



Genetic analysis for farrowing rate and litter size for Landrace and Yorkshire sows in South China



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ABSTRACT

Farrowing rate (FR) and litter size (LS) are economically important traits that directly affect the number of weaned piglets per sow per year. This study aimed to estimate genetic parameters and calculate genetic trends for FR and LS at birth in herds of Landrace and Yorkshire sows in South China. We analyzed 16,451 Landrace sows with 58,091 observations and 33,953 Yorkshire sows with 101,486 observations for FR, and we analyzed 15,079 Landrace sows with 47,831 litters and 31,470 Yorkshire sows with 83,974 litters for LS traits. We used a single-trait threshold model to analyze FR. A joint multi-trait linear-threshold model was used to analyze three LS traits simultaneously: total number of piglets born (NBT), number of piglets born alive (NBA), and number of piglets born dead (NBD). Estimated heritability values for FR were 0.112 ± 0.012 in Landrace and 0.120 ± 0.010 in Yorkshire sows. For the three LS traits, the highest heritability was estimated for NBT, followed by NBA and NBD in both breeds, with values ranging from 0.044 ± 0.004 to 0.109 ± 0.008 in Landrace and from 0.039 ± 0.004 to 0.108 ± 0.007 in Yorkshire. Estimated correlations between NBT and NBA ranged from 0.861 ± 0.018 to 0.949 ± 0.010 in Landrace and from 0.895 ± 0.009 to 0.933 ± 0.009 in Yorkshire for random additive genetic effects, random permanent effects, and random service sire effects. Estimates of correlations between NBT and NBD ranged from -0.010 ± 0.092 to 0.353 ± 0.058 in Landrace and from 0.253 ± 0.065 to 0.516 ± 0.044 in Yorkshire. Estimates of correlations between NBA and NBD were not significantly different from 0 in either population, except for additive genetic effects in Yorkshire sows (0.267 ± 0.059). Among the genetic trends, NBT and NBA showed persistent improvements in both breeds, whereas NBD shows no apparent improvement in either population. Genetic trends for FR showed slight declines over time in both populations. The estimated genetic parameters suggest the possibility of improving these reproductive traits by selection. Our results confirm that the selection criterion for LS should be NBA rather than NBT. Despite its low effect, the effect of service sire should be included as a random effect in the statistical model. Finally, due to the genetic downtrend for FR, this trait should be included in future pig breeding goals in South China.

1. Introduction

Economic efficiency of swine production systems is directly related to reproductive performance. In recent decades, pig breeding programs have sought to increase the number of weaned piglets per sow per year (Imboonta et al., 2007), which is directly influenced by farrowing rate (FR) and litter size (LS) at weaning. Due to cross-fostering, however, it is difficult to obtain accurate records for LS at weaning. Owing to the positive genetic correlation between the number of piglets born and the number of piglets weaned, genetic gains in LS at weaning can be supported by selecting for LS at birth (Pires et al., 2000; Su et al., 2007; Ventura et al., 2015). Performing genetic analyses for FR and LS at birth can be very useful when seeking to increase the number of weaned

piglets per sow per year and the economic profits for pig breeding companies.

The LS at birth is usually recorded in terms of total number of piglets born (NBT), number of piglets born alive (NBA), and number of piglets born dead (NBD) in most pig breeding farms. Thus, we used these three traits to measure LS at birth in the present study. Most previous studies have treated piglet mortality as a continuous trait and ignored its categorical property. A better alternative to a traditional Gaussian linear model is to use a threshold model to account for the non-Gaussian distributions of the phenotypes, which should lead to better parameter estimates. However, to date, few studies have used a joint multi-trait linear-threshold model to investigate traits related to LS at birth.

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Table 1
Descriptive statistics for reproductive traits of Landrace (LL) and Yorkshire (YY) sows.

Trait ^a	Breed	No. of sows	No. of observations	Mean	SD	CV, %	Max	Min
FR	LL	16,451	58,091	0.823	0.381	46.294	1	0
NBT	LL	15,079	47,831	12.048	3.781	31.383	21	5
NBA	LL	15,079	47,831	10.897	3.673	33.707	20	4
NBD	LL	15,079	47,831	0.693	1.533	221.212	6	0
FR	YY	33,953	101,486	0.827	0.378	45.707	1	0
NBT	YY	31,470	83,974	12.528	4.085	32.607	23	5
NBA	YY	31,470	83,974	11.286	3.875	34.335	22	5
NBD	YY	31,470	83,974	0.786	1.632	207.634	6	0

^a FR = farrowing rate; NBT = total number of piglets born; NBA = number of piglets born alive; NBD = number of piglets born dead.

The FR can be defined as becoming pregnant from one insemination record and maintaining pregnancy until farrowing, according to Bloemhof et al. (2012). Because FR reflects whether an animal is farrowed or not in a particular insemination cycle at an individual level, this trait should be considered as a binary trait and should be investigated by using a threshold model.

Genetic parameter estimates from previous studies showed a high degree of variability. To a certain extent, these estimates reflected population-specific parameters related to population structures (Falconer and Mackay, 1996). China has the largest hog slaughter capacity in the world and predominates in pork producers and consumers (Cheng et al., 2011). Genetic parameters in the Chinese swine breeding industry should be obtained from the Chinese population because parameters obtained from other populations may deviate from the true values and may be unfavorable for Chinese swine breeding programs.

