

Genetic parameters for reproductive traits of VCN03 breed

Sang Van Le*, Pham Duy Pham, Hong Son Trinh

Thuy Phuong Pig Research Center, National Institute of Animal Science, Vietnam

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Abstract:

This study was conducted in Thuy Phuong Pig Research Center (TPPRC), Vietnam to determine the genetic parameters of four reproductive traits including numbers born alive (NBA), litter birth weight (LBW), number of weaned pigs (NW) and litter weaning weight (LWW). The reproductive performance of 254 sows of VCN03 breed from four generations between 2010 and 2017 was collected and used in this study. Data from NBA, LBW, NW and LWW were subjected to repeated-measures of ANOVA in PROC MIXED in SAS with four reproductive traits and generations as fixed factors. Data from heritabilities and genetics and phenotypic correlations were plotted using the ASReMl. It was concluded that the heritabilities of the four traits ranged from low to moderate, resulting from 0.134 to 0.267. The heritabilities of NBA, LWW, LBW and NW were 0.264, 0.267, 0.137 and 0.134, respectively. The genetic and phenotypic correlations among the four traits were moderate to high positive. The genetic correlations ranged from 0.467 to 0.991, with the highest estimate for the genetic correlation being between LBW and NW and the lowest estimate for the genetic correlation being between NBA and LWW. The genetic correlation between NBA and NW was 0.67, between NBA and LBW was 0.774, between LBW and LWW was 0.69 and between LWW and NW 0.51.

Keywords: genetic parameters, litter birth weight, litter weaning weight, number born alive, number weaned pigs.

Classification number: 3.1

Introduction

Reproductive traits are the major component in pig production, and genetic improvement is important in swines' breeding objective. Genetic improvement of sow productivity was mainly focused on NBA and NW [1]. However, an increase in NBA was associated with a decrease in LBW and survival [2]. In addition, low average piglet weight at birth led to an increase in mortality [3]. Therefore, to increase pig production via genetic improvement, the reproductive traits of sows such as LBW and LWW should be taken as main objectives in breeding programs. Furthermore, it is necessary to comprehend the knowledge of genetic parameters to accurately estimate breeding values, optimise breeding programs and predict genetic responses to economic selection [4].

Synthetic Duroc breed, namely VCN03, have been imported from PIC (Pig Improvement Company) in the United Kingdom to Vietnam since 1997. This breed has played an important role in a breeding structure in TPPRC as a final sire line in breeding with the objective of creating commercial crossbred pigs containing five different breeds. However, the potential use of the VCN03 breed to increase pig productivity in Vietnam has received little attention.

This study aims to obtain genetic parameters such as heritabilities and genetic as well as phenotypic correlations between reproductive traits including NBA, LBW, NW and LWW in the VCN03 breed.

Materials and methods

Data and animals

A total of 254 sows from the VCN03 breed in TPPRC's program were used to study genetic parameters for reproductive traits of sows including NBA, LBW, NW and LWW.

The data was recorded between 2010 and 2017, and each year was divided into two seasons (Spring-Summer season

*Corresponding author: Email: lesang86@gmail.com.

from February to July and Autumn-Winter season from August to January). All animals were raised in the same units and sows were farrowed by artificial insemination. The summary statistics for four traits and covariates used in this model are shown in Table 1.

Table 1. Factors included (✓) in the repeated animal models.

Factors	Type of factor	NBA	LBW	NW	LWW
Generation	F	✓	✓	✓	✓
Parity	F	✓	✓	✓	✓
Age of farrowing	F	✓			
Season	F	✓	✓	✓	✓
Year	F	✓	✓	✓	✓
Season * Year	F	✓	✓	✓	✓
Date of weaning	F				✓
Boar genotype	F		✓		✓
Animal	A	✓	✓	✓	✓
Permanent environment effect of sow	R	✓	✓	✓	✓
Residual effect	R	✓	✓	✓	✓

A = random animal additive genetic effect, R = random, F = fixed effect.

Analysis

Data from NBA, LBW, NW and LWW were subjected to repeated-measures of ANOVA in PROC MIXED in SAS, version 9.2 with four reproductive traits and generations as fixed factors. Data from heritabilities and genetics and phenotypic correlations were plotted using the ASReml procedure at the School of Rural and Environmental Science, UNE, Armidale, Australia.

