

Milk somatic cells monitoring in Russian Holstein cattle population as a base for determining genetic and genomic variability

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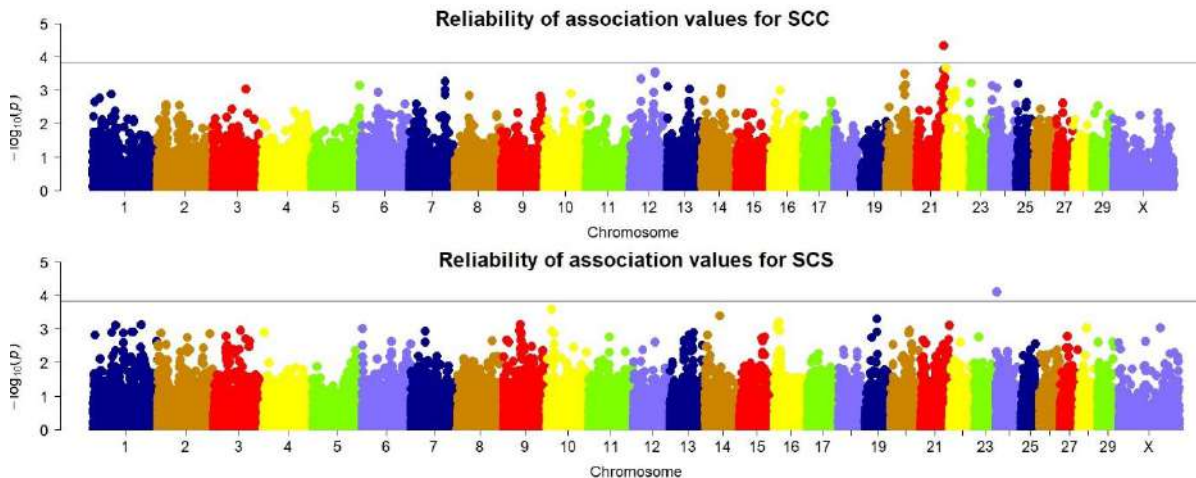
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INTRODUCTION. Health traits in dairy cattle have crucial meaning to produce high quality milk. Despite of fertility problems and metabolic disorders in cows, the mastitis has a bigger economic losses influence to include it as selection criteria in cattle breeding. Somatic cell count (SCC) in that case are the good predictor for monitoring udder health cows under whole population level or separate herd.

The aim of our study was to assess genetic and genomic components for SCC and their scores (SCS) using experimental dataset by seven herds with the subsequent QTL identification.

MATERIAL AND METHODS:

- For six-month observation the **5824 cows** with **19786 test-day records** were included into analysis.
- Then EBVs by offspring assessing of **139** genotyped **Holstein sires** were calculated trough TD Model (BLUPF90; Misztal I., 2002) and then it adopted as pseudo-phenotypes for GWAS.
- After quality control using Plink 1.90 (Chang C., 2015), we used **≈39K SNPs** (Illumina 50K).



RESULTS. The average values for SCC and SCS were 351±7 thousands cells/ml and 2.86±0.02 score respectively. Heritability coefficients revealed low genetic variation for SCC – 0.119 and moderate for SCS – 0.211. Daily yield for cows with SCC >1000×10³ cells/ml was low by -4.0 kg milk to compare individuals with SCC <100×10³ cells/ml. At the same time lactose content and freezing point were decreasing by 4.93 to 4.69% and -0.635 to -0.618°C.

BTA	Position, bp	p-value	Genes	QTL
Somatic cells count				
3	81774972	0.0009	ROR1	somatic cell score, milk protein percentage, udder attachment, Udder depth, Udder height
9	96693865	0.0018	EZR	length of productive life
13	55449134	0.0009	OSBPL2	milk protein percentage, milk yield
13	54397045	0.0022	DNAJC5	milk protein percentage, milk yield
13	54464448	0.0022	ZBTB46	milk protein percentage, milk yield
13	55529589	0.0030	MTG2	milk protein percentage, milk yield
14	7342696	0.0021	KHDRBS3	milk fat percentage, milk protein percentage, milk protein yield, milk vitamin B-12 content, milk yield
22	3840934	0.0002	RBMS3	milk fat yield
Somatic cells score				
13	55449134	0.0021	OSBPL2	milk protein percentage, milk yield
14	38095683	0.0004	KCNB2	milking speed
14	7928189	0.0015	ZFAT	milking speed
19	16578349	0.0018	ASIC2	milk conjugated linoleic acid content
23	10688252	0.0017	CPNE5	milk protein yield

CONCLUSION. By Cattle QTL data base we identified some causal genes for SCC on BTA3 (ROR1), BTA9 (EZR), BTA13 (OSBPL2, DNAJC5, ZBTB46, MTG2), BTA14 (KHDRBS3) and BTA22 (RBMS3). But more relevant GWAS calls were found for SCS by BTA14 (KCNB2, ZFAT) as QTL associated to the milking speed that has unfavorable genetic correlation with clinical mastitis or SCS. Thereby, genes detected under experimental study, are the valuable and informative markers to implementation genomic selection methods for cattle health in creating Russian bulls' reference population.

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