The aim of this study was to estimate variance components and genetic parameters for reproductive traits in Landrace and Yorkshire sows by using data from South China. For each breed, we applied a single-trait threshold model to estimate genetic variations for FR, followed by a joint multi-trait linear-threshold model to estimate genetic parameters for NBT, NBA, and NBD simultaneously.

2. Materials and methods

Animal Care and Use Committee approval was not obtained for this study because the data were obtained from existing databases of performance records.

2.1. Populations and data

Purebred Landrace and Yorkshire sows were analyzed. The typical sow feeding regimen of South China was used. Herds underwent similar procedures in mating, farrowing, and culling. After weaning at 21 days of age, sows were examined twice a day for estrus by using boar contact. In all herds, artificial insemination was applied 12 and 36 h after the first detection of estrus. Real-time ultrasound devices were used to detect pregnancy at 23–30 days after insemination. Pregnancy rates among sows ranged from 85% to 88%. Pregnant sows were transported from gestation units to farrowing houses ~5 to 10 days before the expected farrowing date. After weaning their piglets at 21 days of age, sows were either returned to the central unit to be mated for the next reproductive cycle or sent to culling. Thermometers were installed to ensure comfortable temperature for pigs in each kind of house. Curtains and suction fans were used together to cool animals on hot summer days.

Data were collected from six nuclear farms of Landrace and Yorkshire sows in South China from January 2006 to April 2016. Pedigrees for sows were traced back three generations. Yang and Su (2016) and Zanella et al. (2016) found no differences for genetic estimations in pigs when using complete pedigrees and only three generations. All mating took place by artificial insemination. Sows ranged in parity from 1 to 8.

Litter records at farrowing were available for NBT, NBA, and NBD. A piglet was defined as being born dead when it was found dead behind the sow at or immediately after farrowing. The NBD did not include mummified piglets. As NBT included mummified piglets, this trait was not always equal to, and sometimes was larger than, NBA plus NBD. The NBT, NBA, and NBD were recorded before cross-fostering was assigned and, therefore, were real numbers for each sow under analysis for LS at birth. The NBD showed a strong asymmetrical distribution. For Landrace sows, NBD was 0 for ~68.6%, 1 for 16.0%, 2 for 7.2%, and 3 or more for 8.3% of litters. For Yorkshire sows, NBD was 0 for 65.5%, 1 for 16.4%, 2 for 8.5%, and 3 or more for 9.6% of litters. Thus, NBD was treated as a categorical trait with four categories, as defined above, similarly to Arango et al. (2005).

For each first insemination record per cycle, the following information was available: sow identification number, line, date of birth, farm, parity, date of first insemination in that specific cycle, service sire, service sire breed, and FR. The FR was a binary trait, defined as 1 if the first insemination resulted in a pregnancy and the NBT from the first insemination was at least 1, and 0 otherwise. Records of reproductive performance were summarized for Landrace and Yorkshire sows. The structure of the dataset is shown in Table 1.

2.2. Statistical analysis

Genetic analyses for the aforementioned reproductive traits were performed for Landrace and Yorkshire sows using the following models.

2.2.1. Single-trait threshold model for farrowing rate

To estimate variance components for FR, the following repeatability model was used:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}\boldsymbol{\alpha} + \mathbf{Wp} + \mathbf{Us} + \mathbf{e} \quad (1)$$

where \mathbf{y} is a vector of liabilities to FR. Vector \mathbf{b} represents fixed effects, including sow line (Danish or American; 1 or 2), farm (1–6), insemination year (2006–2016), insemination month (1–12), parity (1–8), and service sire breed (Danish or American, Landrace or Yorkshire; 1–4). Vectors $\boldsymbol{\alpha}$, \mathbf{p} , \mathbf{s} , and \mathbf{e} represent random animal genetic effects, random permanent nongenetic effects, random service sire effects, and random residual effects, respectively. \mathbf{X} , \mathbf{Z} , \mathbf{W} , and \mathbf{U} are incidence matrices associating vectors \mathbf{b} , $\boldsymbol{\alpha}$, \mathbf{p} , and \mathbf{s} , respectively, with vector \mathbf{y} .

Variances were defined as follows:

$$\text{Var} \begin{bmatrix} \boldsymbol{\alpha} \\ \mathbf{p} \\ \mathbf{s} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma_a^2 & 0 & 0 & 0 \\ 0 & \mathbf{I}_{pe}\sigma_{pe}^2 & 0 & 0 \\ 0 & 0 & \mathbf{I}_s\sigma_s^2 & 0 \\ 0 & 0 & 0 & \mathbf{I}_e\sigma_e^2 \end{bmatrix}$$

where \mathbf{A} is the additive relationship matrix; \mathbf{I}_{pe} , \mathbf{I}_s , and \mathbf{I}_e are identity matrices; and σ_a^2 , σ_{pe}^2 , σ_s^2 , and σ_e^2 are animal additive genetic, permanent environmental, service sire, and residual variances, respectively.

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