The statistical models in the data analysis can be written as a repeated model:

$$Y = Xb + Z_1a + Z_2p + e$$

where, Y is the vector of observations, b is the vector of fixed effects that includes year, parity for NBA and herd and parity for NW, X is the incidence matrix of fixed effects, a is the vector of random additive genetic effects, Z_1 is the incidence matrix of random genetic effects, p is the vector of random permanent environmental effects, Z_2 is the incidence matrix of random permanent environmental effect and e is the vector of random residual effects.

Results and discussion

Reproductive performance traits

The descriptive statistics of this study with the least squares means and standard errors for traits are presented in Table 2.

Table 2. Estimated least squares means and standard errors of NBA, NW, LBW and LWW of VCN03 across parities.

Parity	NBA	NW	LBW	LWW
	LSM±SE	LSM±SE	LSM±SE	LSM±SE
1	8.81 ^b ±0.17	8.72 ^c ±0.16	13.39 ^a ±0.28	55.10 ^{cd} ±1.19
2	8.95 ^b ±0.18	8.82 ^{bc} ±0.18	13.70 ^a ±0.28	57.01 ^{bc} ±1.22
3	10.20 ^a ±0.2	9.86 ^a ±0.19	14.07 ^{ab} ±0.29	58.65 ^{ab} ±1.23
4	10.08 ^a ±0.22	9.59 ^a ±0.21	13.65 ^c ±0.32	60.30 ^a ±1.39
5	9.96 ^a ±0.24	9.04 ^{ab} ±0.22	14.37 ^a ±0.34	57.60 ^{bc} ±1.47
6	9.57 ^a ±0.26	8.65 ^{cd} ±0.25	14.12 ^a ±0.38	56.49 ^a ±1.61
7	8.32 ^b ±0.3	8.23 ^d ±0.28	13.54 ^a ±0.43	59.22 ^{ab} ±1.83
8	8.17 ^b ±0.38	8.05 ^d ±0.36	13.89 ^{bc} ±0.56	53.36 ^d ±2.39
9	6.33 ^c ±1.58	6.33 ^e ±1.49	-	-

The different letters such as a, b, c, d and e in the same column show the difference of value with the statistical significance $p < 0.05$.

The average NBA of VCN03 was 8.9 piglets per litter, ranging from 6.33 to 10.2 piglets per litter across the first nine parities. This result was similar to the study by [5], but it was higher than the reports by Luan and Linh (1988) [6], with 7.9 piglets per litter, and Doanh (1979) [7], with 7.8 piglets per litter. However, the NBA of VCN03 in this report was lower than the reports by Hung and Binh (2008) [8], with 10.61 piglets per litter, and Tholen, et al. (1996) [9], with 10.78 piglets per litter.

The NBA increased from the lowest at the first parity to the highest at the third parity, from 8.8 to 10.2 piglets per litter, varying from 9.57 to 10.2 piglets per litter from the third parity to the sixth parity and then, it decreased from the seventh to ninth parities from 8.32 to 6.33 piglets per litter. This changing pattern was in agreement with [4, 10]. The NBA from the third to sixth parities was significantly higher than in the first, second, seventh, eighth and ninth parities. These results agreed with the findings by [11, 12].

The NW ranged from 6.33 piglets per litter at the ninth parity to 9.59 piglets per litter at the third parity, and the average was 8.15 piglets per litter. This result was lower than the report by [8], with 9.72 piglets per litter, and [13], with 10.46 piglets per litter, but it was higher than the report

of 7.98 piglets per litter by [14]. Additionally, the effect of parities on NW was similar to the NBA with an increase from 8.72 piglets per litter at the first parity to 9.86 piglets per litter at the third parity. This significant effect of parity on NW in this study agreed with the report by [15].

The lower values in the NBA and NW of VCN03 could be explained by a number of factors such as high air temperatures, relative humidity and diseases. The high proportion of piglets that died during the nursing period was a result of being starved and overlain by the sows. Furthermore, the influence of heat and humidity and low lactational nutrition contributed to a direct effect on milk production of lactating sows. Another reason is that VCN03 was a sire line in the breeding program in which more selection was emphasised on growth traits.

The LBW and LWW per litter were 14.1 kg and 58.56 kg, respectively. The LBW per piglet was 1.56 kg, which is similar with LBW of other breeds in Vietnam [8, 11, 13, 14]. However, an average of 6.72 kg per piglets LBW of VCN03 on average of 22.6 weaning days was significantly higher than the reports by [8, 13].

