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# Estimation of genetic parameters for birth weight, preweaning mortality, and hot carcass weight of crossbred pigs<sup>1</sup>

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**ABSTRACT:** Genetic parameters for birth weight (BWT), preweaning mortality (PWM), and HCW were estimated for a crossbred pig population to determine if BWT could be used as an early predictor for later performances. Sire genetic effects for those traits were estimated to determine if early selection of purebred sires used in crossbreeding could be improved. Data were recorded from 1 commercial farm between 2008 and 2010. Data were from 24,376 crossbred pigs from Duroc sires and crossbred Large White × Landrace dams and included 24,376 BWT and PWM records and 13,029 HCW records. For the analysis, PWM was considered as a binary trait (0 for live or 1 for dead piglet at weaning). A multitrait threshold-linear animal model was used, with animal effect divided into sire genetic and dam effects; the dam effects included both genetic and environmental variation due to the absence of

pedigree information for crossbred dams. Fixed effects were sex and parity for all traits, contemporary groups for BWT and HCW, and age at slaughter as a linear covariable for HCW. Random effects were sire additive genetic, dam, litter, and residual effects for all traits and contemporary group for PWM. Heritability estimates were 0.04 for BWT, 0.02 for PWM, and 0.12 for HCW. The ratio between sire genetic and total estimated variances was 0.01 for BWT and PWM and 0.03 for HCW. Dam and litter variances explained, respectively, 14% and 15% of total variance for BWT, 2% and 10% for PWM, and 3% and 8% for HCW. Genetic correlations were -0.52 between BWT and PWM, 0.55 between BWT and HCW, and -0.13 between PWM and HCW. Selection of purebred sires for higher BWT of crossbreds may slightly improve survival until weaning and final market weight at the commercial level.

**Key words:** birth weight, crossbred, genetic parameter, performance, pig, threshold

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## INTRODUCTION

Economic gain in commercial swine production results mainly from the sale of pigs reaching full market value. Sow prolificacy has been emphasized in many breeding programs with the intent of increasing the number of pigs reaching full market value while maintaining the same number of sows within the herd. This selection objective has resulted in a significant in-

crease in the number of pigs born alive per litter. As a result of increased litter size, there has been a decrease in individual pig birth weight (**BWT**; Quiniou et al., 2002). Several studies have reported that piglet BWT is related to performances (e.g., piglet survival, growth rate, carcass composition, meat quality) and therefore is an important economic trait in pig production. Low BWT is related to a higher preweaning mortality (**PWM**), reduced weight gain from weaning to the finishing period, and a fatter carcass (Fix et al., 2010). Therefore, pigs with low BWT require more days on feed to reach market weight and potentially produce a lower-quality carcass (Gondret et al., 2005; Bérard et al., 2008; Rehfeldt et al., 2008; Fix et al., 2010). Economic loss associated with low BWT may be attributed to inefficient subsequent performance

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throughout the fattening period. However, selection for higher piglet BWT should be implemented carefully because of the negative relationship between BWT and litter size, which results in the necessity to select both traits simultaneously (Fix et al., 2010).

The ability to make genetic improvement at the commercial level depends heavily on selection programs implemented on purebred lines at the nucleus level. Therefore, the genetic influence of both purebred parents on the commercial performance of crossbred progeny must be determined. Piglet BWT and PWM are strongly influenced by maternal effects (Arango et al., 2006); therefore, genetic parameters for these traits have historically been estimated from dam components, although a genetic effect of the sire is possible (Knol et al., 2002; Hamann et al., 2004). Knowledge of paternal genetic effects and heritabilities for BWT and survival could have a large economic impact if the inclusion of a paternal component is beneficial to implement within a commercial pig breeding program (Hamann et al., 2004). Moreover, a better understanding of the paternal genetic effect on piglet traits may lead to the ability to identify sires at an earlier age.

The objective of this study was to estimate genetic parameters for BWT, PWM, and HCW for commercial crossbred pigs to assess the influence of paternal effects and to determine if BWT could be a good early predictor for subsequent performances.

## MATERIALS AND METHODS

### Data

Animal Care and Use Committee approval was not obtained for this study because data were obtained from an existing database.

Data were provided by Smithfield Premium Genetics (Rose Hill, NC). After discarding records with incomplete or inconsistent data, information recorded from 2008 through 2010 on 1 commercial farm was available for 24,376 crossbred pigs. Crossbred animals were produced from the mating of purebred Duroc boars with crossbred Large White × Landrace sows. Pedigree data were not available for crossbred dams.

