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RESEARCH ARTICLE

## Heritabilities and genetic and phenotypic correlations of litter uniformity and litter size in Large White sows



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ZHANG Tian\*, WANG Li-gang\*, SHI Hui-bi, YAN Hua, ZHANG Long-chao, LIU Xin, PU Lei, LIANG Jing, ZHANG Yue-bo, ZHAO Ke-bin, WANG Li-xian

Key Laboratory of Farm Animal Genetic Resources and Germplasm Innovation, Ministry of Agriculture/Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing 100193, P.R.China

### Abstract

Litter uniformity, which is usually represented by within-litter weight coefficient of variation at birth (CVB), could influence litter performance of sows and the profitability of pig enterprises. The objective of this study was to characterize CVB and its effect on other reproductive traits in Large White sows. Genetic parameters and genetic correlation of the reproductive traits, including CVB, within-litter weight coefficient of variation at three weeks (CVT), total number born (TNB), number born alive (NBA), number born dead (NBD), gestation length (GL), piglet mortality at birth ( $M_0$ ), piglet mortality at three weeks ( $M_3$ ), total litter weight at birth ( $TLW_0$ ), and total litter weight at three weeks ( $TLW_3$ ) were estimated for 2032 Large White litters. The effects of parity and classified litter size on CVB, CVT, TNB, NBA, NBD, GL,  $M_0$ ,  $M_3$ ,  $TLW_0$ , and  $TLW_3$  were also estimated. The heritabilities of these reproductive traits ranged from 0.06 to 0.17, with the lowest heritability for CVB and the highest heritability for  $TLW_0$ . Phenotypic and genetic correlations between these reproductive traits were low to highly positive and negative (ranging from  $-0.03$  to  $0.93$ , and  $-0.53$  to  $0.93$ , respectively). The genetic correlations between TNB and CVB, and between  $M_0$  and CVB were 0.32 and 0.29, respectively. In addition, CVB was significantly influenced by parity and litter size class ( $P < 0.05$ ). All the results suggest that piglet uniformity should be maintained in pig production practices and pig breeding programs.

**Keywords:** genetic parameter, litter uniformity, litter size, piglets mortality

## 1. Introduction

Over the past few decades, pig litter size at birth has sharply increased with the selection of prolificacy. However, both natal and post-natal mortality increased as litter size increased, resulting in substantial economic loss. Previous genetic studies have shown that pre-weaning piglet mortality is mainly affected by piglet litter uniformity and birth weight (Milligan *et al.* 2002; Quiniou *et al.* 2002; Damgaard *et al.* 2003).

Previous researches also showed that piglets with low birth weight have less chance of survival because of delayed

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ZHANG Tian, E-mail: [lfmsfe@126.com](mailto:lfmsfe@126.com); WANG Li-gang,  
E-mail: [wangligang01@caas.cn](mailto:wangligang01@caas.cn); Correspondence WANG Li-xian,  
Tel: +86-10-62816011, Fax: +86-10-62818771, E-mail: [iaswx@263.net](mailto:iaswx@263.net); ZHAO Ke-bin, Tel: +86-10-62816011, Fax: +86-10-62818771, E-mail: [iaszkb@sina.com](mailto:iaszkb@sina.com)

\*These authors contributed equally to this study.

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and lower colostrum intake (Milligan *et al.* 2002; Quiniou *et al.* 2002; Damgaard *et al.* 2003) and a disadvantage in competing with heavier littermates at the udder (Puppe and Tuchscherer 2000; Quesnel *et al.* 2012). In addition, piglets with low birth weight are physiologically compromised in terms of energy reserves and thermoregulatory capacity, which increases their susceptibility to chilling, starvation, and crushing by the sow compared to heavier piglets. Low litter uniformity (e.g., low within-litter weight coefficient of variation at birth (low CVB)) is associated with low piglet survival because litters with low uniformity contain more low birth weight piglets (Milligan *et al.* 2002; Quiniou *et al.* 2002). Moreover, decreased piglet survival with decreasing litter uniformity in birth weight is especially evident in litters with low mean birth weight (Milligan *et al.* 2002). In addition, piglets with poor uniformity require more complicated management. Wolter *et al.* (2002) reported that small pigs require more number of days than larger littermates to reach market weight, which increases the cost of feeding pigs. Furthermore, piglets with poor litter uniformity contain more low birth weight piglets and low birth weight has a detrimental effect on meat quality (Gondret *et al.* 2006).

