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Evaluating service sire effects on genetic parameter estimation for reproductive traits in Duroc, Landrace and Yorkshire pig populations

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Introduction

Reproductive traits are fundamental components of productivity and profitability in commercial pig production systems, as they directly influence litter performance, sow longevity, and overall production efficiency. Despite their economic importance, most reproductive traits in pigs are characterized by low heritability and substantial environmental influence, which limits the rate of genetic improvement through selection (Rothschild, 1996). Consequently, improving the structure of genetic evaluation models and incorporating additional relevant sources of variation are essential to enhance the accuracy of breeding value prediction for these traits. Conventional genetic evaluation models for reproductive traits primarily focus on sow additive genetic and permanent environmental effects (Wolf and Wolfová, 2012). However, increasing evidence suggests that the service sire can also contribute to variation in dam's reproductive traits, through mechanisms associated with semen quality, sperm functionality, and fertilization efficiency (Cieleń and Sell-Kubiak, 2024). While the service sire effect is relatively modest compared with other sources of variation, ignoring it may lead to incomplete partitioning of phenotypic variance and result in suboptimal model fit. Therefore, the objective of this study was to estimate genetic parameters for five economically important reproductive traits, including total number born (TNB), number born alive (NBA), total number weaned (TNW), number of stillborn piglets (STB), and number of mummified piglets (MUM); as well as to quantify the contribution of the service sire effect to phenotypic and genetic variance in commercial pig populations.

Materials & Methods

Phenotypic data consisted of records from 5,883 Duroc (DD), 7,556 Landrace (LL), and 11,363 Yorkshire (YY) sows, with up to 16,005, 24,890, and 40,182 litter records per trait, respectively. A complete pedigree was available for 124,345, 160,962, and 325,808 animals in each breed, respectively. The datasets were provided by the Fujian Yongcheng Breeding Technology Group Corporation (Fuqing, Fujian Province, China), and were collected from three farms between 2009 and 2025. Quality control was performed individually for each trait, and inconsistent records were removed. The summary statistics for each trait, after quality control, are shown in Table 1.

Statistical Models. Two repeatability animal models were fitted for each trait to estimate genetic parameters and breeding values. The models were specified as follows:

$$\text{Model 1: } \mathbf{y} = \mathbf{Xb} + \mathbf{Z_a a} + \mathbf{Z_{pe} pe} + \mathbf{e}$$

$$\text{Model 2: } \mathbf{y} = \mathbf{Xb} + \mathbf{Z_a a} + \mathbf{Z_{pe} pe} + \mathbf{Z_{ss} ss} + \mathbf{e}$$

where $\mathbf{y}$ is the vector of observations; $\mathbf{b}$ is the vector of fixed effects, which included contemporary group (defined as farm–year–biweekly period), parity (levels 1 to >6), and age at first farrowing (AFF). For total number of weaned piglets (TNW), the number of piglets after cross-fostering was also considered as a fixed effect. The vectors $\mathbf{a}$, $\mathbf{pe}$, and $\mathbf{ss}$ represent the additive genetic, permanent environmental, and service sire effects, respectively; and $\mathbf{e}$ is the vector of residuals. Matrices $\mathbf{X}$, $\mathbf{Z_a}$, $\mathbf{Z_{pe}}$, and $\mathbf{Z_{ss}}$ are the corresponding incidence matrices for fixed, additive genetic, permanent environmental, and service sire effects, respectively.

Table 1. Summary statistics for total number born (TNB), number born alive (NBA), total number weaned (TNW), number of stillborn piglets (STB), and number of mummified piglets (MUM) in Duroc (DD), Landrace (LL) and Yorkshire (YY).

