GENOME-WIDE SEARCH FOR GENOMIC REGIONS UNDER PUTATIVE SELECTION IN TWO RUSSIAN NATIVE CATTLE BREEDS USING HIGH-DENSITY SNP BEAD CHIP

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Figure 1. Photos of Yaroslavl and Kholmogor bulls

Material and Methods

Fifty-six animals of Yaroslavl (n=31) and Kholmogor (n=25) breeds were selected for the study. The Illumina Bovine HD BeadChip (777,962 SNPs) was used for genotyping. High-density SNP genotypes for Holsteins (n=25) were used as the reference. Three methods (F_{ST}, hapFLK, and ROH) were implemented to detect the genomic regions to be under putative selection.

Introduction

National livestock genetic resources are the valuable source of genetic variability, which are necessary to ensure the sustainability of the local animal production systems. The aim of our work was to characterize the genomic architecture and to detect signatures of selection in two oldest Russian native cattle breeds, using high-density DNA arrays.
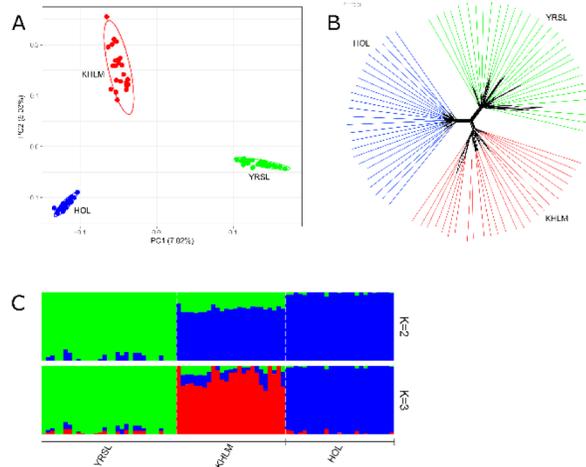

Figure 2. PCA (A), Neighbor-Net (B), Admixture (C) analyses

Results

The results of the PCA-plot, Neighbor-Net analysis and Admixture clustering showed genetic differences between Yaroslavl and Kholmogor as well as between them and Holsteins. Comparison of the results produced by different methods showed that of twelve regions in genome of Yaroslavl and nine regions in genome of Kholmogor breeds, each region was confirmed at least by two methods. We have identified six regions under putative selection in genome of Yaroslavl cattle and six regions in genome of Kholmogor cattle, which were described previously based on medium-density SNP genotypes, herewith the flanking positions of the most of these regions were expanded. Additionally, we detected three new putative genomic regions affected by selection in each studied breed, which were localized on chromosomes 4, 15 and 17 in Yaroslavl breed and on chromosomes 12, 15 and 18 in Kholmogor breed. The functional annotation of genes localized within identified regions was carried out. Our research results can be useful for genetic improvement of the studied cattle breeds and for developing the programs for their conservation.
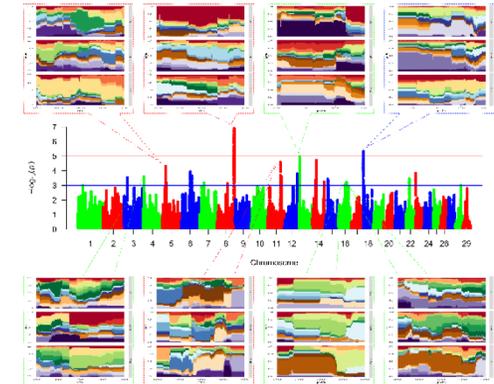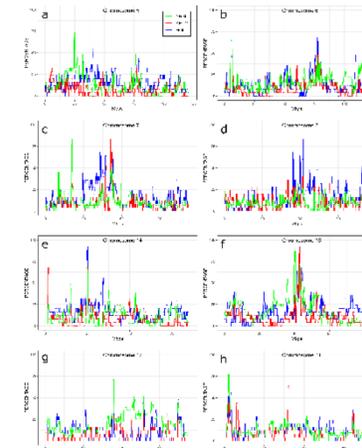
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Figure 3. hapFLK analysis

Figure 4. ROH analysis indicates contiguous stretches of homozygotes on chromosomes 5, 6, 7, 8, 14, 16, 17, 21 in Yaroslavl, Kholmogor and Holstein cattle

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