



PSXI-3

Genome-wide association study for MIR-predicted milk fatty acids composition in Russian Holstein cattle population

Sermyagin A.A., Lashneva I.A., Ignatieva L.P., Kositsin A.A., Gladyr E.A., Ermilov A.N., Yanchukov I.N., Zinovieva N.A.
L.K. Ernst Federal Research Center for Animal Husbandry, Podolsk, Russia, alex_sermyagin85@mail.ru



INTRODUCTION. Milk fatty acids (FA) derived from infrared spectra are a new type of traits that allow fast and predictability use their in dairy breeding and herd cattle management. The Holstein animals feature are the high milk yield, but milk composition traits can be different according to population or country origin.

The purpose of our study was to find out genetic variation for milk FA and detect QTLs associated with Holstein sires' EBV in Russian cattle population.

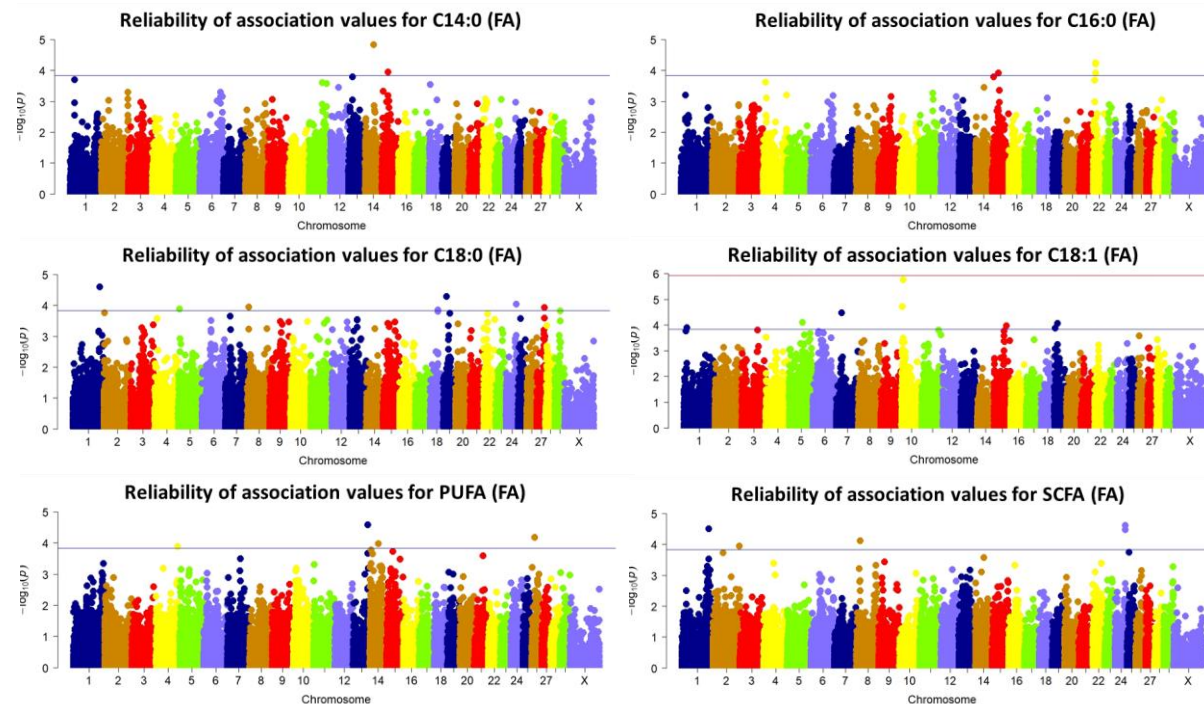
MATERIAL AND METHODS.

- For this analysis, we used an experimental dataset for **36982 milk test records** from **14 breeding herds** in the Moscow region.
- Individual milk samples per animal analyzed routinely by MilkoScan7 for different FA types: **C14:0, C16:0, C18:0, C18:1, saturated (SFA), mono- (MUFA) and polyunsaturated (PUFA), short- (SCFA), medium- (MCFA) and long-chain (LCFA).**
- Total number of bulls consisted **778 individuals** including **222 animals with genotypes (39051 SNPs, Illumina 50K),** genes annotation - **CattleQTLdb** (Zhi-Liang Hu, 2019).
- For calculating EBV by Sire Model, we applied BLUPF90 (Misztal I., 2002).
- Plink 1.90 performed quality check control and GWAS procedure (Chang C., 2015).

Table - Phenotype and genetic parameters for milk fatty acids composition

Trait	$\bar{X} \pm m$	σ	C_v	h^2
C14:0, g/100 g	0,680±0,001	0,148	21,8	0,155
C16:0, g/100 g	1,845±0,003	0,633	34,3	0,071
C18:0, g/100 g	0,585±0,001	0,195	33,4	0,125
C18:1, g/100 g	0,875±0,001	0,281	32,2	0,196
SFA, g/100 g	3,600±0,004	0,861	23,9	0,083
MUFA, g/100 g	1,002±0,001	0,213	23,0	0,176
PUFA, r/1g/100 g	0,005±0,000	0,011	238,8	0,018
SCFA, g/100 g	0,538±0,001	0,113	21,1	0,114
MCFA, g/100 g	2,206±0,003	0,652	29,6	0,125
LCFA, g/100 g	1,486±0,002	0,463	31,2	0,155

RESULTS. GWAS revealed most significant ($p < 0.001-0.00001$) frequently QTLs associated with FA content for BTA5 (CHST11, C18:1), BTA6 (KCNIP4, C18:1; PPRAGC1A, C18:0), BTA11 (NRXN1, LPIN1, C18:1; NBAS, C18:0), BTA26 (PCDH15, PUFA; PRKG1, C18:1)



CONCLUSION. These genes were responsible for synthesis milk fat, fertility, udder conformation traits, lauric, myristic, myristoleic, palmitoleic, oleic and other types of FA. In addition, we identified several QTLs for C14:0, C16:0, SFA, MUFA, SCFA, LCFA on BTA1 (137.32 Mb), BTA10 (5.50 Mb, 9.79 Mb), BTA14 (44.35 Mb), BTA19 (17.57-17.89 Mb) and BTA22 (14.02-14.06 Mb, 20.29-20.45 Mb). Our results are the first steps toward to understanding genetic and genomic mechanisms for using FA in selection processes to improve milk quality for Holstein cattle in Russia.

The study was funded by RSF (project No.21-76-20046)