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Genetic parameter estimates for selected type traits and milk production traits of Holstein cattle in southern China

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Abstract: Phenotypic and genetic parameters among udder traits (udder depth, UD; median suspensory line, MS; fore udder attachment, FUA; rear udder height, RUH; rear udder width, RUW), final score (FS), and milk production traits (305-day milk yield, 305 DM; 305-day milk-fat yield, 305 DF; 305-day milk-protein yield, 305 DP) were estimated using a derivative-free restricted maximum likelihood procedure with an animal model. The results showed that heritability estimates for selected traits ranged from 0.11 to 0.24. Strong positive genetic correlations were observed for MS, RUH, and RUW with FS (0.42–0.72). A positive genetic relationship was also estimated between MS and 305 DM (0.79). The genetic correlation between UD and 305 DM was –0.20. Positive genetic correlations were found between RUW and milk production traits (0.44–0.89). RUH also had positive genetic relationships with 305 DM (0.27) and 305 DF (0.16). Moderate positive genetic correlations were estimated between FS and milk production traits (0.25–0.35). The genetic parameters calculated from field records will provide valuable information for genetic improvement in type and milk production traits of Holstein cattle in southern China.

Key words: Dairy cattle, udder traits, milk production traits, genetic parameter

1. Introduction

Chinese Holstein dairy cattle, which originated from the upgrading of Holstein to Chinese yellow cattle, have a complicated genetic background (1). They have been raised in southern China for more than 60 years, and they have adapted to the hot and humid climate in southern China. Breeders were interested in udder traits because of their influence on the applicability of mechanical milking (2), udder health (3), and milk yield (4). Moreover, final score (FS) and udder traits have had strong relationships with functional survival (5,6). So far, the genetic parameters among udder traits, FS, and milk production traits have been reported for some breeds of dairy cattle (7–10). However, these parameters might be different in different dairy cattle breeds (11). Accurate genetic parameter estimates of selected traits would be beneficial for organizing a genetic improvement program. The literature on genetic parameters of udder traits, FS, and milk production traits of Holstein cattle in southern China is scarce (12). Therefore, the objective of this study was to estimate the genetic and phenotypic parameters of selected udder traits, FS, and milk production traits of Holstein cattle in southern China.

2. Materials and methods

All of the data were collected from 2 Holstein herds in the city of Wuhan participating in the Chinese National Dairy Herd Improvement (DHI) program with animal feed for total mixed ration. Wuhan is located in the center of Hubei Province, southern China. The altitude is about 200 m above sea level and the air temperature, rainfall, relative humidity, sunlight length, and frost-free period annually averaged 18 °C (ranging from –4 °C to 39 °C), 1200 mm, 85%, 2000 h, and 260 days, respectively. Linear type traits were evaluated using the guidelines of the China Holstein Association and 971 records were collected during 2006 and 2007 (scored on a scale from 1 to 9 points). Milk production data came from DHI records of 971 cows in their first 3 lactations from 2001 to 2007. All the linear type traits were identified by 1 classifier,

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and the pedigree data information were traced back more than 5 generations. The fixed effects of selected type traits were analyzed using the general linear model procedure (SAS 8.1). The effects of linear type traits included in the models were herd, year, lactation months, and parity at classification. The fixed effects of milk production traits were herd-year-season and parity. The (co)variance components and genetic parameters were estimated using the MTDFREML program of Boldman et al. (13). Heritabilities were estimated using single trait analyses, and genetic and phenotypic correlations were analyzed using a bivariate animal model. The following model was used to analyze the data of all traits: $y = \mathbf{X}b + \mathbf{Z}a + e$, where y is a vector of the observations, b is a vector of the fixed effects associated with matrix **X**, a is a vector of the direct genetic effect associated with matrix **Z**, and e is a vector of residual effect.

3. Results

The overall means and standard deviations (SDs) of linear udder traits (udder depth, UD; median suspensory line, MS; fore udder attachment, FUA; rear udder height, RUH; rear udder width, RUW), FS, and milk production traits (305-day milk yield, 305 DM; 305-day milk-fat yield, 305 DF; 305-day milk-protein yield, 305 DP) are presented in Tables 1 and 2. A structure model and a significance test of effects used to analyze selected type traits are showed in Table 3. The results of the variance analysis indicated that herd, year, lactation month, and parity at classification were important sources of variation for the selected type traits. The parameters among the selected type traits and production traits of Holstein cattle in southern China are presented in Table 4. Generally the heritabilities estimation of all milk production traits measured ranged moderately from 0.21 to 0.24. The heritability estimations of UD, MS,

Table 1. Descriptive statistics of selected type traits of Holstein cattle in southern China.

Items	1	9	Number	Mean	SD
UD	Shallow	Deep	971	5.65	2.12
MS	Shallow	Deep	971	5.67	1.96
FUA	Weak	Strong	971	5.74	2.11
RUH	Short	High	971	5.84	1.61
RUW	Narrow	Wide	971	4.58	1.22
FS	–	–	971	79.2	2.67

UD = Udder depth, MS = median suspensory line, FUA = fore udder attachment, RUH = rear udder height, RUW = rear udder width, and FS = final score.

Table 2. Descriptive statistics of milk production traits in different lactations of Holstein cattle in southern China.

Items	Parity	Number	Mean	SD
305 DM, kg	1	971	6353	1142
	2	971	6826	1486
	3	971	7066	1582
305 DF, kg	1	971	212	46
	2	971	236	53
	3	971	251	66
305 DP, kg	1	971	190	34
	2	971	206	44
	3	971	212	46

305 DM = 305-day milk yield, 305 DF = 305-day milk-fat yield, and 305 DP = 305-day milk-protein yield.

Table 3. Structure model and significance test of effects on selected type traits of Holstein cattle in southern China.

