LTBW**. Estimates of heritabilities for **MTM-SPAR** were low for all traits, ranging from 0.04 ± 0.01 (first and second parity) to 0.09 ± 0.02 (third to last parity) for **NBA**, 0.06 ± 0.02 (second parity) to 0.08 ± 0.02 (third to last parity) for **LTBW**. Estimates of genetic correlations in **MTM-PAR** were high for **NBA** (0.50 ± 0.18 to 0.96 ± 0.02) and **LTBW** (0.72 ± 0.1 to 0.93 ± 0.07), except between **NBA** in the first parity with the second (0.29 ± 0.24) and in the fourth parity (0.50 ± 0.18). Estimates of genetic correlations for **MTM-SPAR** were low to moderate for **NBA** (0.11 ± 0.19 to 0.54 ± 0.21) and **LTBW** (0.12 ± 0.17 to 0.23 ± 0.18), but high between **LTBW** in the first and the second parities (0.83 ± 0.11). Genetic correlations for **NBA** and **LTBW** were higher for **MTM-PAR** than for **MTM-SPAR**. Results suggested that the **MTM** that treated each parity as a different trait should be used for genetic evaluation and selection for **NBA** and **LTBW** in this swine herd.

INTRODUCTION

Number of piglets born alive (**NBA**) and litter birth weight (**LTBW**) are economically important traits in commercial swine production, thus they are considered for selection in breeding programs. Values of these traits vary among animals and among parities within an animal. Genetic evaluation for these two traits has been frequently based on repeatability models. Alternatively, measurements of these traits in different parities could also be treated as different traits (multiple traits animal model) because of differences in the growth and development stages of sows in the production system (Oh et al., 2006). *Therefore, the objectives of this research was to estimate genetic parameters for NBA and LTBW in different parities using multiple trait animal models in a Thai Landrace-Yorkshire swine population.*

MATERIALS AND METHODS

Data, animals and traits. The dataset was obtained from a commercial swine farm in Northern Thailand (Lat: 18.478392, Long: 98.797586). Sow production records from the first to the fourth parity were included in the analyses. Each sow record contained identification number, breed group, sire, dam, birth date, farrowing date, weaning date, **NBA** and **LTBW** (n = 14,604). Sow records that contained missing, erroneous, or incomplete information were eliminated. In addition, gilts with their first farrowing recorded before 350 days or after 550 days were removed. After these edits, the final dataset contained 49,145 production records from 9,830 sows (1,359 boars) collected from 1989 to 2013.

Four breed groups of sows were included in the analysis: Landrace (L; n = 2,124), Yorkshire (Y; n = 724), Landrace × Yorkshire (LY; n = 2,650), and Yorkshire × Landrace (YL; n = 4,332). Purebred L and Y sows were the progeny of 640 sires (395 L and 245 Y) and 1,319 dams (895 L and 424 Y). Crossbred LY and YL sows were the progeny of 969 sires (608 L and 361 Y) and 2,674 dams (1,608 L and 1,066 Y). Lastly, 260 Duroc (D) boars were represented in the dataset as sires for the three-breed terminal cross. The production records were analyzed as **NBA** and **LTBW**.

Climate, nutrition and management. Seasons were classified as winter (November to February), summer (March to June) and rainy (July to October). All gilts and sows were kept in an open-house system. Boars were housed in barns equipped with an evaporative cooling system. Feed was provided twice a day to gilts and non-lactating sows (approximately 2.5 kg/d of feed with 16% crude protein and 3,200 to 3,500 kcal/kg). Nursing sows were fed four times a day (approximately 5 to 6 kg/d of feed with 17% to 18% crude protein and 4,060 kcal/kg). Gilts and sows were artificially inseminated twice (first insemination 12 hours after the onset of estrus; second insemination 12 hours later). Pregnant gilts and sows were housed in gestating stalls until 7 d before farrowing, when they were moved to farrowing pens. After weaning, sows were moved to mating stalls. Piglets were weaned when they reached 5 to 7 kg of body weight or 26 to 30 d of age.

Statistical analysis. Variance and covariance components were estimated using Restricted Maximum Likelihood (REML) procedures, and were computed using an Average Information Restricted Maximum Likelihood (AI-REML) algorithm with program ASREML. Two multiple-trait-animal-model analyses were performed. The first analysis treated each parity as a separate trait (**MTM-PAR**). The second analysis considered three traits: trait 1 (first-parity records), trait 2 (second-parity records), and trait 3 (sum from the third to the last parity; **MTM-SPAR**).

$$y = Xb + Z_{ga}g_a + Z_{gn}g_n + Z_a a_a + e$$
$$\begin{bmatrix} y \\ a_a \\ e \end{bmatrix} \sim \text{MVN} \left(\begin{bmatrix} Xb + Z_{ga}g_a + Z_{gn}g_n \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} Z_a G_a Z_a' + R & Z_a G_a & R \\ G_a Z_a' & G_a & 0 \\ R & 0 & R \end{bmatrix} \right)$$

The mixed model for each trait included fixed effects of contemporary group (farrowing year-season), additive genetic group of the sow, heterosis of the sow, heterosis of the litter and age at first farrowing. The random effects in the mixed model were sow, boar, and residual. The estimated variance and covariance components were used to compute heritabilities for all traits, and genetic and phenotypic correlations between traits.



