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Genetic variability in sperm quality traits for Norwegian Red bulls

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Introduction

Semen production and sperm quality are crucial traits for AI bulls. Traits related to bull fertility are heritable (Butler *et al*., 2020), but these traits have not been included in the routine genetic evaluations so far. Computer-assisted sperm analysis (CASA) is used for quality control at AI centers and provides objective measures of semen production and sperm quality. Despite the growing use of CASA in AI centers, genetic analyses of such data remain limited. Access to CASA data offers new opportunities to define objective phenotypes related to sperm motility and morphology that could be used in genomic selection. This study aimed to estimate genetic parameters for an initial subset of sperm quality measures derived from CASA for Norwegian Red bulls.

Materials & Methods

The data were from the production facilities at Geno's AI center and included CASA measures on fresh semen for all collected ejaculates from Norwegian Red AI bulls between November 2021 and September 2025. CASA is part of the routine quality control procedure implemented by Geno. The dataset included CASA-derived measurements from 8,615 ejaculates collected from 278 bulls. The number of records per bull varied from 1 to 361, with an average of 31.

Traits. Aggregated CASA data were used, summarizing single-cell observations into one record per ejaculate. Four semen quality traits were analyzed: percent motile sperm (mot%), percent progressive motile sperm (prog%), proportion of sperm with defects, and proportion of sperm with cytoplasmic droplets. On average, 85 % of sperm exhibited motility (movement), 82 % showed progressive motility (moving actively forward), 3.2 % of the sperm had defects (head, tail, or midpiece abnormalities), and 6.7 % had droplets (proximal and distal).

Model. Variance components were estimated using the DMU software (Madsen and Jensen, 2013), applying single-trait linear animal repeatability models. Fixed effects included bull age, days since the previous semen collection, and collection date. Bull age at the time of semen collection was categorized into 20 classes: ≤12 months were assigned to the first class, >30 months to the final class, and the remaining ages were grouped in one-month intervals. The interval since the previous semen collection was categorized into 10 classes: daily intervals from 1 to 7 days, followed by grouped intervals of 8–14 days, 15–21 days, and >21 days. Collection date was modeled with 801 classes and accounted for seasonal variation and effect of personnel involved in semen collection and laboratory analysis. The model had random permanent environment and additive genetic effect of animal. Pedigree information of the bulls with data was traced back five generations and included a total of 4597 animals.

Results & Discussion

The estimated variance components are given in Table 1. Heritabilities were 0.04 and 0.05 for the motility traits and 0.02 for defects, but with a standard error (SE) of 0.05 they were not significantly different from zero. Low heritability estimates for motility traits were in line with the mean pooled heritability estimate of 0.054 for sperm motility reported from a meta-analysis by Berry *et al*. (2014). Olsen *et al*. (2021) estimated heritability for subjectively scored motility traits for Norwegian Red bulls ranging from 0.02 to 0.08.

The proportion of sperm with droplets had the highest heritability (SE) of 0.27 (0.07). Retained cytoplasmic droplets may indicate immature sperm. Moderate heritability for droplet was in agreement with Druet *et al*. (2009) who reported a heritability (SE) of 0.19 (0.08) from a genetic analysis of semen characteristic traits of Holstein bulls.

Table 1. Estimated additive genetic (σ^2_a), permanent environment (σ^2_{pe}), and residual (σ^2_e) variances with standard error (SE) together with the corresponding heritability[2] (h^2) and repeatability (rep) for sperm quality traits.

Trait[1]	σ^2_a	SE	σ^2_{pe}	SE	σ^2_e	SE	h^2	SE	rep
Mot%	2.28	2.60	11.13	2.71	36.89	0.60	0.05	0.05	0.27
Prog%	2.65	3.25	14.99	3.44	41.94	0.68	0.04	0.05	0.30
Defects	0.13	0.30	1.75	0.35	4.30	0.07	0.02	0.05	0.30
Droplets	6.86	1.84	3.03	1.43	15.31	0.25	0.27	0.07	0.39

1. Traits: percent motile sperm (mot%), percent progressive motile sperm (prog%), proportion of sperm with defects, and proportion of sperm with cytoplasmic droplets.
2. Heritability: $h^2 = \sigma^2_a / (\sigma^2_a + \sigma^2_{pe} + \sigma^2_{e.})$. Repeatability: $rep = (\sigma^2_{a+} + \sigma^2_{pe}) / (\sigma^2_a + \sigma^2_{pe} + \sigma^2_e)$.

Table 1 shows that the repeatability was moderate for all traits. For mot%, prog%, and defects, the permanent environment variance is much larger than the additive genetic variance. A similar pattern was reported by Negai *et al*. (2022) from analyses of semen traits in Japanese Black and in Holstein bulls. Their results suggested that repeatability was largely explained by non-additive genetic effects, and epistatic effects were detected for all analyzed semen traits in both breeds.

In our study we used data collected during production at the AI center. Norwegian Red young bulls undergo a test of andrology before they are selected and enter the AI center. Active AI bulls are therefore preselected for andrology and may not fully represent the variation in sperm quality in the entire Norwegian Red population.

Use of CASA for routine quality control in production at the AI center provide large scale standardized phenotypic data valuable for genetic evaluation. Further research should investigate potential associations between phenotypes derived from CASA and field fertility outcomes, such as conception rate. The available data also allows for expanding the analysis to a broader set of motility and morphology traits. Semen production and quality traits are crucial traits for AI bulls. Genomic breeding values for traits related to sperm motility and morphology could be useful when recruiting bull calves to become future AI bulls and can also be used to monitor genetic trends in bull fertility.

Conclusion

The results demonstrate that CASA measures of semen production and sperm quality offer opportunities to identify new phenotypes related to sperm motility and morphology, which can be used in genomic selection.

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Notes

We confirm that none of the authors have any conflicts of interest to declare that are relevant to the content of this article. This article does not contain any studies of human or animal subjects that require approval.

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