

# Genetic parameters for six semen characteristic traits of young Norwegian Red bulls, 772.

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## Summary

Genetic parameters for the semen characteristic traits volume, density (before and after 2013), and motility (in fresh samples and after storing for 24 and 48 hours) were estimated by restricted maximum likelihood applied to an animal model using records from young Norwegian Red bulls (10 to 14 months old). Number of observations per trait varied from 14905 for volume to 4002 for motility 48 hours. Each bull had between 1 and 9 observations per trait and the pedigree consisted of 27437 animals. Volume and density after 2013 had moderate heritability (0.14, 0.15), while density before 2013, a categorical trait, had lower heritability (0.07). Motility (0, 24 and 48 h) also had lower heritabilities (0.03, 0.06 and 0.09). The heritability of motility seemed to increase with time stored.

*Key words: semen characteristic, andrology, Norwegian Red, cattle*

## Introduction

Bovine fertility is highly complex and depends on the fertility of the cow, management of the herd, timing of insemination as well as the quality of the semen. Female fertility traits have been included in the breeding goal for Norwegian Red since the 1970's and is now included in breeding goals in many countries. On the other hand, male fertility has received much less attention in dairy cattle breeding programs.

Druet *et al.* (2009) estimated genetic parameters for sperm volume and concentration in fresh samples and motility (%) after thawing, based on data from 515 Holstein bulls at age 12 to 18 months. They found moderate heritabilities for volume (0.22) and concentration (0.19) and high heritability for motility (0.43). Mathevon *et al.* (1998) estimated heritabilities of 0.24, 0.52 and 0.31 for volume, concentration and motility in fresh samples. These estimates were based on information from 198 Holstein bulls between 11 and 30 months. A dataset with 1957 Normand bulls between 12 and 15 months of age was analyzed by Ducrocq & Humblot (1995). Estimated heritability of volume, concentration and motile spermatozoa after thawing were 0.65, 0.37 and 0.24 respectively.

For Norwegian Red, sperm quality is assessed for the first time at the performance test station when the bulls are around 12 months old. Here the libido of the young bulls are tested, as well as a number of andrology traits to ensure acceptable semen quality. Bulls pass this test, and become an AI bull, by achieving at least 3 out of 5 in an overall grade based on the results from

all the andrology traits. Andrology data from the performance test station is particularly interesting for genetic analyses because here the young bulls are unselected with respect to male fertility

The aim was to estimate genetic parameters of male fertility traits in Norwegian Red.

## Materials and methods

Data from the initial tests of sperm quality of Norwegian Red young bulls were available from Geno, where ejaculates have been evaluated for the physical characteristics: volume (in ml.), density and percentage of motile sperm cells. Density was measured by a spectrophotometer and given as  $10^3$  number of spermatozoa in 1ml diluted (100 times) solution. The diluted samples were then evaluated under a phase contrast microscope (magnification 10x to 100x) and percentage of motile sperm cells were registered subjectively. The values ranged from 0 to 80, with intervals of 10, and gives minimum motility in the sample. Afterwards the samples were stored in a refrigerator until they were reactivated and evaluated again after 24 hours and finally after 48 hours.

Data from 1994 until early in 2017 were available and included 21304 observations. 4524 of these did not contain any information on semen characteristics and were deleted. For estimation of genetic parameters, volume was required to be  $> 0$ . Samples with volume  $> 12$  and density  $> 3000$  were considered erroneous and excluded. Only bulls with group number and group year information and bulls between 330-450 days old at the day of testing were kept. A total of 1163 observations were duplicates and removed. Data edits were done in SAS (2012).

Density showed a skewed distribution, peaking at 390, with 22% of the observations. Closer examination revealed few observations lower than 390 before 2013 because the photometer used before April 2013 could not register density lower than 390. In this period, density was set to 390 if the photometer showed 0, but cells were found during microscope evaluation. Density was therefor defined as two traits, before and after April 22. 2013, hereafter called density1 and density2. Density2 were kept as recorded, while density1 was divided into 10 categories (0, 1-390, 391-590, 591-790, 791-990, 991-1190, 1191-1390, 1391-1590, 1591-1790,  $> 1790$ ).

The final dataset included 14914 observations from 3914 bulls between 10 and 14 months with mean 12. Number of observations per bull ranged from 1-11 with mean 2.8. Number of observations per trait is given together with summary statistic in Table 1.

*Table 1. Descriptive statistics<sup>1</sup> for the six semen characteristic traits.*

	N	Mean	Std Dev	Median	Min	Max
Volume (ml)	14905	2.6	1.5	2.5	0.5	12
Density1 <sup>2</sup>	12057	2.9	1.8	3	0	9
Density2 <sup>3</sup>	2837	475.2	306.2	440	0	1745
Motility Fresh (%)	14511	64.9	21.3	70	0	80
Motility 24h (%)	9998	61.2	19.0	70	0	80
Motility 48h (%)	4002	55.6	20.3	60	0	80

<sup>1</sup> Number of observations, mean, standard deviation, median and minimum and maximum value.

<sup>2</sup> Density recorded before 22.04.13 and categorized in 10 classes (0, 1-390, 391-590, 591-790, 791-990, 991-1190, 1191-1390, 1391-1590, 1591-1790, > 1790).

<sup>3</sup> Density recorded after 22.04.13 given as  $10^3$  spermatozoa in a 1ml diluted solution (x100).

General linear models were run with the GLM procedure in SAS (2012) to test whether the explanatory variables ejaculate number (first in life=1, second=2, etc.), age in months and group-year had a significant effect (p-value  $\leq 0.05$ ) for the different andrology traits.

