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Genetic Correlation of Conformation Traits with Semen Traits in Chinese Holstein Bulls: A Preliminary Investigation

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ABSTRACT

The current study conducted a preliminary investigation of genetic correlations in Chinese Holstein bulls to improve their semen quantity and quality by indirect selection of conformation traits. The results of seven semen traits and nine conformation traits showed that the heritability estimates of semen traits ranged from 0.24 (post-thaw motility) to 0.63 (volume per ejaculation), while the conformation traits ranged from 0.29 (pin width) to 0.80 (withers height). Phenotypic correlation between scrotal circumference (SC) and semen concentration per ejaculation (SCPE), SC and total number of sperm per ejaculation (TNS), and SC and total number of motile sperm per ejaculation (TNMS) was 0.22, 0.25, and 0.24, respectively. Genetic correlation between SC and SCPE, SC and TNS, and SC and TNMS was 0.41, 0.40, and 0.38, respectively. To summarize, moderate or high heritability of semen traits indicated that genetic improvement of semen quality by selection is feasible, where SC could be a useful trait for indirect selection or as correlated information to improve semen quantity and production.

Keywords: Chinese Holstein bull, conformation trait, genetic analysis, genetic correlation, semen trait

1. INTRODUCTION

The widespread use of frozen semen from bulls for artificial

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insemination largely contributes (up to 70%) to genetic progression in dairy cattle [1, 2]. As semen quality directly determines the conception rate, the reproductive performance of bulls needs to be continually improved in order to supply high-quality semen for efficient production; therefore, selection is necessary for high-quality and large-quantity semen from genetically superior sires [3–5]. Recently, inconsistent heritability estimates of Holstein semen traits were reported in different studies [6–14]. Kawakami et al. [8] showed that the heritability estimates of semen volume, motility, and concentration traits were 0.12, 0.20, and 0.13, respectively. However, Yin et al. [15] reported that the heritability estimates of the above three traits were 0.15, 0.12, and 0.22, respectively. Due to the genetic and environmental differences among different populations, genetic parameters in previous studies were estimated inconsistently. Therefore, the current study aims to estimate the genetic parameters of semen traits and body conformation traits in Chinese Holstein bulls. The preliminary results could be used potentially for the genetic improvement of semen production and quality in the selection programs of Holstein population.

2. MATERIALS AND METHODS

The phenotype records of semen and conformation traits were collected from 270 Chinese Holstein bulls covering a period of nine (09) years from one herd in Shandong OX Livestock Breeding Co., Ltd., in Shandong province, China. The seven semen traits included semen volume per ejaculation (SVPE), semen concentration per ejaculation (SCPE), sperm motility per ejaculation (SMPE), total number of sperm (TNS), total number of motile sperm (TNMS), percentage of abnormal sperm (PAS), and post-thaw motility (PTM). The nine conformation traits included body weight (BW), withers height (WH), body length (BL), chest girth (CG), abdominal circumference (AC), tube circumference (TC), pin width (PW), hip height (HH), and scrotal circumference (SC). Semen was collected twice a week from each bull using an artificial vagina and then immediately stored at 37℃ in a water bath. The fresh semen traits of SVPE (ml), SCPE (10^8/mL), SMPE (%), and PAS (%) were evaluated by skilled technicians, where TNS = SVPE (ml) × SCPE (10^8/ml) and TNMS = TNS (10^8) × SMPE (%). After

5-7 days of cryopreservation, two straws of each bull were randomly taken and thawed at 38℃ for 20 seconds. Immediately, PTM (%) were evaluated under a light microscope.

Nine (09) conformation traits were measured in the middle of the month. BW (kg) was measured using electronic balance on the morning of the test day. WH (cm) was measured with a measuring stick as the vertical distance from the highest point of the armor to the ground. BL (cm) was measured with a tape measure from the shoulder to the end of the sciatic bone. CG (cm) was measured with a tape measure as the vertical circumference of the body at the posterior scapula. AC (cm) was measured with a tape measure as the circumference around the abdomen. TC (cm) was measured with a circular gauge as the upper third of the tube in the left lead limb. PW (cm) was measured with a circular gauge as the maximum width of the hip joint. HH (cm) was measured with a measuring stick from the center of the two waist angles to the ground. SC (cm) was measured with a special measuring ruler as the circumference of the most prominent part of the middle part of the scrotum.

