RESEARCH ARTICLE

Genetic parameters and trends for production and reproduction traits of a Landrace herd in China

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Abstract

The objectives of this study were to estimate the genetic parameters and the breeding progress in a Landrace herd in China, and to predict the potential benefits by applying new breeding technology. Hereby, the performance records from a Landrace swine herd in China, composing over 33 000 pigs born between 2001 and 2013, were collected on six economically important traits, i.e., average daily gain between 30–100 kg (ADG), adjusted backfat thickness at 100 kg (BF), adjusted days to 30 kg (D30), adjusted days to 100 kg (D100), number born alive (NBA), and total number born (TNB). The genetic parameters were estimated by restricted maximum likelihood *via* DMU, and realized genetic trends were analyzed. Based on the real population structure and genetic parameters obtained from this herd, the potential genetic trends by applying genomic selection (GS) were predicted *via* a computer simulation study. Results showed that the heritability estimates in this Landrace herd were 0.55 (0.02), 0.42 (0.01), and 0.12 (0.01), for BF, D100, and TNB, respectively. Favorable genetic trends were obtained for D100, BF, and TNB due to direct selection, for ADG and NBA due to indirect selection. Long-term selection against D100 did not improve D30, though they are highly genetically correlated (0.64). Appling GS in such a swine herd, the genetic gain can be increased by 25%, or even larger for traits with low heritability or individuals without phenotypes before selection. It can be concluded that conventional breeding strategy was effective in the herd studied, while applying GS is promising and hence the road ahead in swine breeding.

Keywords: genetic parameter, genomic selection, swine, genetic trend

1. Introduction

Reliably estimated variance components are critically important in animal breeding practice. Estimates of heritability or environmental effects are a function of variance components and are population specific (Falconer and Mackay 1996). Such as the heritability of reproduction traits is ~0.1 in most population (Roehe and Kennedy 1995; Kapell *et al.* 2011), while it is ~0.2 in several cases (Banville *et al.* 2014; Hsu and Johnson 2014; Skorput *et al.* 2014). Hence, population parameter estimates are essential in an efficient breeding system.

Genetic trend can be expected in an effectively organized breeding system after long-term selection. Since the meat production is the main aim in pig industry, production and

reproduction traits, such as days to 100 kg and litter size, were intensively selected during the past decades in most pig breeding herds to pursue a quick genetic changes. For example, genetic advance on the days to 100 kg is ~–1.0 d yr^{-1} for Duroc, during the past 30 years in Canada according to the annual report of Canadian Center for Swine Improvement (CCSI, http://www.ccsi.ca/). While, in China, the genetic change for this trait is ~–0.5 d yr^{-1} for Duroc during the past five years according to the report from the Center of National Swine Genetic Evaluation of China (CNSGE, http://www.cnsge.org.cn/). Hence, genetic trends can be variable in different regions and in different breeding farms.

The recent development of high-throughput genotyping technology for almost all livestock species has facilitated the implementation of genomic selection (GS) (Meuwissen *et al.* 2001; Goddard and Hayes 2009; Zhang *et al.* 2011) in these species. Due to the promising features of GS, it has been widely implemented in national and international dairy cattle genetic evaluation (Harris and Montgomerie 2009; Hayes *et al.* 2009; VanRaden *et al.* 2009). In the industries of swine and other livestock species, applying GS is frequently referred to, however, the performance of GS should be carefully evaluated before implemented (Van Eenennaam *et al.* 2014).

In the swine breeding industry of China, genetic parameters obtained from literatures or other populations are used in genetic evaluation of many breeding herds, which would be misleading if the parameters used deviate much from their true values. Along with the developing of massive factory pig breeding farms, the increasing in the volume of breeding records are quick and enable variance component estimation within such populations. Additionally, the genomic selection breeding technology is going to be suggestively applied to pig breeding herds with an urgent need on the assessing of the relative performances of such technique.

Hence, the objectives of this study are: by analyzing the dataset from a representative breeding herd in China, (1) to estimate the phenotypic and genetic parameters of six economically important traits; (2) to assess the realized genetic trend in this herd; and (3) to predict the potential genetic trend assuming GS applied in such a herd. Phenotypic/genetic parameters and genetic trends were analyzed based on the real dataset including over 33 000 records (ranged from 33 500 for backfat thickness to 19 981 for total number born), then computer simulation based on the real population structure and genetic parameters from this herd were conducted to assess the potential advantages of applying GS in such a breeding system. The current status and potential advantages of applying new breeding methods in the Chinese swine breeding herds were discussed.

2. Results

2.1. Data summary

There are four production traits and two reproduction traits analyzed in the present study. Means, standard deviations, number of recorders per trait, and minimum and maximum for each production and reproduction trait are shown in Table 1. Most individuals were recorded on all traits within trait group. For the production traits, the number of records in each year ranged from 884 in 2002 to 5 219 in 2012 with average of 2 798 records per year, while for reproduction traits, it ranged from 539 in 2003 to 3 152 in 2009 with average of 1 851 records per year.

2.2. Heritability and correlations

The estimated heritability and correlations are shown in Table 2. The heritability for the three selected traits, adjusted backfat thickness (BF), adjusted days to 100 kg (D100), and total number born (TNB), were 0.55, 0.42, and 0.12, respectively. And were 0.34, 0.33, and 0.10, for average daily gain (ADG), adjusted days to 30 kg (D30), and number born alive (NBA), respectively. D100 is highly genetically correlated with ADG (–0.72) and D30 (0.64), while the genetic correlation between other production traits are low (Table 2). TNB is highly correlated with NBA (0.98).

2.3. Realized genetic trends

Genetic trends for production traits from 2002 to 2013, and reproduction traits from 2000 to 2012 are shown in Fig. 1. The three target traits selected during the past decade, D100, BF, and TNB, showed a persistent improvement with the amount of +6.87 d, +1.40 mm, and 1.01 piglets, respectively (Fig. 1-B, D, and E). And the annual genetic trends were –0.63 d yr^{-1}, –0.13 mm yr^{-1}, and +0.08 piglets litter^{-1} yr^{-1}, for D100, BF, and TNB, respectively. In addition, ADG and NBA were continuously improved with an average

Table 1 Phenotypeic parameters for reproductive and growing traits in the Landrace herd

Trait[1]	*n*	Mean	SD	Min	Max	Median
ADG	32 359	840.84	84.47	523.44	1 178.45	838.02
BF	33 462	13.96	2.22	7.10	22.88	13.79
D30	32 439	72.90	7.18	44.27	101.42	72.88
D100	33 500	156.99	9.98	120.42	197.02	156.34
TNB	19 981	11.04	3.02	1	20	11
NBA	19 985	10.12	3.04	0	20	10

[1] The traits are average daily gain from 30 to 100 kg (ADG), backfat thickness at 100 kg (BF), days to 30 kg (D30), and days to 100 kg (D100), total number born (TNB), and number born alive (NBA). The same as below.