

GENOME-WIDE ASSOCIATION STUDY

FOR BULLS' FERTILITY TRAITS IN RUSSIAN HOLSTEIN CATTLE POPULATION

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INTRODUCTION

Holsteins are the most widely distributed cattle breed in Russia. To achieve improvement of both milk production and fertility traits, principles were elaborated to use genomic approaches together with breeding strategies to develop a common breeding index. Combining semen-quality measures for sires with the cows' reproduction records makes it possible to resolve the problems with decreased conception rates and semen production.

Our objective was to search the genomic regions and associated markers for bulls' fertility traits in Russian Holstein cattle.

MATERIALS AND METHODS

Genotyping:

- Illumina Bovine SNP50 v2 BeadChip (selected 41,435 SNPs, Plink 1.07). The common dataset with genotypes consisted of 282 bulls.
- The data set consisted of 14,490 records, which varied between 10 and 328 per animal, with 104 sires' observations in the data set. The average age of sires was 80.1 ± 0.3 months. **Traits under study:** semen volume (SV, $h^2=0.322$), sperm concentration (SC, $h^2=0.202$), average SV for multiple ejaculates collected from one sire (ASV, $h^2=0.366$), motility (Mt, $h^2=0.014$), and number of spermatozoa (NS, $h^2=0.169$)

The following linear model was used (EBV, BLUP AM):

- $y_{ijk} = \mu + YM_i + b_1 A_k + animal_j + e_{ijk}$,
where: μ – population constant, YM_i – “year-month” effect of collecting semen, A_k – bull's age in months at testing.

To increase the prediction reliability of associations genomic EBVs as the animal's pseudo-phenotypes for young bulls were calculated (DGV, GBLUP):

- $DRP = Xb + Zu + e$

Bonferroni correction test: $P < 1.21 \times 10^{-6}$

For calculating (co)variance components REMLF90 was used (Misztal I. et al, 2002).

RESULTS AND DISCUSSION

Two QTL for Mt including 11 SNP were detected on BTA1 (146.3–146.9 Mb) and BTA9 (76.9–77.1 Mb)

Table 1. Results of GWAS for significant SNPs

	SNP	MAF	p-value	R ² , %	Closest gene
Semen volume:	BTA-89872-no-rs	0.480±0.021	6.0×10^{-8}	10.1	SUGCT succinyl-CoA:glutarate-CoA transferase
Motility:	ARS-BFGL-NGS-4700	0.414±0.018	2.7×10^{-9}	12.1	UMODL1 uromodulin like 1
	BTA-84317-no-rs	0.489±0.022	1.1×10^{-6}	8.6	PERP TP53 apoptosis effector
Sperm concentration:	ARS-BFGL-NGS-57433	0.272±0.019	7.4×10^{-7}	8.5	ARHGAP20 Rho GTPase activating protein 20
Number of spermatozoa:	ARS-BFGL-NGS-84969	0.173±0.016	1.4×10^{-6}	8.1	EPT1 CDP-ethanolamine-specific
Average SV:	BTA-30092-no-rs	0.469±0.022	9.8×10^{-7}	8.9	SOX5 SRY-box 5

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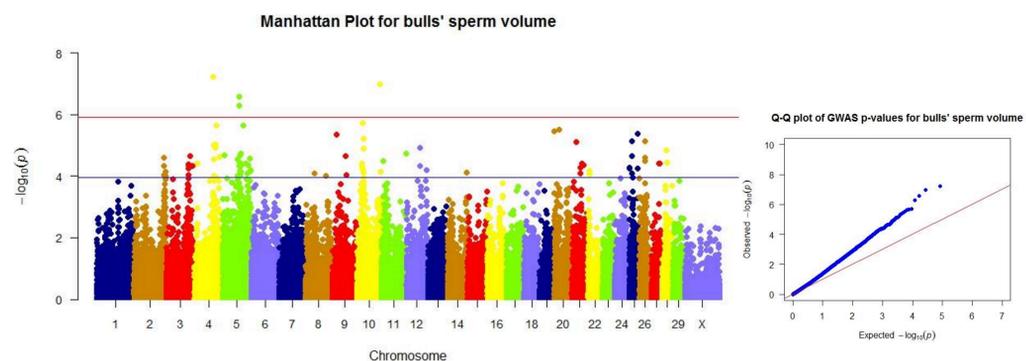


Figure №1. Manhattan plot for bulls' EBV of semen volume

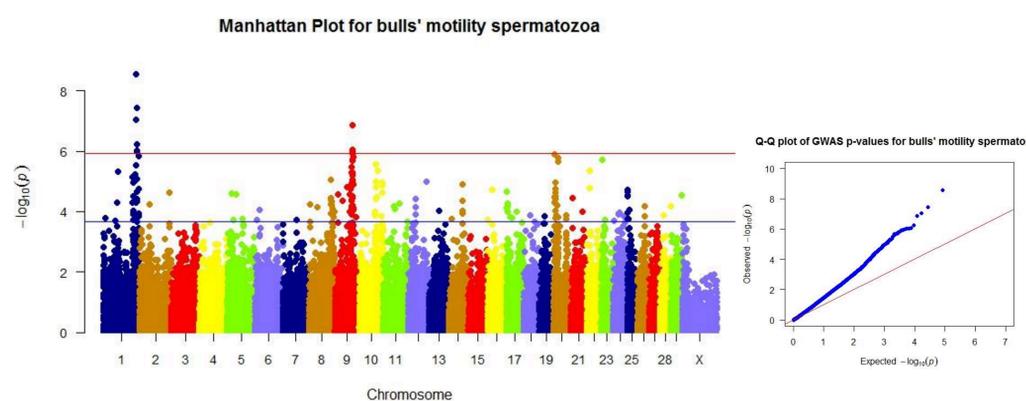


Figure №2. Manhattan plot for bulls' EBV of motility spermatozoa

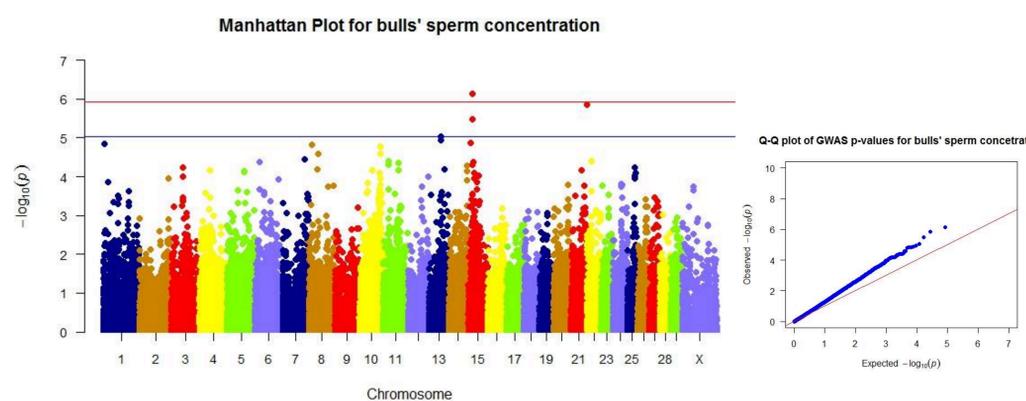


Figure №3. Manhattan plot for bulls' EBV of sperm concentration

CONCLUSION

The genes SOX5 (BTA12), PERP (BTA9), and EPT1 (BTA11) were associated with embryonic development, cell death, or apoptosis and synthesis of selenoproteins. Our results may be used to select donor cows for oocytes or embryo collection in the focus of genomic selection.