

INTRODUCTION

The cost of fodder is the major part in expenditure in pork industry. In this regard, improving the feed efficiency is the main goal of breeding programs for the most of pig breeds. Residual feed intake (RFI) is an alternative measure for feed efficiency, which is accepted in different livestock species including pigs. RFI is defined as the difference between the observed and predicted feed intake based on average daily gain and (additionally) back fat thickness.

MATERIALS

The object of research was the boars of the Duroc breed (n = 766), tested at feed stations. The studies involved clinically healthy animals that were not treated, periodically examined by veterinary specialists. Samples were taken from all cartilages for molecular genetic studies.



GENOME-WIDE ASSOCIATION STUDY OF FEED EFFICIENCY IN RUSSIAN DUROC BOARS

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PHENOTYPES

The average daily gain in studied boars was 957 g with variation in individual animals from 424 to 1508 g. Feed conversion rates averaged to 2.21 kg/kg with variation from 1.8 to 3.7 kg/kg.

GENOTYPING

Full genome genotyping was performed using a Porcine GGP HD DNA chip (Illumina, USA) containing ~ 70 k. SNP. Quality control and filtering of genotyping data for each SNP and each sample was performed using the PLINK software package v1.9

Based on the results of the quality control conducted, 43,199 SNPs were selected for GWAS.

GWAS results (fig. 3) showed the presence of 48 SNPs, which were significantly ($p < 0.00001$) associated with RFI, including 15 SNPs on SSC2, 9 SNP – SSC4, 2 SNPs – SSC6, 21 SNPs – SSC9, and 1 SNP – SSC17. A search for genes located within 0.4 Mb window (0.2 Mb down-stream to 0.2 Mb up-stream from identified SNP) revealed several putative candidates. Functional annotation of the obtained candidates showed the presence of genes involved in protein metabolism (*ADAMTS2*, *UIMC1* on SSC2; *NTNG1* on SSC4), regulation of glucose and bile acid metabolism (*FGFR4* on SSC2), neuronal development (*ENC1* on SSC2; *NTRK1*, *MEF2D* on SSC4), vitamin D and K pathways (*BGLAP* on SSC4).

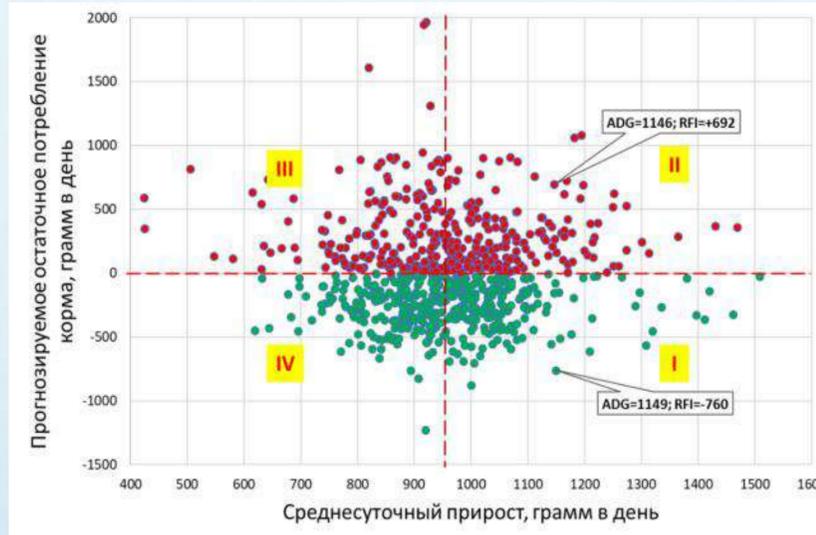


Fig 2. Distribution of phenotypic values of average daily gain (ADG) and deviation from residual feed intake (RFI) according to the boars group compared (*Sus scrofa*) of Duroc breed by ratio RFI and ADG

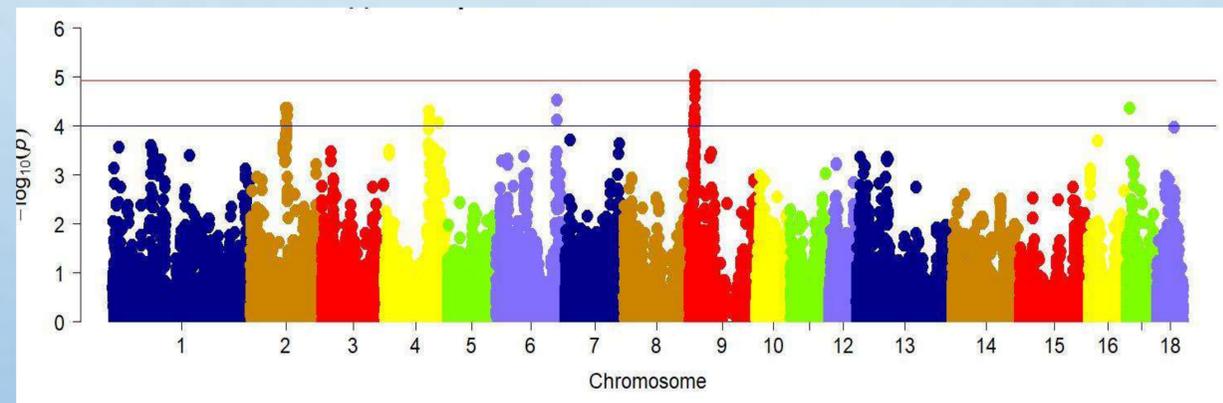


Fig 3. GWAS results for RFI scores in the studied Duroc breed boars sample

Note: X axis — number of pigs chromosome; axis Y — reversed decimal logarithm of validity level $-\log_{10}(p)$; upper horizontal line — confidence threshold for full genome associations, $-\log_{10}(p) = 1,2 \times 10^{-6}$; lower horizontal line - validity threshold for accreditation associations $-\log_{10}(p) = 1,02 \times 10^{-5}$.

CONCLUSION

The predicted residual feed consumption, combined with average daily feed growth and conversion, is the most reliable result for determining the number of livestock in the reproduction or fattening groups. The effect of predicted residual feed intake with average daily gain on reproductive qualities of offspring will be examined. In the future, it is planned to increase the number of livestock and expand the breeds according to these studies, as well as to introduce the indicator of the predicted residual consumption of feed in the production process.



Fig 1. Duroc boars on automatic feed station.