

Assessment of genomic inbreeding in Russian local and commercial dairy breeds of cattle.

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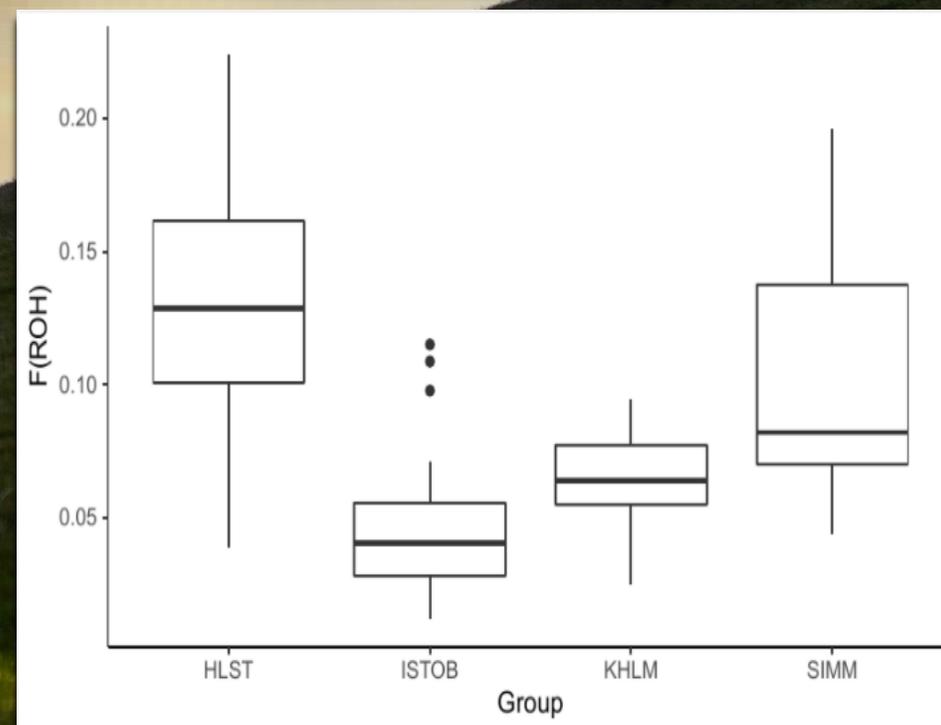
Introduction. Drastic decline of population size of Russian local cattle breeds observed during last three decades has led to the decrease of genetic diversity. Due to the limited number of bulls used for artificial insemination, inbreeding in herds can be increased, which can lead to the decrease of reproduction capacity and adaptability of animals.

Aim. Our aim was to assess genomic inbreeding in two Russian local cattle breeds, including Kholmogor (n = 26) and Istoben (n = 21).

Materials and methods. Two transboundary cattle breeds used for milk production in Russia including Holstein (n = 49) and Simmental (n = 38) were chosen for comparison. SNP genotyping was performed using the Bovine GGP 150K BeadArray (Illumina, CA, USA). After the quality control, 117591 autosomal SNPs were selected for analyzes. The degree of genomic inbreeding was assessed by calculations of inbreeding coefficient based on run of homozygosity (F(ROH)) and multilocus heterozygosity (sMLH).

Results. We found the strong negative correlations between the F(ROH) and sMLH values in animals of all of studied breeds ($r^2 = -0.805$). The average F(ROH) values were 0.065 ± 0.003 for Kholmogor, 0.048 ± 0.006 for Istoben, 0.129 ± 0.007 for Holstein, and 0.102 ± 0.007 for Simmental breed. The sMLH values in Kholmogor, Istoben, Holstein and Simmental breeds varied from 0,99 to 1,076, from 0,829 to 1,102, from 0,890 to 1,069 and from 0,866 to 1,041, and averaged to 1.030, 1.013, 1.000, and 0.974, respectively.

Conclusions. Two studied Russian cattle breeds are characterized by lower levels of genomic inbreeding compared to transboundary cattle breeds. Our results will be helpful for developing the conservation programs for Russian Kholmogor and Istoben cattle breeds.



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