Breed	n1	n2	n3	Trait	Mean	SD	Min	Max
				TNB	9.1074	2.8936	1	20
				NBA	7.8266	2.6701	1	18
DD	16,005	5,883	426	TNW	6.3987	2.977	0	14
				STB	1.0341	1.3899	0	16
				MUM	0.3157	0.8174	0	13
				TNB	12.348	3.4728	1	32
				NBA	11.0279	3.1822	1	23
LL	24,890	7,556	304	TNW	10.3748	2.2672	0	17
				STB	1.146	1.5439	0	20
				MUM	0.2135	0.6616	0	14
				TNB	12.0826	3.1913	1	26
				NBA	10.7621	2.9476	1	22
YY	40,182	11,363	466	TNW	9.7526	2.7935	0	16
				STB	1.1065	1.5469	0	17
				MUM	0.2625	0.7773	0	18

n1: number of records; n2: number of sows; n3: number of services sires; Min: minimum; Max: maximum; Mean: phenotype mean; SD: standard deviation.

Models Comparison. Model comparison was performed using the Akaike Information Criterion (AIC) and the likelihood ratio test (LRT). The AIC was calculated as:

$$\text{AIC} = 2k - 2\ln(L),$$

where L is the maximized likelihood of the model, and $k$is the number of estimated parameters. Models with lower AIC values are preferred. The LRT statistics were computed as:

$$\text{LR} = -2[\ln(L_1) - \ln(L_2)],$$

where L_1 and L_2 denote the maximized likelihoods of the reduced (Model 1) and full (Model 2) models, respectively. The LR statistic was assumed to follow a chi-square distribution with degrees of freedom equal to the difference in the number of parameters between the two models.

Results & Discussion

Table 2 shows the differences in AIC between Model 2 (i.e., model with service sire effects) and Model 1 (i.e., model without service sire effects), along with the results of likelihood ratio tests for each trait and breed. Across most traits and breeds, inclusion of the service sire effect resulted in lower AIC values and significantly improved model fit. The only exception was TNW in DD, for

which the service sire effect was not statistically significant. Estimates of variance components and heritability for all traits across breeds are summarized in Table 3. Heritability estimates were generally low, ranging from 0.01 to 0.13 across traits and breeds. For TNB and NBA, heritability estimates were relatively higher than for other traits, with values ranging from 0.10 to 0.13 in DD, 0.09 to 0.12 in LL, and 0.08 to 0.10 in YY. In contrast, heritability estimates for TNW and MUM were consistently low across breeds, highlighting the substantial influence of non-genetic factors on these traits.

Table 2. Model comparison between repeatability models with and without service sire effects based on ΔAIC and likelihood ratio tests.

Trait	Breed	ΔAIC	LRT Sig.
MUM	DD	-11.38	***
	LL	-25.59	***
	YY	-3.03	*
NBA	DD	-131.36	***
	LL	-27.93	***
	YY	-357.11	***
STB	DD	-32.43	***
	LL	-34.72	***
	YY	-109.03	***
TNB	DD	-290.38	***
	LL	-21.45	***
	YY	-446.80	***
TNW	DD	0.49	ns
	LL	-24.15	***
	YY	-6.18	**

ΔAIC represents the difference in AIC between Model 2 and Model 1. Negative values indicate an improved model fit when including service sire effects. LRT Sig. denotes the significance of the likelihood ratio test: ns, not significant ($P > 0.05$); * $P < 0.05$; ** $P < 0.01$; ** $P < 0.001$.

The proportion of phenotypic variance attributable to service sire effects was small, accounting for less than 1% of the total variance for TNW and MUM and approximately 3 to 6% for TNB and NBA. Interestingly, the highest contributions of sire effects were observed in the YY breed. For STB, service sire effects explained approximately 1.0 to 1.3% of the phenotypic variance across breeds. Although modest in magnitude, these effects were sufficient to improve model fit in most cases. The lack of a significant service sire effect for TNW in DD might be explained by data structure limitations. From TNW records in DD, the coverage of service sires within contemporary groups was markedly lower than that observed for other traits and breeds, resulting in limited information to disentangle service sire effects from other sources of variation. Consistent with this speculation, the estimated service sire variance for TNW in DD was small and associated with a relatively large standard error (0.0008 ± 0.0007), indicating comparatively limited precision and instability of the estimate.