The screening criteria of qualified semen were as follows: SVPE ≥ 2ml, SCPE ≥ 3×10^8/ml, SMPE ≥ 0.6, and PTM ≥ 0.3. Due to the large phenotypic loss of semen traits that imbalanced each individual, 1,106 month-averaged records of semen traits were used for genetic analysis, after merging the averaged phenotype records of semen traits with conformation traits in the same month. The analysis was conducted in four seasons, that is, spring (March, April, and May), summer (June, July, and August), autumn (September, October, and November), and winter (December, January, and February).

Two-trait model was used to estimate variance and covariance components of both semen and conformation traits using average information restricted maximum likelihood (AI-REML) in the DMU package [11]. The model is described as follows:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix},$$

where y_1 and y_2 are the vectors of phenotypes (semen or conformation traits), X_1 and X_2 are the design matrices for fixed effects, b_1 and b_2 are the vectors of fixed effects (year-season and age effects), Z_1 and Z_2 are the design matrices for additive genetic effects, a_1 and a_2 are the vectors of the additive genetic effects that satisfy $a_1 \sim N(0, A\sigma_{a1}^2)$ and $a_2 \sim N(0, A\sigma_{a2}^2)$ (where σ_{a1}^2 and σ_{a2}^2 are additive genetic variances and A is the relationship matrix calculated using pedigree information), e_1 and e_2 are the vectors of random environmental effects that satisfy $e_1 \sim N(0, I\sigma_{e1}^2)$ and $e_1 \sim N(0, I\sigma_{e1}^2)$ (where σ_{e1}^2 and σ_{e2}^2 are residual variances).

The variances of additive genetic effects and genetic covariance for the two traits (semen or conformation traits) are $\begin{bmatrix} A\sigma_{a1}^2 & A\sigma_{a12} \\ A\sigma_{a12} & A\sigma_{a2}^2 \end{bmatrix}$. Then, the heritability h^2 of the two traits was estimated as $h_1^2 = \frac{\sigma_{a1}^2}{\sigma_{a1}^2 + \sigma_{e1}^2}$ and $h_2^2 = \frac{\sigma_{a2}^2}{\sigma_{a2}^2 + \sigma_{e2}^2}$. Genetic correlation r_{a} and phenotypic correlation r_{p} were estimated as $r_{\mathrm{a}} = \frac{\sigma_{a12}}{\sigma_{a1}\sigma_{a2}}$ and $r_{\mathrm{p}} = \frac{\sigma_{p12}}{\sigma_{p1}\sigma_{p2}}$, respectively, where σ_{a12} and σ_{p12} refer to the additive genetic covariance and phenotypic covariance between the two traits that were calculated based on multiple trait models.

3. RESULTS AND DISCUSSION

The heritability (diagonal) estimate, genetic correlation (upper diagonal), and phenotypic correlation (lower diagonal) of semen and conformation traits are presented in Figure 1.

