

# PSXI-2 Genome-wide association study and possibilities for genomic selection of Simmental cattle breed in Russia

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## OBJECTIVES

The implementation of genomic selection methods in dairy cattle is limited due to the size of the reference population, quantitative traits variability and genetic structure of population. The Simmental cattle and related breeds in Russia occupy the third place by registered cows - 87.6 thousand, and are bred from the western borders of central Russia to Yakutia in Siberia.

**THE STUDY AIM** was to search for QTL using as a pseudo phenotype sires' EBV to validate the effectiveness of genomic assessments for Simmental cattle in Russia.

## MATERIALS AND METHODS

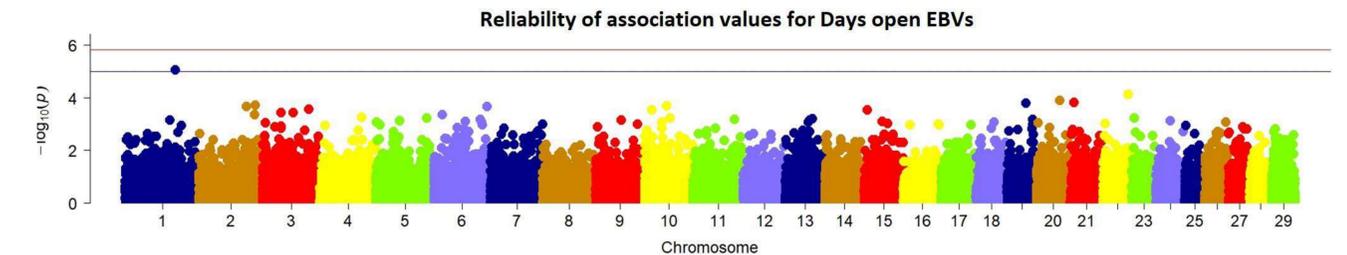
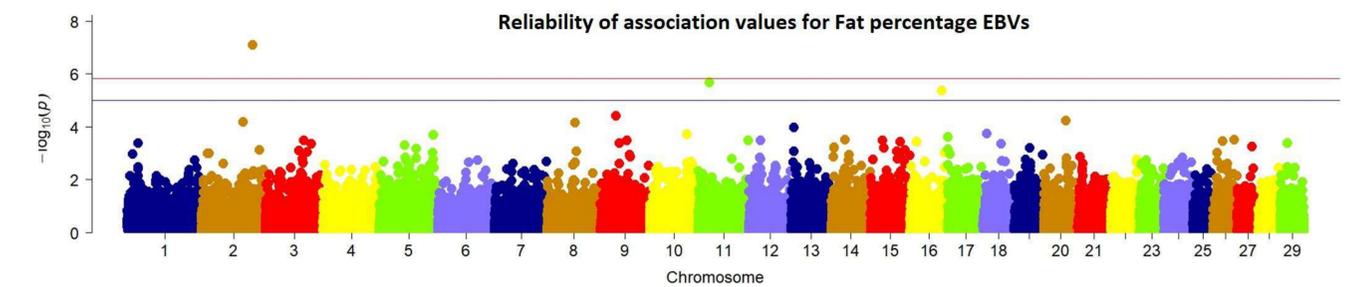
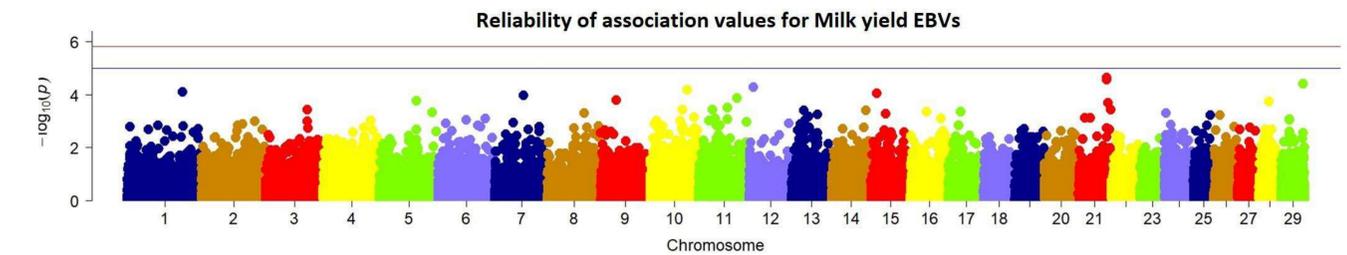
- Reference group based on **358** bulls from different Russian regional populations was formed.
- By the dataset of **61976** cows, using BLUP Animal Model approach, animals' EBV were calculated (BLUPF90; Misztal I., 2002).
- The GBLUP procedure was used to get genomic prediction (DGV).
- Genotype quality control selected of **37143** SNPs (Illumina 50K, GGP 150K).
- GWAS analysis was performed by Plink 1.90.