The estimate of heritability for reproductive traits

The heritabilities with standard errors and variance components for reproductive traits of the VCN03 sows are presented in Table 3. The heritability of NBA was moderate, being 0.264. Previous studies have reported a large range in heritability for NBA (0.04 to 0.66). The result of this study is in agreement with previous studies [16-19]. This result was higher than the reports of [20-24]. In contrast, the heritability of NBA in this study was lower than the report of 0.66 by [25]. The moderate heritability of NBA in this study could be explained by a better control experimental population when compared to the use of field data in the previous studies.

Table 3. Heritabilities with standard errors and variance components for NBA, NW, LBW, and LWW of VCN03 breed.

	σ_A^2	σ_E^2	σ_P^2	$h^2 \pm SE$
NBA	2.192	6.098	8.290	0.264±0.056
LBW	0.002	0.012	0.014	0.137±0.044
NW	0.926	5.999	6.926	0.134±0.037
LWW	0.216	0.591	0.807	0.267±0.051

The estimated heritability for LBW was 0.137. This estimate is in agreement with that reported by [11, 26-28]. In contrast, Hermes, et al. (2000) [23], Kerr and Cameron (1995) [29] and Ferraz and Johnson (1993) [30]

found the heritability of LBW to be 0.08, 0.09 and 0.06, respectively. However, a high estimate of heritabilities with a range of 0.47-0.54 were reported by [16-18], which were higher than the estimated heritability of LBW in this study. Rydhmer, et al. (1992) [3] reported that an early weighing of the litter after birth is important, and delay in recording litter birth weight in field data might be the reason for lower heritabilities.

The estimate of heritability for NW was 0.134. This heritability is in agreement with that reported by [29, 31]. Higher mean estimates for NW found by [9, 17, 25] were 0.48, 0.25, and 0.3, respectively. In contrast, the result of this study is greater than the estimates reported by [4, 20, 21, 29], ranging from 0.03 to 0.1. The differences of heritability for NW among studies could be explained by the varied swine breeds and the research data.

The LWW recorded in this study was moderate heritability (0.267), which was in agreement with the estimates reported by [11, 18, 32, 33]. However, the result of this research's finding is smaller than the estimates reported by [34] for LWW (0.34), as well as the prediction of 0.38 reported by [25]. Additionally, a higher estimate for this trait (0.38) was found by [35]. The LWW in this study had a higher heritability in comparison with the estimates presented by previous studies [9, 14, 22, 24, 27].

Heritability is the proportion of phenotypic variance due to additive genetic effects. The more heritable a trait is, the more the observed variation is due to genetic rather than environmental effects. The heritabilities of NBA, NW, LBW and LWW in this study ranged from 13.5% to 26.5%. These results mean that the major difference between animals is due to environmental effects. Therefore, increasing the NBA and NW can be done through crossbreeding, especially crossbred dam, due to the benefit of heterosis. In addition, the creation of a good environment may be another solution to increase NBA and NW.

Although the effect of parities on heritability was not examined in this study, previous studies [23, 31] found that the heritabilities of reproductive traits were influenced by parities. The heritability for NBA in the first three parities was lower than these estimates in the fourth and fifth parities [14]. Hermes, et al. (2000) [23] reported that heritability for LBW in the first parity of Large White and Landrace was smaller than that in the second and third parities (0.08 as opposed to 0.22 and 0.20, respectively). Gilts' uterine capacity are smaller than those of multiparous sow. Therefore, this may have a restriction on the expression of their genetic potential in LBW [36]. The heritability

increased with parity number in some reports [9, 22], but not in other research [2, 22].

Genetic and phenotypic correlations for reproductive traits

Genetic and phenotypic correlations between reproductive traits of the VCN03 sows are shown in Table 4. The estimated values of genetic and phenotypic correlations between NBA and NW were positive at 0.627 and 0.45, respectively, indicating that survival is not a heritable trait. These estimates of correlations between NBA and NW were lower than the range of 0.8 to 0.96 reported by [11, 25, 27, 31, 33]. However, the correlations in this study were higher than 0.59 found in the Mong Cai breed [14], 0.48 in the Duroc breed [27] and 0.38 in the Yorkshire breed [33]. Furthermore, Bushman (2007) [34] reported that the genetic correlation between NBA and NW was negative (-0.38). The difference in genetic correlations among studies was the result of the use of field data and different breeds. Another reason for the differences between this study and the previous ones is that cross-fostering was not practiced in the previous populations but was a common management practice in this study.