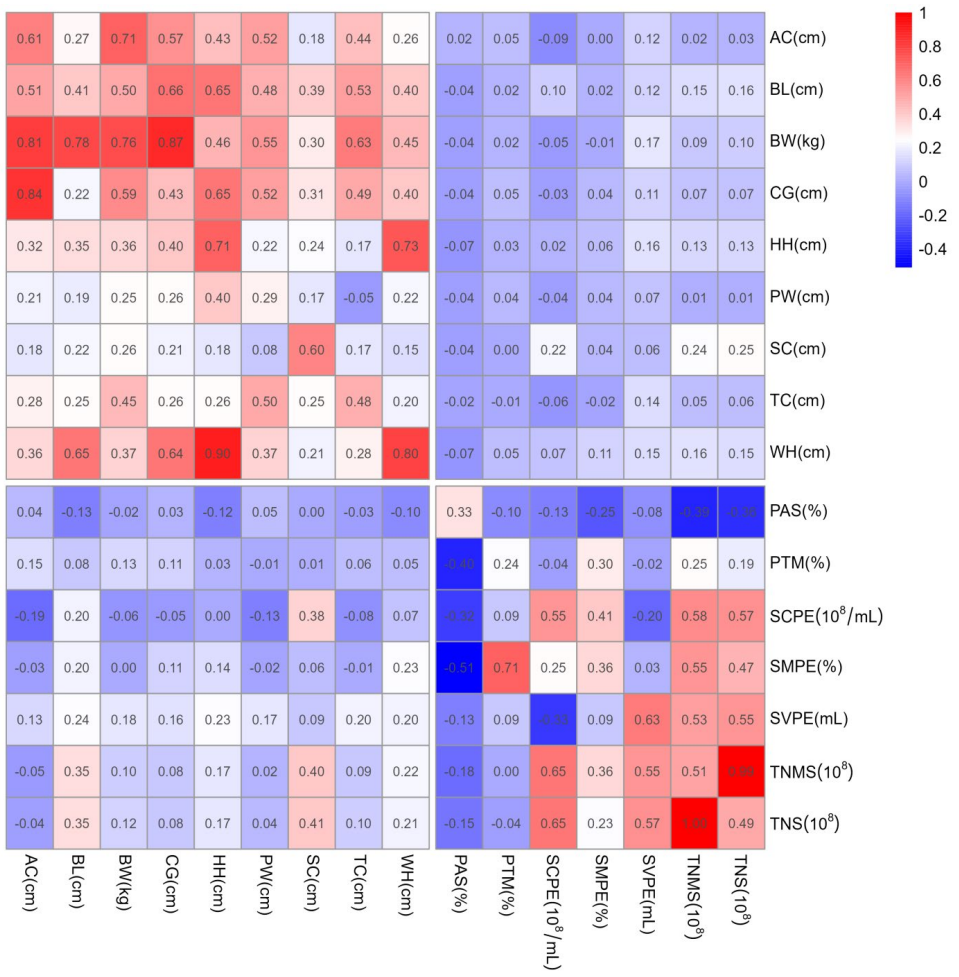

Figure 1. Heritability (Diagonal), Genetic Correlations (Upper Diagonal), and Phenotypic Correlations (Lower Diagonal) of semen and conformation traits.

Note. AC = Abdominal circumference, BL = Body length, BW = Body weight, CG = Chest girth, HH = Hip height, PAS = Percentage of abnormal sperm, PTM = Post-thaw motility, PW = Pin width, SC = Scrotal circumference, SCPE = Semen concentration per ejaculation, SMPE = Sperm motility per ejaculation, SVPE = Semen volume per ejaculation, TC = Tube circumference, TNMS = Total number of motile sperm, TNS = Total number of sperm, WH = Withers height.

It shows that semen traits had medium to high heritability estimates ranging from 0.24 to 0.63, while conformation traits had relatively high heritability estimates ranging from 0.41 to 0.80, except for the PW trait (0.29). Phenotypic correlation among semen traits ranged from -0.25 to 0.99, where TNS showed a high correlation (0.99) with TNMS. Phenotypic correlation among conformation traits ranged from -0.05 to 0.73. They were all positively correlated except PW and TC (-0.05). However, phenotypic correlation between semen traits and production traits was quite weak or close to zero in general, except for the correlation of SC with SCPE, TNS, and TNMS, which was 0.22, 0.25, and 0.24, respectively (Figure 1).

Genetic correlation among semen traits ranged from -0.51 to 1.00, where TNS showed a high correlation (1.00) with TNMS. Genetic correlation among conformation traits was positive and ranged from 0.17 to 0.90, where HH correlated with WH (0.90), BW correlated with CG (0.87), AC correlated with CG (0.84), and BW correlated with AC (0.81), showing strong correlation. Genetic correlation between semen traits and conformation traits ranged from -0.19 to 0.41. Notably, genetic correlation of SC with SCPE, TNS, and TNMS was 0.38, 0.41, and 0.40, respectively. This indicates that larger SC can lead to higher SCPE, TNS, and TNMS. Furthermore, BL also had a moderate genetic correlation (0.35) with TNS and TNMS (Figure 1).

In this study, SVPE heritability (0.63 ± 0.03) was found to be higher than other studies (0.04 ~ 0.43) and SCPE heritability (0.55±0.03) was also found to be higher than other studies (0.1 ~ 0.26) [10]. The heritability estimates of conformation traits in the Holstein bull population were moderate or high, which indicates that genetic improvement of semen production and quality by selection could be feasible, if their genetic correlation with conformation traits is strong. Kealey et al. [10] determined that the genetic correlation of SC with semen volume and contraction was 0.20 and 0.77, respectively in Hereford cattle. It is worth mentioning that in the current study, SC was found to be positively correlated with semen traits in general and moderately correlated with SCPE (0.38), TNS (0.41), and TNMS (0.40) (Figure 1). The results are consistent with those in the

literature [7, 15]. Therefore, the selection of those conformation traits could help improve semen production and quality in Holstein bulls.

3.1. Conclusion

Positive but low level genetic correlation of scrotal circumference (SC) was preliminarily determined with semen concentration per ejaculation (SCPE), total number of sperm per ejaculation (TNS), total number of motile sperm per ejaculation (TNMS), and other semen traits. These findings indicate that genetic improvement of semen production and quality traits by selection is feasible and SC could be used as an indicator trait for indirect selection, or as an assistant trait to improve selection accuracy for semen production and quality.

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