A description of the data is shown in Table 1. Piglet BWT and PWM status (dead or alive) were available for the 24,376 animals. The piglet BWT was recorded within 24 h of birth on the commercial farm. Of those pigs, 13,029 had subsequent HCW records. Mean age at slaughter was  $192 \pm 12$  d. Pedigrees were traced back 2 generations, and a total of 26,136 animals and 2,016 litters were included. A total of 193 different sires and 1,671 dams had progeny with a recorded BWT and PWM status, and 191 sires and 1,639 dams had prog-

**Table 1.** Description of data

Item	Value
No. of records	24,376
No. of animals in pedigree	26,136
No. of litters	2,016
No. of dams	1,671
No. of sires	193
No. of contemporary groups	15
Parity	
Mean	3.54
SD	1.90
Age at slaughter, d	
Mean	192.37
SD	12.12

eny with HCW. Distributions of records by sire and dam family are shown in Tables 2 and 3, respectively. On average, each sire was mated with 8.7 dams, and each dam had 1.2 litters. Sows had records for  $\leq 10$  parities, but records for parities 7 through 10 (<7% of records) were grouped together. The mean number of parity was  $3.5 \pm 1.9$ . Among the 1671 dams, 1413 had pigs recorded in parity  $> 1$ . Contemporary groups (15) were defined on the basis of piglets born during the same year and month.

### Statistical Analysis

An animal model was used to estimate genetic parameters. To separate the animal additive genetic effects into sire and dam components as in Zumbach et al. (2007), a model with sire additive genetic effects and dam effects was considered. This allowed the estimation of sire genetic covariance based on their crossbred progeny. Moreover, this model was better adapted as the dam effect had to include both genetic and environmental variations due to the lack of pedigree information for the crossbred dams. The equation for the general multiple-trait model was

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{s} + \mathbf{U}\mathbf{d} + \mathbf{W}\mathbf{l} + \mathbf{Q}\mathbf{c} + \mathbf{e},$$

where  $\mathbf{y}$  is a vector of observations (BWT, PWM status, or HCW),  $\boldsymbol{\beta}$  is a vector of fixed effects,  $\mathbf{s}$  is a vector of additive genetic effects of the sire,  $\mathbf{d}$  is a vector of dam effects composed of dam additive genetic effects and dam environmental effects,  $\mathbf{l}$  is a vector of common litter effects assigned by litter of the dam and assumed to be uncorrelated,  $\mathbf{c}$  is a vector of random contemporary group effect,  $\mathbf{X}$ ,  $\mathbf{Z}$ ,  $\mathbf{U}$ ,  $\mathbf{Q}$ , and  $\mathbf{W}$  are incidence matrices that relate observations to effects, and  $\mathbf{e}$  is a vector of residual effects. For the observed traits, BWT and HCW were continuous, but PWM status was a binary trait (0 if the piglet was still alive at weaning or 1 if the piglet died before weaning).

Fixed effects were sex and parity number for all traits. Contemporary groups were fitted as a fixed effect

**Table 2.** Distribution of records by sire family for birth weight (BWT), preweaning mortality (PWM), and HCW

Trait	Mean	SD	Minimum	Maximum
BWT ( <i>n</i> = 193)	126.30	118.72	6	741
PWM ( <i>n</i> = 193)	126.30	118.72	6	741
HCW ( <i>n</i> = 191)	68.21	67.49	2	398

for BWT and HCW but as a random effect for PWM status to avoid the “extreme category problem” that would occur with contemporary groups with no dead piglets at weaning (Misztal et al., 1989). Age at slaughter was included as linear covariable for HCW only.

For all traits, sire additive genetic, dam, common litter, and residual effects were included as random effects. In this model, the animal additive effect is partitioned into sire additive genetic effect, dam additive genetic effect included in the dam effect, and Mendelian sampling included in the residuals. The variance of the sire genetic effects describes 1/4 of the total additive genetic variance and represents the genetic component of the model. The residual variance for the binary trait was fixed to 1. The (co)variance matrices were assumed to be

$$\text{Var} \begin{bmatrix} \mathbf{s}_1 \\ \mathbf{s}_2 \\ \mathbf{s}_3 \end{bmatrix} = \mathbf{A} \otimes \begin{bmatrix} \sigma_{s_1}^2 & \sigma_{s_1, s_2} & \sigma_{s_1, s_3} \\ & \sigma_{s_2}^2 & \sigma_{s_2, s_3} \\ & & \text{Symm} & \sigma_{s_3}^2 \end{bmatrix},$$