## RESULTS

To prove DGV we used verification procedure to comparison with EBV in training population dataset that showed slightly moderate repeatability for 305-milk yield - 37.6%, milk fat - 39.8% and milk protein - 43.6%. Significant SNPs associated with bulls EBV according to milk production and fertility traits revealed for: 305-milk yield on BTA5 (ACO2,  $p=0.0005$ ), BTA29 (NAP1L4,  $p=0.00004$ ; KCNQ1,  $p=0.00004$ ); fat percentage on BTA3 (ROR1,  $p=0.0003$ ), BTA14 (CRH,  $p=0.0003$ ; TRIM55,  $p=0.0003$ ; DNAJC5B,  $p=0.0003$ ; REX2,  $p=0.0020$ ; ZFH4,  $p=0.0020$ ) BTA17 (TLR2,  $p=0.0011$ ); days open on BTA1 (TNIK,  $p=0.0007$ ; FNDC3B,  $p=0.0007$ ), BTA21 (IGF1R,  $p=0.0002$ ). Using Cattle QTL Database, the identified genes were associated with milk yield, fat and protein percentage,

protein yield, somatic cell score, protein-to-fat ratio, stearic fatty acid content, calving ease, daughter pregnancy rate, stillbirth and inseminations per conception (table).

No	Gene candidate	p-value	BTA	QTL
<b>MILK YIELD</b>				
1	ACO2	0.00050	5	milk fat percentage, milk protein percentage, milk protein yield, milk yield
2	NAP1L4	0.00004	29	udder balance
3	KCNQ1	0.00004	29	luteinizing hormone level, somatic cell score, udder depth
<b>MILK FAT PERCENTAGE</b>				
4	ROR1	0.0003	3	body depth, calving ease, calving ease, daughter pregnancy rate, length of productive, milk protein percentage, Net merit
5	CRH	0.0003	14	PTA type, rump width, somatic cell, stature stillbirth (maternal), stillbirth, strength, udder attachment, udder depth, udder height
6	TRIM55	0.0003	14	average daily gain, carcass weight, conformation score, connective tissue amount, longissimus muscle area, marbling score, muscle PH, subcutaneous fat
7	DNAJC5B	0.0003	14	carcass weight
8	PEX2	0.0020	14	calf suckling reflex, carcass weight
9	ZFH4	0.0020	14	milk yield
10	TLR2	0.0011	17	feet and legs conformation, milk yield
<b>DAYS OPEN</b>				
11	TNIK	0.0007	1	bovine tuberculosis susceptibility, m. paratuberculosis susceptibility, milk protein-to-fat ratio, milk stearic acid content, somatic cell score
12	FNDC3B	0.0007	1	milk protein yield
13	IGF1R	0.0002	21	calving ease, dairy form, daughter pregnancy rate, dry matter intake, length of productive life, milk protein percentage, milk protein yield, Net merit, residual feed intake, somatic cell score, stillbirth, udder cleft
				age at puberty, body size, body weight, body weight (weaning), body weight (yearling), bovine respiratory disease susceptibility, inseminations per conception, milk fat percentage, milk fat yield, milk protein percentage, milk protein yield, milk yield



## Genome-wide association study for milk and fertility traits in Simmental cattle population

## CONCLUSION

GWAS results identified significant SNPs associated with milk production and fertility traits that will allow in the nearest future improve reliability for genomic prediction of young bulls and boost genetic trend in the Russian Simmental cattle population.

## ACKNOWLEDGMENTS:

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