Linear animal models were used to estimate variance components with the DMU software (Madsen & Jensen, 2012). For the andrology traits assessed, the model was:

$$Y_{ijklmno} = \mu + \text{age}_i + \text{groupyear}_j + \text{ejaculatenum}_k + \text{testday}_l + a_m + \text{pe}_n + e_{ijklmno};$$

where  $Y_{ijklmno}$  = observation on one of the six andrology traits;  $\text{age}_i$  is the fixed effect of the i-th age in months,  $i=10,11,\dots,14$ ;  $\text{groupyear}_j$  is the fixed effect of the j-th group and year the bull entered the test station,  $j(1,\dots,132)$   $\text{ejaculatenum}_k$  is the fixed effect of k-th ejaculate number,  $k=1,2,3,\dots,11$  (not used in the model for motility 48h);  $\text{testday}_l$  is the random effect of testday,  $l \sim N(0, \sigma^2_{td})$ ;  $a$  is the random genetic effect of bull  $\sim N(0, \sigma^2_a)$ ;  $\text{pe}$  is the random permanent environment effect of bull  $\sim N(0, \sigma^2_{pe})$ ; and  $e$  is the residual  $\sim N(0, \sigma^2_e)$ . The additive relationship included pedigree of 27437 animals.

## Results and discussion

The heritability of volume and density<sup>2</sup> was moderate (0.14 and 0.15), while the categorical trait density<sup>1</sup> gave a lower heritability (0.07). Heritability of motility increased with time stored and ranged from 0.03-0.09.

Table 2. Variance components<sup>1</sup> with standard error (SE), repeatability ( $w^2$ ) and heritability ( $h^2$ ) for the six semen characteristic traits.

	$\sigma^2_{td}$ (SE)	$\sigma^2_a$ (SE)	$\sigma^2_{pe}$ (SE)	$\sigma^2_e$ (SE)	$w^2$	$h^2$
Volume (ml)	0.06 (0.01)	0.27 (0.05)	0.29 (0.04)	1.29 (0.02)	0.29	0.14
Density <sup>1</sup> <sup>2</sup>	0.10 (0.14)	0.20 (0.06)	0.70 (0.06)	1.84 (0.04)	0.32	0.07
Density <sup>2</sup> <sup>3</sup>	2499.63 (719.80)	13765.96 (6014.78)	25946.04 (5323.81)	49718.46 (1622.80)	0.43	0.15
Motility Fresh (%)	9.28 (1.68)	11.91 (4.77)	76.50 (5.68)	311.36 (4.42)	0.22	0.03
Motility 24h (%)	15.08 (2.30)	20.40 (5.99)	39.87 (6.14)	271.17 (4.85)	0.17	0.06
Motility 48h (%)	20.77 (4.59)	37.47 (15.34)	68.20 (16.00)	270.60 (9.80)	0.27	0.09

<sup>1</sup> Variance components for testday ( $\sigma^2_{td}$ ), additive genetic effect ( $\sigma^2_a$ ), permanent environment effect ( $\sigma^2_{pe}$ ) and residual variance ( $\sigma^2_e$ ).  $w^2 = \sigma^2_a + \sigma^2_{pe} / \sigma^2_{td} + \sigma^2_a + \sigma^2_{pe} + \sigma^2_e$  and  $h^2 = \sigma^2_a / \sigma^2_{td} + \sigma^2_a + \sigma^2_{pe} + \sigma^2_e$ .

<sup>2</sup> Density recorded before 22.04.13 and categorized in 10 classes (0, 1-390, 391-590, 591-790, 791-990, 991-1190, 1191-1390, 1391-1590, 1591-1790, > 1790).

<sup>3</sup> Density after 22.04.13 given as 10<sup>3</sup> number of spermatozoa in a 1ml diluted (x100) solution.

The strength of this dataset is the large number of bulls previous to selection for andrology. Volume and density<sup>2</sup> were found with moderate heritability (0.14 and 0.15), but these estimates were lower than in previous studies. Druet *et al.* (2009) had results closest to our findings, with a heritability of 0.22 for volume and 0.19 for concentration, while the estimates of Ducrocq and Humblot (1995) were considerably higher; (0.65) for volume and (0.37) for concentration (0.37). The latter study used mean values from 11.6 ± 3.6 sperm collections. Volume and density have been shown to increase with increasing age (Mathevon *et al.* 1998) and the bulls in our study were younger than the bulls in the other studies mentioned. Still both studies used bulls younger than 19 months. Heritability of motility in fresh samples were 0.03 and increased to 0.06 and 0.09 for motility after storing for 24 and 48 hours. This suggest that the ability of the spermatozoids to survive storing is more affected by genetics than motility in fresh samples. Other studies have found the heritability of percentage motile spermatozoa in fresh samples to be 0.31 (Mathevon *et al.* 1998), while both Ducrocq and Humblot (1995) and Druet *et al.* (2009) examined motility after thawing and estimated heritabilities of 0.24 and 0.43. It is unclear whether the latter traits can be directly compared to the traits in the present study, as these samples were not frozen. The lower heritability estimates found in our study, indicates that the traits were not recorded as precisely at the test station, especially for the subjectively evaluated motility traits that were found to have the lowest repeatability among the traits. Further, we used data from the performance test station, so the bulls were young and not acquainted to the procedure, which may have contributed to a lower heritability for semen characteristics than for bulls in semen production. Still most of the traits have a strong genetic basis and a good resource for further study of male fertility in Norwegian Red.

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