$$\text{Var} \begin{bmatrix} \mathbf{d}_1 \\ \mathbf{d}_2 \\ \mathbf{d}_3 \end{bmatrix} = \mathbf{I} \otimes \begin{bmatrix} \sigma_{d_1}^2 & \sigma_{d_1, d_2} & \sigma_{d_1, d_3} \\ & \sigma_{d_2}^2 & \sigma_{d_2, d_3} \\ & & \text{Symm} & \sigma_{d_3}^2 \end{bmatrix},$$

$$\text{Var} \begin{bmatrix} \mathbf{l}_1 \\ \mathbf{l}_2 \\ \mathbf{l}_3 \end{bmatrix} = \mathbf{I} \otimes \begin{bmatrix} \sigma_{l_1}^2 & 0 & 0 \\ & \sigma_{l_2}^2 & 0 \\ & & \text{Symm} & \sigma_{l_3}^2 \end{bmatrix},$$

$$\text{Var}[\mathbf{c}_2] = \mathbf{I} \otimes \sigma_{c_2}^2, \quad \text{Var} \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \\ \mathbf{e}_3 \end{bmatrix} = \mathbf{I} \otimes \begin{bmatrix} \sigma_{e_1}^2 & 0 & 0 \\ & \sigma_{e_2}^2 & 0 \\ & & \text{Symm} & \sigma_{e_3}^2 \end{bmatrix},$$

where  $\mathbf{A}$  is the additive relationship matrix and  $\mathbf{I}$  is an identity matrix; traits 1, 2, and 3 refer to BWT, PWM, and HCW, respectively.

Estimations of (co)variance components were obtained with a Gibbs sampling algorithm, using the THRGIBBSF90 program (Misztal et al., 2002; Montpellier, France) with flat priors for (co)variances. This program allows the estimation of (co)variance components and genetic parameters in threshold mixed models with combinations of categorical and continuous traits (Lee et al., 2002). The program POSTGIBBSF90 (Misztal et al., 2002; Montpellier, France) was used for post-Gibbs analysis. A single chain of 250,000 cycles with a burn-in of the first 50,000 iterations was run for the analysis. The stationary stage was confirmed by

**Table 3.** Distribution of records by dam family for birth weight (BWT), preweaning mortality (PWM), and HCW

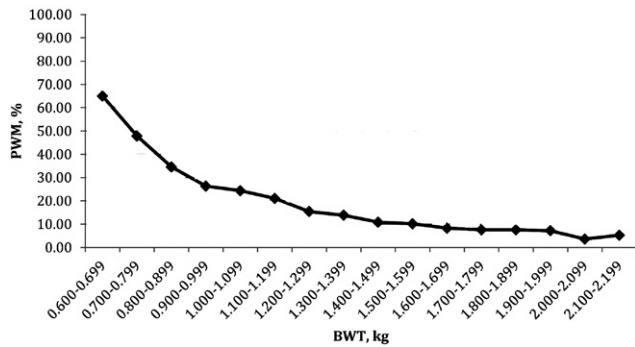
Trait	Mean	SD	Minimum	Maximum
BWT ( <i>n</i> = 1671)	14.59	7.19	1	61
PWM ( <i>n</i> = 1671)	14.59	7.19	1	61
HCW ( <i>n</i> = 1639)	7.95	4.63	1	36

graphical inspection of plots of sampled values vs. iterations. Every 10th sample was retained to compute mean and SE, obtained as SD of the posterior distribution. Starting values for (co)variance components were obtained from preliminary analyses using linear models implemented with restricted maximum likelihood and bivariate threshold-linear analyses.

