Genome-wide association studies for growth and carcass traits in Russian sheep

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INTRODUCTION: Breeding of intensively growing sheep with good carcass is beneficial for lamb producers. However, genomic selection for relevant traits is still lagging in Russian sheep industry. In this regard, detection of the QTLs and candidate genes specific for local sheep is of great scientific and practical interest in Russia.

THE AIM: In our research, we aimed to perform GWAS for growth and carcass traits in the QTL-mapping sheep population obtained from crossing slow- and fast-growing breeds.

MATERIALS: Backcrosses from (Katahdin× Romanov) × Romanov mapping sheep population from experimental farm **(Fig.1).**

Fig 1. Backcrosses at the age of 90 days

Table 1. Significant SNPs and neighboring genes

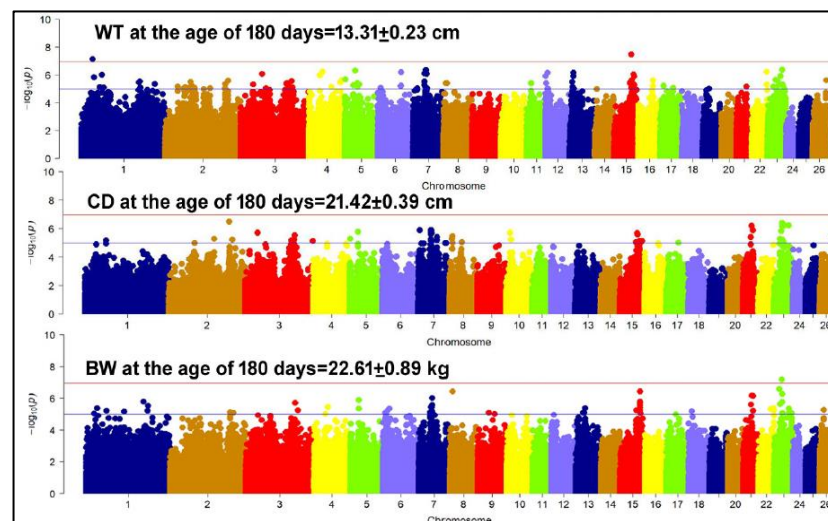| OAR	SNP	p-value	Gene
2	oar3_OAR2_148067154	$5.21*10^{-06}$ (CD);	PDK1
	oar3_OAR2_148075957	$9.70*10^{-06}$ (WT)	ITGA6
	oar3_OAR2_148077728		RAPGEF4
	s30510.1	$7.10*10^{-06}$ (CG)	
4	oar3_OAR4_45680479	$3.74*10^{-06}$ (BW)	GNAT3
7	oar3_OAR7_44462236	$2.66*10^{-06}$ (BW); $8.40*10^{-07}$ (WT)	
	oar3_OAR7_44496608	$7.92*10^{06}$(CD)	
	oar3_OAR7_44975375	$8.60*10^{-07}$ (WT)	PYGL
	oar3_OAR7_45012432	$2.15*10^{-06}$(CD); $7.24*10^{-06}$ (BW)	

Fig 1 . GWAS results for WT, CD and BW at the age of 180 days

GENOTYPING: We used Ovine Infinium HD SNP BeadChip (Illumina, USA). The Manhattan plots were visualized in R package qqman. Quality control in PLINK v.1.9 resulted in 459,868 SNPs which were used for GWAS. Threshold p-value for Bonferroni genome-wide significance was estimated as $p = 1.09x10^{-7}$.

PHENOTYPES: The measurements were recorded at the age of 6, 42 and 180 days and included body weight (BW) , chest depth (CD), chest width (CW) , chest girth (CG) and width at the iliac tubercle (WT).

RESULTS: Several significant SNPs were associated with WT at age of 180 days. One SNP on chromosome 4 and four SNPs on chromosome 7 suggestively associated with BW at age of 180 days. In addition, genomic regions located on chromosome 7 and chromosome 2 contained SNPs associated with CD at age of 180 days as well as with WT at age of 180 days **(Tab. 1 and Fig,2).**

Genes were annotated: **PDK1** is important lipid kinase and may play role in in osteoclast formation. **ITGA6** is involved in bone metabolism. **RAPGEF4** is involved in endocrine processes and has role in cardiac functions. **GNAT3** is involved in energy metabolism in muscle**. PYGL** is involved in carbohydrate metabolism.

CONCLUSION: The first results for GWAS in the QTL-mapping sheep population are promising. Because next series of backcrosses will be genotyped in the end of 2020 year, we will continue our studies on a larger sample. Thus, our work creates a base for genomic selection in sheep breeding in Russia.

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