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RESULTS AND DISCUSSION

Heritability estimates for **NBA** and **LTBW** from **MTM-PAR** and **MTM-SPAR** are shown in **Table 1** and **Table 2**, respectively. The estimates of heritability from **MTM-PAR** ranged from 0.04 ± 0.01 (second parity) to 0.09 ± 0.02 (fourth parity) for **NBA**, 0.07 ± 0.02 (second parity) to 0.16 ± 0.02 (third parity) for **LTBW**. Similarly, estimates of heritabilities for **MTM-SPAR** ranged from 0.04 ± 0.01 (first and second parity) to 0.09 ± 0.02 (third to last parity) for **NBA**, 0.06 ± 0.02 (second parity) to 0.08 ± 0.02 (third to last parity) for **LTBW**. The heritabilities estimated here for **NBA** and **LTBW** with **MTM-PAR** model were somewhat lower than those estimated in other countries (Oh et al., 2006; Fernández et al., 2008; Skorput et al., 2014). However, the estimates of heritability for NBA1 and NBA3+ in the **MTM-SPAR** were higher than those reported by Skorput et al. (2014). The levels of genetic variation found in this commercial herd indicated that these traits would respond to genetic selection.

Table 1 Estimates of heritabilities ($\pm$ SE; diagonal), genetic correlations ($\pm$ SE; above diagonal), and phenotypic correlations ($\pm$ SE; below diagonal) for number of piglets born alive (NBA) and litter birth weight (LTBW) using a four-trait model

Trait ^a	Parity			
	1	2	3	4
Number of piglets born alive (piglets)	NBA1	NBA2	NBA3	NBA4
NBA1	0.05 ± 0.01	0.29 ± 0.24	0.70 ± 0.16	0.50 ± 0.18
NBA2	0.09 ± 0.01	0.04 ± 0.01	0.86 ± 0.2	0.96 ± 0.02
NBA3	0.10 ± 0.01	0.09 ± 0.01	0.07 ± 0.02	0.94 ± 0.13
NBA4	0.12 ± 0.01	0.14 ± 0.01	0.15 ± 0.01	0.09 ± 0.02
Litter birth weight (kg)	LTBW1	LTBW2	LTBW3	LTBW4
LTBW1	0.10 ± 0.02	0.81 ± 0.12	0.92 ± 0.07	0.72 ± 0.01
LTBW2	0.16 ± 0.01	0.07 ± 0.02	0.93 ± 0.10	0.84 ± 0.12
LTBW3	0.17 ± 0.01	0.15 ± 0.01	0.16 ± 0.02	0.93 ± 0.07
LTBW4	0.13 ± 0.01	0.15 ± 0.01	0.21 ± 0.01	0.13 ± 0.02

Estimates of genetic correlations between first four parities from **MTM-PAR** ranged from 0.29 ± 0.24 to 0.94 ± 0.13 for **NBA** and 0.72 ± 0.01 to 0.93 ± 0.07 for **LTBW** (**Table 1**). Correlations estimated here for **NBA** using the **MTM-PAR** were within the range of estimates of genetic correlation between parities in Slovenia (0.67 to 0.99 ; Luković et al., 2004), Spain (0.49 ± 0.07 to 0.92 ± 0.04 ; Noguera et al., 2002) and The Netherlands (0.55 to 0.99 ; Hanenberg et al., 2001). Estimates of genetic correlations for **MTM-SPAR** were low to moderate for **NBA** (0.11 ± 0.19 to 0.54 ± 0.21) and **LTBW** (0.12 ± 0.17 to 0.23 ± 0.18), but high between **LTBW** in the first and the second parities (0.83 ± 0.11 ; **Table 2**). These positive correlations were somewhat lower than genetic correlation estimates in Spain (0.84 ± 0.05 ; Fernández et al., 2008). Additionally, genetic correlations obtained with **MTM-PAR** were higher than estimates obtained with **MTM-SPAR** for **NBA** and **LTBW**. Thus, if the selection target continued to be the improvement of **NBA** and **LTBW**, a multiple-trait genetic evaluation program that treated each parity as a separate trait would be appropriate.

Table 2 Estimates of heritabilities ($\pm$ SE; diagonal), genetic correlations ($\pm$ SE; above diagonal), and phenotypic correlations ($\pm$ SE; below diagonal) for number of piglets born alive (NBA) and litter birth weight (LTBW) using a three-trait model where the third trait represented sums of records from third to last parity

Trait ^a	NBA1	NBA2	NBA3+
Number of piglets born alive (piglets)			
NBA1	0.04 ± 0.01	0.54 ± 0.21	0.11 ± 0.19
NBA2	0.11 ± 0.01	0.04 ± 0.01	0.51 ± 0.18
NBA3+	0.05 ± 0.01	0.07 ± 0.01	0.09 ± 0.02
Litter birth weight (kg)	LTBW1	LTBW2	LTBW3+
LTBW1	0.08 ± 0.02	0.83 ± 0.11	0.12 ± 0.17
LTBW2	0.17 ± 0.01	0.07 ± 0.02	0.23 ± 0.18
LTBW3+	0.08 ± 0.01	0.08 ± 0.01	0.06 ± 0.02

^a NBA1 = number of piglets born alive in the first parity; NBA2 = number of piglets born alive in the second parity; NBA3+ = sum of number of piglets born alive from third to last parity; LBW1 = litter birth weight in the first parity; LBW2 = litter birth weight in the second parity; LBW3+ = sum of litter birth weight from third to last parity



FINAL REMARKS

- Estimates of heritability of **NBA** and **LTBW** indicated that enough additive genetic variation existed in this population for a genetic improvement program.
- Heritabilities and genetic correlations for **NBA** and **LTBW** from **MTM-PAR** were higher than from **MTM-SPAR**
- Genetic correlations between **NBA** and **LTBW** in the first, second and the sum from the third to the last parity indicated that **NBA** and **LTBW** from first-parity sows should be analyzed as a different trait from those of later parities

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