Table 3. Heritabilities and variance components estimated using the repeatability models including service sire effects.

Traits	Breed	σ_a^2	σ_{pe}^2	σ_{ss}^2	σ_e^2	h^2	$\frac{\sigma_{ss}^2}{\sigma_p^2}$(%)
TNB	DD	0.8690±0.1027	0.5540±0.0816	0.3769±0.0415	5.0098±0.0728	0.1276±0.0141	5.53
	LL	1.2058±0.1287	0.6203±0.0923	0.0706±0.0194	8.4731±0.0913	0.1163±0.0116	0.68
	YY	0.9302±0.0914	1.0526±0.0711	0.3710±0.0362	6.9196±0.0582	0.1003±0.0093	4.00
NBA	DD	0.6416±0.0754	0.3428±0.0621	0.1771±0.0243	4.0068±0.0597	0.1241±0.0137	3.43
	LL	0.7844±0.0934	0.4459±0.0712	0.0737±0.0179	6.9755±0.0757	0.0947±0.0107	0.89
	YY	0.6390±0.0685	0.7702±0.0556	0.2645±0.0270	5.8177±0.0493	0.0853±0.0087	3.53
TNW	DD	0.0087±0.0022	0.0015±0.0029	0.0008±0.0007	0.2400±0.0040	0.0345±0.0087	0.32
	LL	0.0072±0.0022	0.0090±0.0033	0.0042±0.0011	0.4791±0.0054	0.0145±0.0044	0.84
	YY	0.0053±0.0014	0.0057±0.0021	0.0012±0.0005	0.4210±0.0037	0.0121±0.0032	0.27
MUM	DD	0.0113±0.0032	0.0064±0.0043	0.0034±0.0011	0.4600±0.0063	0.0236±0.0066	0.70
	LL	0.0044±0.0013	0.0047±0.0019	0.0008±0.0004	0.3135±0.0033	0.0137±0.0040	0.26
	YY	0.0109±0.0018	0.0016±0.0019	0.0008±0.0004	0.3930±0.0032	0.0269±0.0043	0.19
STB	DD	0.0794±0.0153	0.0883±0.0160	0.0202±0.0045	1.3603±0.0188	0.0513±0.0096	1.30
	LL	0.1042±0.0143	0.0789±0.0127	0.0160±0.0037	1.5172±0.0160	0.0607±0.0080	0.93
	YY	0.1057±0.0112	0.0684±0.0097	0.0225±0.0033	1.5015±0.0122	0.0622±0.0063	1.33

Heritability (h^2), additive genetic variance (σ_a^2), permanent environment variance (σ_{pe}^2), service sire variance (σ_{ss}^2) and residual variance (σ_e^2) estimates are presented for each trait. In addition, the proportion of phenotypic variance attributable to service sire effects was calculated as $\frac{\sigma_{ss}^2}{\sigma_p^2}$. Values are reported as estimates ± standard errors.

Conclusions

Reproductive traits in DD, LL, and YY pig populations exhibited generally low heritability, reflecting the substantial contribution of non-genetic factors and the inherent difficulty of achieving rapid genetic improvement through selection. Inclusion of the service sire effect had minimal impact on estimates of genetic parameters, which remained highly consistent across models, but consistently reduced AIC values. The likelihood ratio test results suggested that the extended models (i.e., models including service sire effects) captured additional sources of variation that were not accounted for in conventional models. Consequently, despite its relatively small contribution to phenotypic variance, incorporating the service sire effect significantly improved overall model fit and may enhance the robustness and reliability of genetic evaluations for low-heritability reproductive traits in commercial DD, LL, and YY pig populations.

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