Traits	Herd	Year	Lactation month	Parity
UD	ns	*	*	**
MS	*	ns	**	**
FUA	**	**	ns	**
RUH	*	**	**	**
RUW	**	**	**	**
FS	ns	**	**	**

UD = Udder depth, MS = median suspensory line, FUA = fore udder attachment, RUH = rear udder height, RUW = rear udder width, and FS = final score.
ns = P > 0.05, * = P < 0.05, and ** = P < 0.01.

Table 4. Parameter estimates among selected type traits and production traits of Holstein cattle in southern China.

Traits	305 DM	305 DF	305 DP	UD	MS	FUA	RUH	RUW	FS
305 DM	0.23 (0.03)	0.82 (0.03)	0.95 (0.03)	−0.15 (0.05)	0.10 (0.03)	−0.07 (0.03)	0.02 (0.02)	0.16 (0.06)	0.12 (0.03)
305 DF	0.77 (0.04)	0.21 (0.03)	0.83 (0.03)	−0.09 (0.04)	0.05 (0.02)	−0.03 (0.01)	0.07 (0.04)	0.16 (0.06)	0.15 (0.05)
305 DP	0.89 (0.01)	0.83 (0.03)	0.24 (0.03)	−0.16 (0.05)	0.05 (0.03)	−0.06 (0.04)	0.02 (0.01)	0.18 (0.04)	0.15 (0.06)
UD	−0.20 (0.04)	−0.01 (0.04)	0.06 (0.05)	0.11 (0.06)	0.03 (0.02)	0.40 (0.10)	0.07 (0.03)	−0.08 (0.04)	0.10 (0.02)
MS	0.79 (0.05)	0.09 (0.02)	−0.06 (0.02)	0.01 (0.01)	0.16 (0.07)	−0.01 (0.01)	0.085 (0.02)	0.16 (0.03)	0.41 (0.05)
FUA	−0.04 (0.02)	0.07 (0.03)	0.01 (0.01)	0.97 (0.12)	−0.67 (0.20)	0.16 (0.08)	0.05 (0.03)	0.06 (0.02)	0.24 (0.06)
RUH	0.27 (0.08)	0.16 (0.05)	−0.32 (0.03)	0.70 (0.10)	−0.59 (0.10)	0.32 (0.06)	0.21 (0.09)	0.17 (0.08)	0.18 (0.05)
RUW	0.82 (0.07)	0.44 (0.06)	0.89 (0.06)	−0.22 (0.08)	−0.01 (0.01)	0.89 (0.12)	−0.05 (0.02)	0.16 (0.03)	0.35 (0.06)
FS	0.29 (0.03)	0.35 (0.08)	0.25 (0.05)	0.27 (0.03)	0.72 (0.06)	0.08 (0.02)	0.42 (0.08)	0.63 (0.07)	0.16 (0.07)

Heritabilities are on the diagonal, genetic correlations are below the diagonal, phenotypic correlations are above the diagonal, and standard error is in parentheses. UD = Udder depth, MS = median suspensory line, FUA = fore udder attachment, RUH = rear udder height, RUW = rear udder width, FS = final score, 305 DM = 305-day milk yield, 305 DF = 305-day milk-fat yield, and 305 DP = 305-day milk-protein yield.

FUA, RUH, and RUW were 0.11, 0.16, 0.16, 0.21, and 0.16, respectively.

4. Discussion

In the current study, the heritability estimations of 305 DM, 305 DF, and 305 DP were 0.23, 0.21, and 0.24, respectively. Similarly, the heritability of milk production traits used by the American Holstein Association in constructing selection indexes was 0.30. Lower heritabilities were reported by DeGroot et al. (14), ranging from 0.09 to 0.22. The value of heritability for FS was close to the finding of Dechow et al. (15), which was 0.21. However, Lee and Whitley (16) reported a higher value of 0.54. The values of heritabilities estimation of UD, MS, FUA, RUH, and RUW were within the range of previous estimations (4,8,10,17). Furthermore, positive genetic correlations among MS, RUH, RUW, and FS were observed (0.42–0.72). The results could be attributed to the fact that genetic selection for FS might be beneficial to improve these traits, and those results were supported by the study of Gengler et al. (18) on Jersey cattle using a repeatability model, in which the genetic correlations between RUH or RUW and FS were 0.67 and 0.69, respectively. In the present study, phenotypic correlations between udder traits and milk production traits were weak. Negative genetic correlations between UD or FUA and milk production traits were observed, and the results were in accordance with some previous research (4,8,10,17). High direct genetic correlations have been estimated between RUW and milk yield trait, and the result was higher than in some other research reported (4,8,14). The results suggested that improved RUW was associated with higher milk production. In the present study, positive and moderate genetic correlations between FS and milk traits were estimated; the results were in agreement with previous reports (12,19). A long-term selection response to sires based on milk and conformation indicated that commercial dairy producers select high predicted transmitting ability for yield without deterioration of conformation (20). Moreover, a nonlinear genetic relationship between 305 DM and FS in first-lactating US Holstein cattle also suggested that selection for FS would improve milk yield (21).

In summary, our results suggested that emphasis on selection for udder traits and FS would bring great benefits to improve milk production in a future selection program. The genetic parameters calculated from field records can provide valuable information for genetic improvement in type traits and milk production traits of Holstein dairy cattle in southern China.

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