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Selection footprints in Russian red cattle identified by linkage disequilibrium blocks based on SNP data

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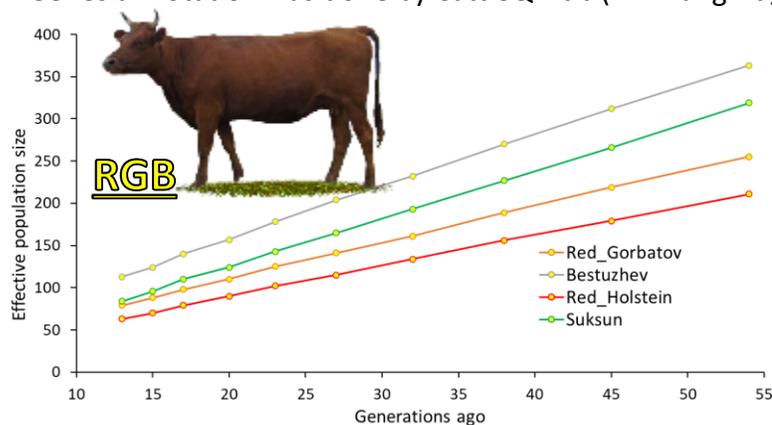


INTRODUCTION Among the variety of cattle breeds in Russia, the Russian red dual-purpose cattle breeds have great importance because of their ability to produce high milk yields as well as to provide excellent milk quality. The low census size of the Russian red cattle breeds requires development of programs for conservation of their biodiversity.

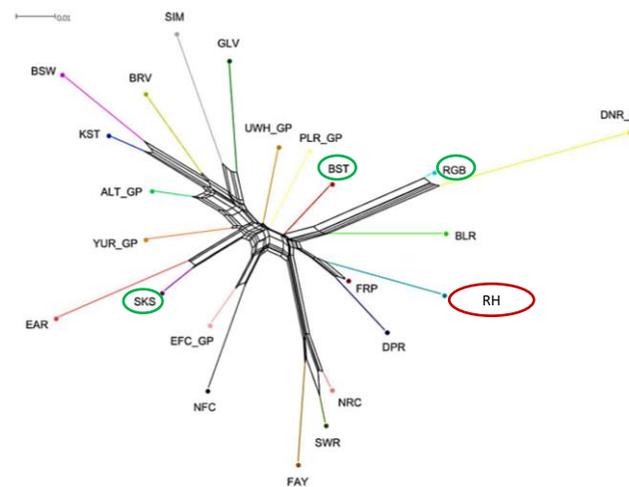
Our study aimed to investigate selection footprints in Russian red cattle breeds using high values of linkage disequilibrium (LD) in SNP haplotype blocks as indicators.

MATERIAL AND METHODS

- For finding LD blocks, we used the genotypes (**≈35K SNPs**, Illumina) of **Red Gorbatov (RGB, n=26)**, **Bestuzhev (BST, n=27)** and **Suksun (SKS, n=17)** breeds, as well as **Red Holstein (RH, n=16)** as an outgroup.
- Quality control and LD calculations for different distances were performed in Plink 1.90 (Chang C., 2015). **Top 0.01% SNP pairs** by LD value ($0.9 \leq r^2 < 1.0$) were selected for further analysis. Comparison of LD values for 70 kb interval between breeds and chromosomes by MANOVA (SAS).
- The effective population size derived from LD patterns was estimated using SNeP tool (Barbato M., 2015).
- Genes annotation was done by CattleQTLdb (Zhi-Liang Hu, 2019)



RESULTS MANOVA pairwise testing significantly distinguished RH/RGB and BST/SKS breeds ($p < 0.05-0.001$). LD values among chromosomes were 0.195-0.287 for RH, 0.194-0.272 for RGB, 0.172-0.237 for BST, and 0.157-0.217 for SKS. The SKS and BST breeds had higher N_e values (84 and 113, respectively) compared to RH (63) and RGB (79). Selection footprints by LD blocks in Russian red cattle genome covered several relevant genes on BTA1 (EPHA6, DGKG), BTA2 (LRP1B, THSD7B, STAT1), BTA5 (CPM, BAIAP2L2), BTA9 (TRDN, UTRN), BTA10 (KCNN2, CAPN3), BTA11 (SH3RF3, RABGAP1, RALGPS1), BTA14 (ZNF16, ARHGAP39, TOX, DGAT1), and BTA19 (MYH10), BTA22 (FHIT).



Neighbor-Net tree constructed based on the F_{ST} genetic distances among studied breeds (doi: 10.1111/age.13102)

Distance (kb)	Breed	SNP pairs	Average r^2 (SD)*	SNP pair with $r^2 > 0.3$ (%)
0-30	RH	9931	0.317 (0.330) ^a	3795 (38.21)
	RGR	8901	0.303 (0.321) ^a	3247 (36.48)
	BST	9565	0.275 (0.306) ^b	3145 (32.88)
	SKS	5212	0.251 (0.286) ^c	1550 (29.74)
30-70	RH	27412	0.238 (0.274) ^a	7787 (28.41)
	RGR	24556	0.219 (0.262) ^c	6317 (25.72)
	BST	26556	0.191 (0.240) ^d	5780 (21.77)
	SKS	14718	0.173 (0.218) ^e	2884 (19.60)
70-100	RH	20087	0.195 (0.233) ^a	4473 (22.27)
	RGR	17963	0.173 (0.217) ^c	3461 (19.27)
	BST	19399	0.142 (0.189) ^d	2814 (14.51)
	SKS	10742	0.130 (0.169) ^e	1378 (12.83)
100-200	RH	65656	0.157 (0.196) ^a	11302 (17.21)
	RGR	58372	0.135 (0.176) ^c	7950 (13.62)
	BST	63455	0.108 (0.150) ^d	5827 (9.18)
	SKS	35121	0.106 (0.140) ^e	3085 (8.78)

Note: *upper right index means a significance level of difference between breeds by distances variants ($p < 0.0001$)

CONCLUSION Detected genes were found to be responsible for milk fat and protein contents, fatty acid composition, somatic cells score, fertility, feet and legs, and udder conformation traits. Our results can be useful for developing the breeding and conservation programs of the Russian red cattle genetic resources.

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