

Genetic Parameter Estimation for Breeding Soundness Examination Traits in Angus Bulls

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Abstract

Scrotal circumference and semen quality traits such as motility, motility score, primary abnormalities, secondary abnormalities, and normal sperm are widely used as phenotypic indicators of bull fertility during a breeding soundness examination (BSE); however, the genetic relationships of these traits are not fully understood. The objectives of this study were to estimate heritabilities, repeatabilities, phenotypic correlations, and genetic correlations between scrotal circumference and semen quality traits to better understand their potential application in a genetic evaluation for improved bull fertility. Eleven purebred Angus operations provided 5,877 BSE records from 4,996 Angus bulls for use in this study. Heritability estimates ranged from 0.05 to 0.36. Repeatability estimates were moderately to highly repeatable, ranging from 0.22 to 0.70. Estimates for phenotypic correlations ranged from no correlation (0.0) to highly correlated (0.94). Low to moderate genetic correlations were estimated between scrotal circumference and semen quality traits, while stronger correlations were estimated between percentage of primary abnormalities and the motility traits. Many genetic correlations had high standard errors, making them not significantly different from zero, and several relationships between semen quality traits were not estimable. These results indicate that it is feasible to improve bull fertility with genetic selection; however, further research is needed to determine the best methodology for developing a genetic evaluation.

Introduction

The breeding soundness examination (BSE) is the most common method for assessing bull fertility. There are three key components of a BSE: a physical examination, reproductive tract examination, and semen quality evaluation (Hopper, 2014). However, BSEs are often only performed before the breeding season, before the sale of the animal, or when a bull's fertility is in question. Additionally, a BSE only measures a bull's fertility on the examination day and may not be representative of his average fertility level throughout the breeding season (Koziol and Armstrong, 2018). The subjective nature of semen quality assessment of the BSE can also introduce biases due to differences in equipment, training, and attention to detail of the practicing veterinarian or

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technician (Hopper, 2014). There are technologies available that can provide more objective measurements of sperm quality, but they are expensive to purchase and often are only owned by artificial insemination semen collection facilities (Tanga et al., 2021). Nevertheless, BSE data can be made readily available by seedstock producers for a large number of bulls, which would be beneficial for a large-scale genetic evaluation. Several studies have reported low to moderate genetic correlations for scrotal circumference and semen quality traits using BSE data; however, those analyses did not include multiple BSE records on a single bull (Smith et al., 1989; Christmas et al., 2001; Garmyn et al., 2011). Therefore, our objective was to estimate heritability and repeatability for scrotal circumference and semen quality traits using BSE data in a repeated records model and examine the relationships between traits.

Experimental Procedures

Eleven purebred Angus breeders provided 5,877 BSE records on 4,996 bulls. While each bull had one BSE, 651 bulls had at least one additional BSE, with a maximum of five exams. Most of the additional exams were for bulls that had failed their initial BSE, but some bulls had additional records from a subsequent breeding season. The data included measurements of scrotal circumference, percentage of progressive motility, gross motility score, percentage of primary abnormalities, percentage of secondary abnormalities, percentage of normal spermatozoa, and percentage of abnormal spermatozoa. Most operations did not report every measurement listed, but rather a combination of the traits. Different veterinarians or technicians conducted the BSEs; however, only a single veterinarian or technician performed all the exams for each operation on a particular day.

Data were filtered to ensure that all measurements recorded as percentages were treated as missing if they were not between 0 and 100. Scrotal circumference measurements needed to be larger than zero, or they were treated as missing. Traits that were not reported by the producer but could be calculated from the existing data were added to the dataset. For example, if normal spermatozoa were not directly reported, it was calculated by subtracting the percentage of primary abnormalities, the percentage of secondary abnormalities, or the percentage of abnormal spermatozoa from 100. Additionally, for breeders who reported motility, but not motility score, motility score was generated based on the guidelines provided by the Society for Theriogenology, with the following classifications (Hopper, 2014): greater than or equal to 70% motility was considered “very good,” 50-69% motility was “good,” 30-49% motility was “fair,” and less than 30% was classified as “poor.” The generated motility score was added to the producer-provided motility score for analysis.

All phenotypic correlations between fertility traits were estimated using the CORR procedure of SAS. Genetic parameters were estimated using single-step genomic best linear unbiased prediction methodologies with the BLUPF90+ suite of programs (Miszta et al., 2014). This is the same statistical software used by the American Angus Association for their genetic evaluations. Model selection for the bull fertility traits was performed in the BLUPF90+ suite using a forward selection procedure, and model fit was evaluated using the likelihood ratio test. The final models included variables of contemporary group, age, genotypes, and pedigree information. For this study, bulls were put into contemporary groups based on the operation they came from and the date the BSE was performed to account for multiple operations providing multiple years of data. The American Angus Association provided a date of birth, genotypic

information, and a three-generation pedigree for all the bulls. Age was only included as a variable in the scrotal circumference and percentage of secondary abnormalities prediction models. Animal was a random variable in all models.

