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Genome-wide screening for SNPs associated with stature in diverse cattle breeds

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Federal Research Center for Animal Husbandry named after Academy Member L.K. Ernst

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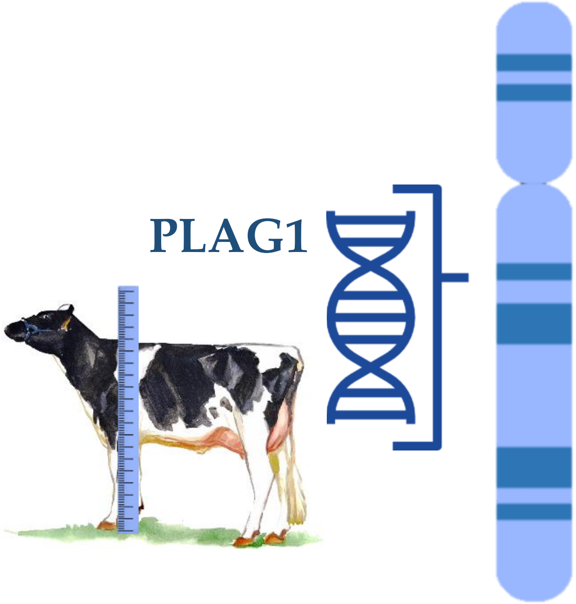
Abstract: Cattle breeds used in industrial production tend to have larger size compared to the local cattle, as the increased dairy and beef productivity is closely related to the stature. The aim of our work was to identify SNPs, which are significantly associated with stature in diverse cattle breeds. Thirteen local and transboundary cattle breeds (n = 670) subjected to our study were divided in two groups according to the stature. The high-stature group included Angus, Ayrshire, Black-and-White, Holstein, Kholmogor, Yaroslavl, Tagil and Istoben breeds. The low-stature group comprised of Jersey, Kalmyk, Kyrgyz, Mongolian and Yakut cattle. The average height at withers was 136.3±1.6 and 121.6±2.8 cm in the high- and low-stature groups, respectively. The samples of 11 breeds were genotyped using high-density DNA arrays (Illumina Inc., USA). The genotypes of two remaining breeds were downloaded from the publicly available WIDDE database [http://widde.toulouse.inra.fr/wide]. Genome-wide association studies revealed four SNPs, which were strongly associated with the stature, including three SNPs at 77.3-77.8 cM on BTA4 (map53144-ss46525999, p<7.747*10-101; BovineHD0400021479, p<1.173*10-91; ARS-BFGL-NGS-116590, p<7.665*10-105) and one SNPs at 25.2 cM on BTA14 (BovineHD1400007259, p<1.324*10-109). Functional annotation showed the localization within identified regions of genes, which are responsible for growth, exterior characteristics, protein and lipid metabolism, and feed intake. Identified SNPs can be considered as useful DNA markers for marker-assistant cattle breeding aimed at increased stature.

Keywords: local cattle, SNP, stature, allele frequency

Animals' stature is closely related to the productivity. Many studies have been conducted, which revealed a large number of loci associated with body size in cattle

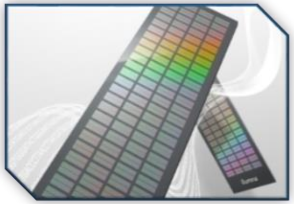
The PLAG1 gene, which is located on chromosome 14 was the one of the most frequently detected genes in such studies. However, the most studies were carried out on commercial breeds of cattle that have been subjected to the strong artificial selection pressures.

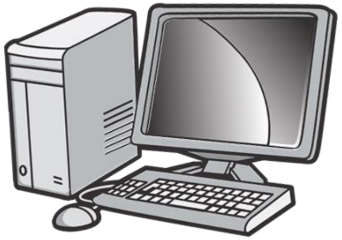


Although comprehensive genome-wide studies of Russian local cattle breeds were carried out, the genetic basis of stature in these breeds was not investigated until now.