## RESULTS AND DISCUSSION

The mean BWT of 1.40 kg with SD = 0.32 kg was similar to mean BWT reported in other studies (Grandinson et al., 2002; Knol et al., 2002; Arango et al., 2006; Fix et al., 2010). The mean HCW of 93.37 kg with a SD = 8.60 kg is in agreement with HCW reported by Fix et al. (2010) but is somewhat higher than the final weight reported by Zumbach et al. (2007) in similar crossbred populations. On average, litter had  $12.1 \pm 3.8$  piglets born alive. The PWM rate for all piglets was 16.99%, rising from 15.26% in parity 1 to 19.58% in parity 7 or later. The PWM rate of 16.99% is higher than the rate of 11.8% reported by Arango et al. (2006) for piglets that were alive after birth but is similar to PWM rates in other studies (e.g., Knol et al., 2002; Quiniou et al., 2002; Cecchinato et al., 2010). In this study, piglets from parities up to 10 were included, with 20% of piglets from parities higher than 5, whereas Arango et al. (2006) reported only 4% of piglets were represented for parities of  $\geq 5$ . Moreover, they found that PWM rate increased only for parities of  $\geq 7$ . Therefore, the higher PWM rate in this study could be the result of the larger proportion of piglets from later parities. Phenotypic correlations were  $-0.25$  between BWT and PWM,  $0.20$  between BWT and HCW, and  $-0.48$  between PWM and HCW. As expected, PWM rate decreased as BWT increased, as shown in Fig. 1.

Estimates of variance components for BWT, PWM, and HCW are in Table 4. Histograms of posterior distributions of estimated (co)variance components (figure not shown) were quasi-normal for all traits, and the Geweke test did not detect any lack of convergence. Estimated sire genetic variance was small for each trait (0.001 for BWT, 0.006 for PWM, and 2.028 for HCW). Estimated sire covariances were negative between BWT and PWM ( $-0.001$ ) and between PWM and HCW ( $-0.014$ ). Estimated sire covariance was positive between BWT and HCW (0.025). Estimated dam and litter variances were similar for BWT (0.015) and were higher than estimated sire variance. For



**Figure 1.** Relationship of preweaning mortality (PWM) rate and birth weight (BWT).

PWM, estimated litter variance was higher than estimated sire variance; moreover, both were higher than estimated dam variance. For HCW, estimated dam variance was on the same order as sire variance but lower than estimated litter variance. Estimated dam covariances had the same sign than estimated sire covariances. Estimated residual variances were high compared to other variance components for each trait (0.070 for BWT, 1.000 for PWM, and 56.228 for HCW). The relatively high residual variances could be due to the variation of the Mendelian sampling, which is not included directly in the model (Zumbach et al., 2007). Therefore, the Mendelian sampling becomes part of the residual and contributes to the increasing of the estimated residual variance.

Estimated heritability was 0.042 for BWT, 0.022 for PWM, and 0.124 for HCW (Table 5). For each trait, the estimated heritability was at the lower range of literature estimates, especially for HCW (e.g., Grandinson et al., 2002; Knol et al., 2002; Lund et al., 2002; Arango et al., 2006; Zumbach et al., 2007; Cecchinato et al., 2010). Comparison with literature estimates is difficult because of the different structures of data sets and different models. In many studies, mortality traits were modeled with linear models (van Arendonk et al., 1996; Knol et al., 2002; Mesa et al., 2006), which ignore the categorical nature of those traits. Also, animals in this study were crossbreds, and some traits in crossbred populations have lower heritabilities than in purebred populations (Lutaaya et al., 2001).

To determine if the sire component of each trait was useful for sire selection in a breeding program, the sire genetic effect was calculated as the ratio of estimated sire variance to total variance. Because the estimated sire genetic variance was small compared with total variance for each trait, the sire genetic effect (Table 5) was small (0.011 for BWT, 0.005 for PWM, and 0.031 for HCW). The larger effect of sire on HCW compared with BWT and PWM could be the result of declining maternal effect over time. Because piglet traits such as BWT and PWM are strongly influenced by maternal effects, most studies have usually included only maternal effects in analyses. However, Hamann et al. (2004)

**Table 4.** Estimates (SE) of (co)variances for sire genetic, contemporary group, dam, litter, and residual effects for birth weight (BWT), preweaning mortality (PWM), and HCW of crossbred pigs<sup>1</sup>

Effect	Trait	BWT	PWM	HCW
Sire genetic	BWT	0.001 (0.0004)	-0.001 (0.0009)	0.025 (0.0091)
	PWM		0.064 (0.0039)	-0.014 (0.0275)
	HCW			2.028 (0.4518)
Contemporary group	BWT			
	PWM		0.028 (0.0278)	
	HCW			
Dam	BWT	0.015 (0.0017)	-0.015 (0.0056)	0.081 (0.0346)
	PWM		0.039 (0.0143)	-0.077 (0.0502)
	HCW			2.209 (0.7247)
Litter	BWT	0.015 (0.0015)		
	PWM		0.102 (0.0165)	
	HCW			4.914 (0.7987)
Residual	BWT	0.070 (0.0007)		
	PWM		1.000 (0.0080)	
	HCW			56.228 (0.7522)

<sup>1</sup>Variances on diagonal; covariances above diagonal.

estimated genetic parameters for litter size, which is a trait strongly affected by maternal effects, as both sow and boar traits. They found that the sire had a small but significant effect on that trait.