Results and Discussion

The heritability estimates with their standard errors, as well as repeatability estimates from multivariate genetic analyses, are presented in Table 1. Heritability describes the proportion of phenotypic variation that can be attributed to genetic differences, showing how strongly related the genetic breeding values are to the observed phenotypic traits. Scrotal circumference was moderately heritable, and semen quality traits such as motility and morphology were lowly heritable. This result was expected, because scrotal circumference is more of a growth trait and less influenced by the environment, while semen quality traits are strongly affected by many outside factors, including bull age, health, nutrition, social interactions, and temperature. Although semen quality traits had low heritability, the estimates were still greater than zero, suggesting potential for genetic improvement in fertility.

Repeatability measures the consistency of repeated records for the same trait. Repeatability was moderate for motility, motility score, percentage of secondary abnormalities, and normal spermatozoa. Scrotal circumference and percentage of primary abnormalities were highly repeatable. These results suggest that individual bulls tend to produce consistent records for these reproductive traits over time.

Table 2 summarizes the genetic and phenotypic correlations between scrotal circumference and semen quality traits measured during the BSE. Genetic correlations measure the strength of the relationship between breeding values for two traits. A favorable genetic correlation was observed between scrotal circumference and the presence of normal spermatozoa. This is beneficial for producers because scrotal circumference is easily measured, and it is easy to select for larger scrotal circumference, which can lead to more normal spermatozoa being produced. In contrast, genetic correlations between scrotal circumference and the primary and secondary abnormality traits were not significantly different from zero, likely due to limited abnormality records. Weak and unfavorable correlations were also detected between scrotal circumference and motility traits. This finding was unexpected because if scrotal circumference can lead to more normal sperm cells, then those sperm should be able to move better with better motility. However, that was not the relationship observed between motility and scrotal circumference. These results suggest that additional research is needed to determine the optimal scrotal circumference range for maximizing semen quality. Favorable correlations were identified between the percentage of primary abnormalities and motility traits, consistent with the expectation that sperm with normal morphology are more likely to exhibit higher motility. Not every genetic correlation could be estimated in this study; however, all phenotypic correlations between the traits were obtained. Many of the phenotypic correlations were consistent with the genetic relationships observed, including inverse associations between motility traits and the percentage of primary abnormalities. In other words, an increase in motility of sperm was associated with a decrease in abnormal sperm morphology. This was similar to an increase in normal spermatozoa being related to a decrease in sperm abnormalities.

Implications

These results indicate that it is feasible to improve bull fertility through genetic selection; however, further research is needed to determine the best methods for developing a commercially available genetic evaluation.

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Table 1. Average heritability estimates $\pm$ standard errors and repeatability estimates calculated from bivariate single-step genomic best linear unbiased predictions

Trait	Heritability $\pm$ standard error	Repeatability
Scrotal circumference	0.36 $\pm$ 0.03	0.68
Percent motility	0.10 $\pm$ 0.03	0.31
Motility score	0.05 $\pm$ 0.02	0.30
Percent primary abnormalities	0.09 $\pm$ 0.03	0.70
Percent secondary abnormalities	0.09 $\pm$ 0.03	0.44
Percent normal sperm	0.06 $\pm$ 0.01	0.22

Table 2. Genetic correlations $\pm$ standard errors above the diagonal, and phenotypic correlations below the diagonal between Angus bull reproductive traits using a bivariate single-step genomic best linear unbiased prediction

	SC ¹	%MOT ²	MOTSC ³	%PRIM ⁴	%SEC ⁵	%NORM ⁶
SC		-0.16 $\pm$ 0.13	-0.02 $\pm$ 0.14	0.00 $\pm$ 0.15	-0.03 $\pm$ 0.16	0.21 $\pm$ 0.12
%MOT	-0.21*		---	-0.73 $\pm$ 0.33	dnc	dnc
MOTSC	0.00	0.94*		-0.98 $\pm$ 0.50	dnc	dnc
%PRIM	0.00	-0.45*	-0.47*		0.25 $\pm$ 0.29	dnc
%SEC	-0.03	-0.40*	-0.40*	0.01		dnc
%NORM	0.18*	0.56*	0.72*	-0.85*	-0.73*	

* Correlation is significantly different from zero at $P < 0.0001$; -- Correlation was not estimated; dnc: Model did not converge.

¹SC: Scrotal circumference.

²%MOT: Percentage of progressive motility.

³MOTSC: Motility score.

⁴%PRIM: Percentage of primary abnormalities.

⁵%SEC: Percentage of secondary abnormalities.

⁶%NORM: Percentage of normal spermatozoa.