The aim of our work was to identify SNPs, which are significantly associated with stature in commercial and local cattle breeds bred in Russia.

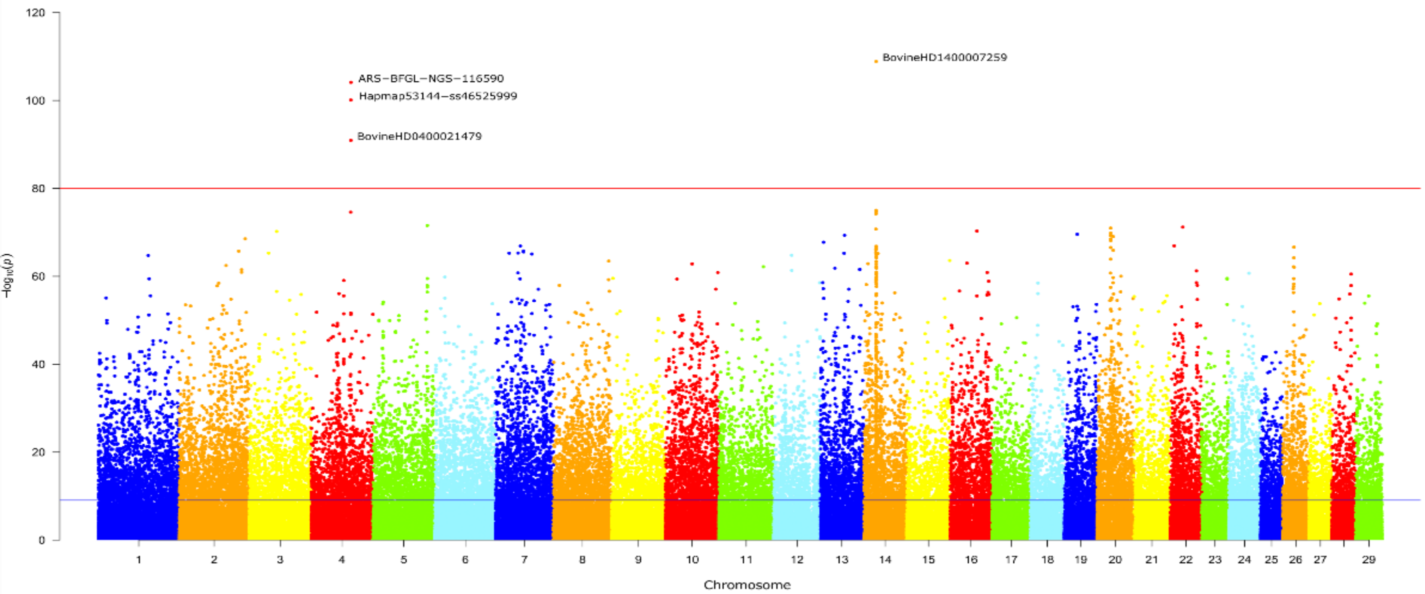
Results





The samples of 11 breeds were genotyped using high-density DNA arrays (Illumina Inc., USA) in the L.K. Ernst Federal Research Center for Animal Husbandry. The genotypes of two remaining breeds were downloaded from the publicly available WIDDE database

Genome-wide association studies revealed four SNPs, which are strongly associated with the stature, including three SNPs at 77.3-77.8 cM on BTA4 (map53144-ss46525999, $p<7.747*10^{-101}$; BovineHD0400021479, $p<1.173*10^{-91}$; ARS-BFGL-NGS-116590, $p<7.665*10^{-105}$) and one SNPs at 25.2 cM on BTA14 (BovineHD1400007259, $p<1.324*10^{-109}$).