The estimated dam effect was defined as the ratio between the estimated dam variance and the total variance (Table 5). Because of the lack of pedigree information for the crossbred dams, the dam effect is composed of genetic and environmental components. Estimated dam effects were higher than direct heritabilities for BWT (0.146) and for PWM (0.033) but lower for HCW (0.034). Also, estimated dam effects were higher than sire genetic effects for BWT and PWM but on the same order of values for HCW. As expected, the dam effect is more important than the sire genetic effect on early recorded traits, especially on BWT compared to PWM (van Arendonk et al., 1996; Grandinson et al., 2002; Knol et al., 2002; Lund et al., 2002; Arango et al., 2006). Moreover, when the dam effects for BWT and HCW are compared, it appears that the maternal influence is attenuated with age. For HCW, the dam effect is of the same magnitude as the sire genetic effect. However, the dam effect contains a genetic part and an environmental part. Therefore, either the sire genetic effect is higher than the dam genetic effect, or the dam effect is mainly genetic rather than environmental in later performances (Zumbach et al., 2007).

The common litter effect was defined as the ratio of estimated litter variance to total variance. The litter effect (Table 5) explained a large portion of total variance for piglet traits (0.143 for BWT, 0.086 for PWM). However, the common litter effect is lower for HCW (0.075) compared to heritability. Cecchinato et al. (2010) found that the litter variance was larger than the sire variance for

**Table 5.** Estimates (SE) of heritability, sire genetic, dam, and litter effects for birth weight (BWT), preweaning mortality (PWM), and HCW of crossbred pigs

Effect	BWT	PWM	HCW
Heritability	0.04 (0.015)	0.02 (0.013)	0.12 (0.024)
Sire genetic	0.01 (0.004)	0.01 (0.003)	0.03 (0.007)
Dam	0.15 (0.016)	0.03 (0.012)	0.03 (0.011)
Common litter	0.14 (0.015)	0.09 (0.014)	0.08 (0.012)

preweaning survival of piglets, which confirms that piglet survival is mainly affected by the litter effects. The smaller common litter effect for HCW compared with BWT indicates that effects common to littermates dissipate with age, like the dam effects. In the literature, the proportion of total variance explained by the litter effect at market age was 4% to 6% for backfat and 5% to 12% for weight per day of age and HCW (Lutaaya et al., 2001; Zumbach et al., 2007). Moreover, the birth litter explained a larger part of the total variance than the dam did for HCW, as found by Zumbach et al. (2007) with a similar model.

A common issue with the dam effect is cross-fostering and possible confounding of maternal and permanent environmental effects. For cross-fostered piglets, the maternal genetic effect is different before and after cross-fostering, BWT vs. PWM, for example. One strategy to deal with that is to include in the model the effect of the adoptive dam. However, in this study, the sow that raised the piglet is assumed to be the real mother of the piglet because of the lack of information available about the adoptive dam. In this case, the effect of the nurse dam for PWM and, to a smaller extent, for HCW is assumed to be part of the common litter effect. Knol et al. (2002) studied piglet survival with the genetic effect of the adoptive dam. They had issues with the estimation of genetic parameters (i.e., negative heritabilities) and convergence.

Piglet BWT was genetically correlated with PWM ( $-0.52 \pm 0.33$ ) and HCW ( $0.55 \pm 0.15$ ). The SE of these correlations were lower than their corresponding estimates and did not include zero, supporting the genetic association between traits. The genetic correlation between PWM and HCW was lower ( $-0.13 \pm 0.24$ ). The SE was greater than its corresponding correlation and did include zero. This indicates no genetic association between PWM and HCW. The greater SE may also be because fewer data were considered. Moreover, such a low correlation might partly be the result of the data structure because dead piglets at weaning had no HCW record. Phenotypic correlations had the same sign than genetic correlations but were lower between BWT and PWM ( $-0.25$ ) and between BWT and HCW ( $0.20$ ) and higher between PWM and HCW ( $-0.48$ ). The dam correlations were also favorable between BWT and PWM ( $-0.62 \pm 0.23$ ) and between BWT and HCW ( $0.45 \pm 0.19$ ). These correlations indicate that piglets from a dam providing favorable genes and

environment have a greater chance to survive until weaning and to reach a high final market weight. The dam correlation between PWM and HCW was low ( $-0.26 \pm 0.17$ ) but stronger than the sire genetic correlation.