To date, few studies have investigated litter uniformity in China, and the genetic correlations between CVB and common reproductive traits, such as total number born (TNB), number born alive (NBA), litter weight at birth (TLW<sub>0</sub>), and piglet mortality at birth (M<sub>0</sub>) remain unclear. The aim of the present study was to determine the heritabilities of CVB, TNB, NBA, M<sub>0</sub>, TLW<sub>0</sub>, within-litter coefficient of variation in piglet weight at three weeks (CVT), number born dead (NBD), litter weight at three weeks (TLW<sub>3</sub>), gestation length (GL), and piglet mortality at three weeks (M<sub>3</sub>). Phenotypic correlation and genetic correlation between all these 10 traits were also determined and the influence of parity and litter size on CVB was analyzed.

## 2. Results

### 2.1. Descriptive statistics and additive genetic variance of reproductive traits

Means and standard error (SE) of the traits investigated in the present study are presented in Table 1. The additive genetic variances of reproductive traits are presented in Table 2. The variation in additive genetic variances of these reproductive traits ranged from 0.000162 to 37.76972, with the minimum additive genetic variance for CVT and the maximum additive genetic variance for TLW<sub>3</sub>. The additive genetic variance for CVB was 0.000301.

**Table 1** Descriptive statistics for selected variables for 2032 litters

Variable <sup>1)</sup>	Mean	SE <sup>2)</sup>	Minimum	Maximum
TNB	11.25	0.08	3.00	23.00
NBA	10.17	0.07	2.00	20.00
NBD	0.84	0.04	0.00	11.00
CVB (%)	16.95	0.14	1.04	41.26
CVT (%)	18.61	0.16	0.68	58.78
M <sub>0</sub> (%)	7.12	0.26	0.00	84.62
M <sub>3</sub> (%)	19.05	0.40	0.00	92.86
TLW <sub>0</sub> (kg)	15.55	0.11	2.25	31.60
TLW <sub>3</sub> (kg)	51.58	0.42	4.87	120.17
GL (day)	114.59	0.04	108.00	130.00
MBW (kg)	1.56	0.006	0.84	2.86
MBWT (kg)	5.91	0.02	2.78	9.76

<sup>1)</sup> TNB, total number born; NBA, number born alive; NBD, number born dead; CVB, within-litter weight coefficient of variation at birth; CVT, within-litter weight coefficient of variation at three weeks; M<sub>0</sub>, piglet mortality at birth; M<sub>3</sub>, piglet mortality at three weeks; TLW<sub>0</sub>, total litter weight at birth; TLW<sub>3</sub>, total litter weight at three weeks; GL, gestation length; MBW, mean weight of live born piglets; MBWT, mean weight of piglets at three weeks. The same as below.

<sup>2)</sup> SE, standard error.

Data are mean values of the reproduction traits.

**Table 2** Additive variance of reproduction traits in population<sup>1)</sup>

Variable	$\sigma_a^2$	$\sigma_s^2$	$\sigma_{pe}^2$	$\sigma_e^2$	$\sigma_p^2$
TNB	1.5299543	0.3615692	0.2362585	9.5658161	11.6935981
NBA	1.3927853	0.2214475	0.3848581	8.4173729	10.4164638
NBD	0.2068375	0.0309596	0.0184100	1.9425277	2.1987348
M <sub>0</sub>	0.0009208	0.0000684	0.0001037	0.0089553	0.0916383
M <sub>3</sub>	0.0023832	0.0000045	0.0002847	0.0239240	0.0896061
CVB	0.0002991	0.0000116	0.0001382	0.0037896	0.0051385
CVT	0.0003752	0.0000129	0.0000067	0.0050174	0.0054122
TLW <sub>0</sub>	3.5456834	0.2561160	0.1866185	17.2596720	21.2480899
TLW <sub>3</sub>	36.5125864	3.8609713	9.0156943	300.6677910	340.0570430
GL	0.3156910	0.1351249	0.0000588	1.9280069	2.2788816

<sup>1)</sup>  $\sigma_a^2$ , additive genetic variance;  $\sigma_s^2$ , mating boar variance;  $\sigma_{pe}^2$ , permanent environment variance;  $\sigma_e^2$ , residual variance;  $\sigma_p^2$ , phenotypic variation.

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