Results

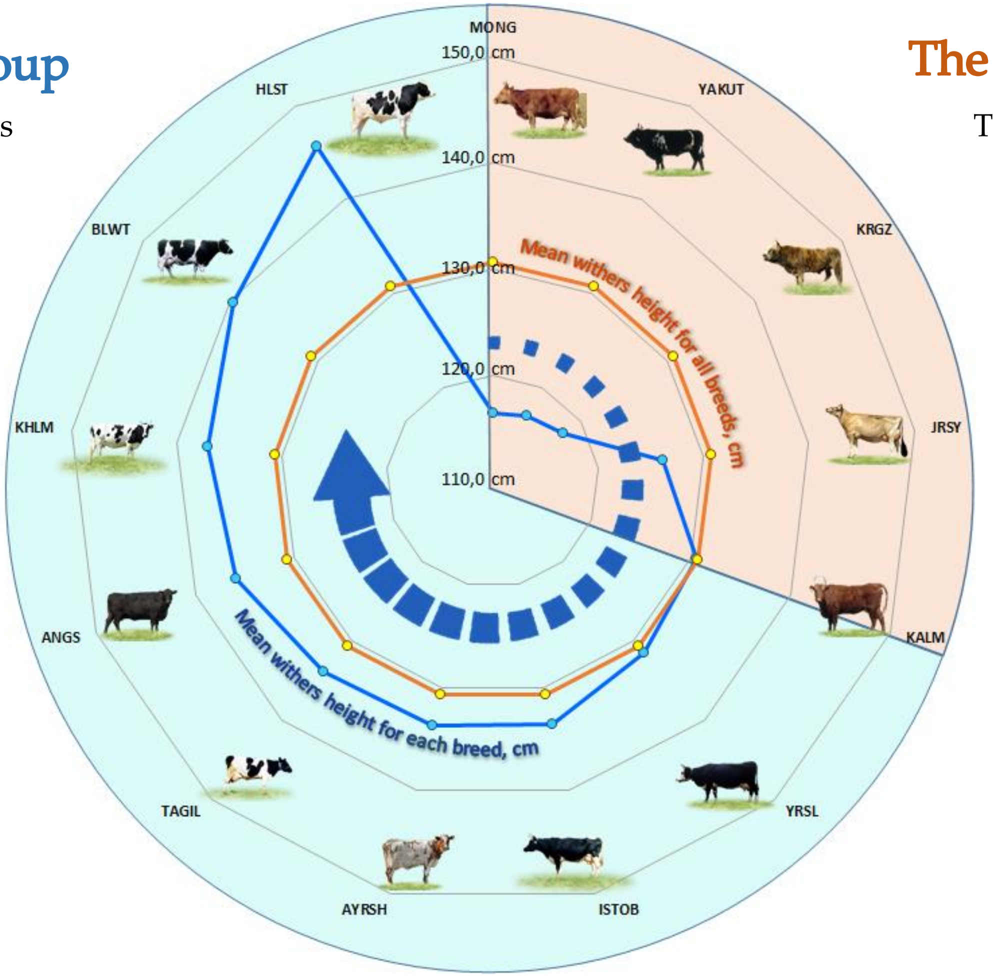
Cattle breeds were divided in two groups according to the stature.

The high-stature group

The average height at withers is 136.3±1.6 cm

SNP	Allele	Allele frequencies
ARS-BFGL-NGS-116590	T	0,204
	G[a]	0,796
Hapmap53144-ss46525999	T[a]	0,795
	C	0,205
BovineHD0400021479	A	0,201
	G[a]	0,799
BovineHD1400007259	T	0,090
	G[a]	0,910

a — alleles are associated with greater height at withers



The low-stature group

The average height at withers is 121.6±2.8 cm

SNP	Allele	Allele frequencies
ARS-BFGL-NGS-116590	T	0,349
	G[a]	0,651
Hapmap53144-ss46525999	T[a]	0,082
	C	0,918
BovineHD0400021479	A	0,309
	G[a]	0,647
BovineHD1400007259	T	0,959
	G[a]	0,041

a — alleles are associated with greater height at withers

Identified SNPs can be considered as useful DNA markers for marker-assistant cattle breeding aimed at increased stature in diverse cattle breeds bred in Russia.

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Acknowledgments

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Thank you for your attention!