The negative genetic correlation between BWT and PWM is in agreement with other studies (Grandinson et al., 2002; Arango et al., 2006; Roehe et al., 2010) and indicates a favorable genetic link between BWT and piglet survival until weaning. However, selection for higher BWT should be carefully undertaken; very high BWT may increase farrowing mortality because of other problems such as dystocia or prolonged parturition (Grandinson et al., 2002). As reported by Herring et al. (2010), BWT is positively correlated with final weight. Thus, BWT may be a good indicator of final market weight, as BWT is heritable and genetically correlated with HCW. Moreover, BWT is expressed earlier in life and is recorded earlier. Therefore, selection on BWT as a way to improve HCW may provide an opportunity to accelerate genetic progress.

The favorable genetic correlations of BWT with PWM and HCW indicate that selection for high BWT can improve survival until weaning and final market weight for crossbred pigs. Therefore, BWT could be used as an early predictor of subsequent performances. However, such selection should not be extreme because of the association between high BWT and higher farrowing mortality (Grandinson et al., 2002; Arango et al., 2006), which is not economically advantageous. Moreover, this situation is more common in sire lines with lower prolificacies, as was evident in this study. Indeed, fewer piglets per litter leads to heavier piglets and a higher frequency of dystocia, and that affects the survival for the whole litter (Ibáñez-Escriche et al., 2009). Therefore, a profitable selection on survival rate needs to balance survival and birth weight. A restricted selection index (Kempthorne and Nordskog, 1959) is often used in such situations where changes in 1 particular trait, such as BWT, are restricted to zero while selecting for correlated traits of direct interest, such as PWM and HCW.

Litter size at weaning is an important economic trait. Many breeding programs focus on selection to increase the number of piglets born per litter as a way to improve litter size at weaning (Grandinson et al., 2002). Selection index often puts large economic values on litter size and PWM (De Vries, 1989). However, selection to increase litter size at birth does not guarantee survival until weaning and larger litter at weaning. Indeed, litter size has a negative impact on preweaning survival and is linked to an increasing number of light piglets per litter and higher variations of piglet BWT within litter (van Arendonk et al., 1996; Milligan et al., 2002). High BWT variations within litter lead to competitive exclusion of light piglets from access to productive teats. Therefore,

differences in BWT between light and heavy piglets are often maintained or even increased until weaning, and smaller piglets at birth have lower survival rates, which has a negative economic impact for producers (Milligan et al., 2002). Therefore, litter size must not be forgotten in the selection goal because it has indirect influence on survival rate (Lund et al., 2002; Arango et al., 2005). However, selection for litter size should be coupled with maintaining a minimum threshold for BWT to avoid too light piglets with more risks of PWM.

Approximate reliabilities of sire breeding values for the 3 traits were computed with the following formula:

$$REL = \frac{ns^2}{(n-1)s^2 + 4},$$

where  $n$  is the total number of progeny of the sire and  $s^2$  is the ratio between the sire genetic variance and the total variance. The mean approximate reliabilities of sire breeding values were 0.21 (0.14) for BWT and PWM and 0.29 (0.18) for HCW. These mean approximate reliabilities are low because of low sire genetic variance. Also, reliability depends on the number of progeny of the sire. Therefore, sires with a large number of progeny will have breeding values with higher reliability. However, the number of progeny per sire is variable (Table 2), which leads to a low mean approximate reliability. Theoretically, reliabilities should be higher with an animal model because of the use of the genetic relationships among all animals instead of only relationships among sires. However, because this is a crossbred population, an animal model would be suboptimal.

The genetic effect of the sire on BWT, PWM, and HCW was low. Thus, on the basis of these results, direct selection of purebred sires may not be very efficient to improve those traits in crossbred populations. Subsequently, it may be easier to improve BWT from the maternal side than from the paternal side. However, BWT was genetically correlated with PWM and HCW. Therefore, selection on BWT could be a way to improve survival of piglets until weaning and final market weight. It could also improve the genetic progress as BWT is recorded earlier in the life of the animal. However, selection should be focused not only on improvement of BWT but also on an optimum combination of BWT, survival, and litter size.

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