Table 4. Genetic correlations with standard errors (above diagonal) and phenotypic correlations with standard errors (below diagonal) between reproduction traits.

	NBA	NW	LBW	LWW
NBA		0.627±0.134	0.774±0.090	0.467±0.165
NW	0.450±0.034		0.991±0.062	0.510±0.137
LBW	0.912±0.021	0.596±0.026		0.690±0.118
LWW	0.338±0.049	0.796±0.018	0.386±0.037	

The genetic correlation between NBA and LBW was high and positive (0.774). This genetic correlation is in agreement with that reported by [27] in the Large White breed. The larger and stronger correlation between NBA and LBW were found by [11] with 0.95 and by [25] with 0.92. However, these results contradicted the negative relationship between NBA and LBW at -0.38, -0.2 and -0.34 in reports of [23, 34, 37], respectively. The differences of genetic correlation between these two traits could be caused by the recording procedure of litter birth weight as well as the cross-fostering procedures.

The genetic correlation between NBA and LWW in this study is in agreement with [25, 27], who found a moderate

positive correlation between the two traits. Negative genetic correlations between NBA and LWW with -0.43, -0.14 and -0.18 in reports by [9, 23, 34], respectively, were much lower than those seen in this study (0.467). However, the genetic correlations between these two traits in reports by [17] with 1.13, [33] with 0.9 and [31] with 0.87 were higher than the result of this study. The difference could be attributed, in part, to the pooled estimates of the three breeds in the study of [17], two breeds in [33] and Mong Cai crosses in the study of [31] compared to purebred VCN03 in this study.

The estimated genetic correlation between NW and LBW in this study (0.99) was similar to those reported by previous studies [17, 27]. The positive genetic correlations between NW and LBW were also found in reports by [18] with 0.55, [27] with 0.48, and [25] with 0.64, but it was lower in comparison with the result of this study. The high positive genetic correlation between these two traits indicates that the higher LBW led to the higher number of piglets weaning.

The positive genetic correlation between LBW and LWW was revealed in this study and in other researches. The estimate of the genetic correlation between these two traits in this study was the same as the studies by [27, 38] in Large White at 0.69. Young, et al. (1978) [25] and Bereskin (1984) [33] showed much greater genetic correlations between LBW and LWW, ranging from 0.92 to 0.95, in comparison to the result of this study. However, this result was higher than the reports by [16, 23, 34]. The moderate to high genetic correlation between LBW and LWW indicate that the heavier litter weight at birth is associated with a higher litter weight at weaning.

The high positive genetic correlation was found between NW and LWW. The result of this study is as large as the genetic correlation between NW and LWW in the report of [25] at 0.51. However, the estimate of genetic correlations between these two traits were greater, ranging from 0.8 to 0.87 in the reports of previous studies by [18, 21, 34, 39, 40] in comparison with the result of this study. In addition, Siewerdt, et al. (1995) [27], Irvin and Swiger (1984) [17] and Bereskin (1987) [41] found a high genetic correlation between LWW and NW, ranging from 0.95 to 0.97. The magnitude of the genetic correlation between these two traits gives rise to the expectation that more piglets weaning per sow per year would result in a heavier LWW.

The genetic and phenotypic correlations of average piglet weight at birth (APWB) with other reproductive traits were not examined in this study, but Rydhmer, et al. (1992) [3] and Hermes, et al. (2000) [23] reported that

APWB had an unfavorable relationship with NBA; their genetic correlation ranged from -0.86 to -0.27. In addition, APWB had a favourable relationship with piglet mortality [3]. Therefore, increasing NBA by selection would lead to decreasing weight of piglet at birth and consequently, lead to low weaning rate.

Conclusions

The results of this study showed low heritabilities for LBW and NW, at 13.7% and 13.4%, respectively, while the heritabilities for NBA and LWW were moderate, at 26.4% and 26.7%, respectively. These low and moderate heritabilities showed potential for subsequent selection such as improvement of environment and crossbreeding program to increase the NBA and NW.

The genetic and phenotypic correlations among the four reproductive traits were moderate to high positive. The genetic correlations between NW and LBW account for 0.99, whilst the genetic correlations between NBA and LWW and between NW and LWW were the lowest with 0.467 and 0.51, respectively. The genetic correlation between NBA and NW and between LBW and LWW were 0.627 and 0.69, respectively. Moderate to high positive genetic associations between these reproductive traits suggest that increasing one trait by selection would lead to the improvement of other traits.

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