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A study of biodiversity of Russian local sheep breeds based on pattern of runs of homozygosity

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

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Abstract: A rapid spreading of cosmopolite breeds leads to decrease of population sizes of Russian local sheep that consequently result in their biodiversity loss. Estimation of runs of homozygosity in local sheep genomes will be informative tool to address their current genetic state. In this work, we aimed to address the distribution of the ROH and to estimate genome inbreeding in Russian local sheep breeds based on SNP-genotyping. Medium-density SNP-genotypes of twenty-three local sheep breeds (n=332) were obtained in our previous study. We used a consecutive runs method implemented in the R package "detectRUNS" to calculate ROH which were estimated for each animal and then categorized in the ROH length classes (1-2 Mb, 2–4 Mb, 4–8 Mb, 8–16 Mb, >16 Mb). The frequency of short ROH segments (≤ 2 Mb) were the highest in all studied breeds (63.15% - 93.10%). The longest segments (> 16 Mb) were the least frequent and were missing in four breeds. The genomic coefficients based on ROH estimation varied from medium (0.114) to low (0.035). Thus, we found that Russian local sheep breeds are characterized by a low level of genomic inbreeding.

Keywords: sheep; genetic diversity; SNPs; genomic inbreeding

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Results and Discussion

The frequency of short ROH segments (≤ 2 Mb) was the highest in all studied breeds (63.15% -93.10%). The longest ROH segments (> 16 Mb) were the least frequent (0.07% - 1.22%).

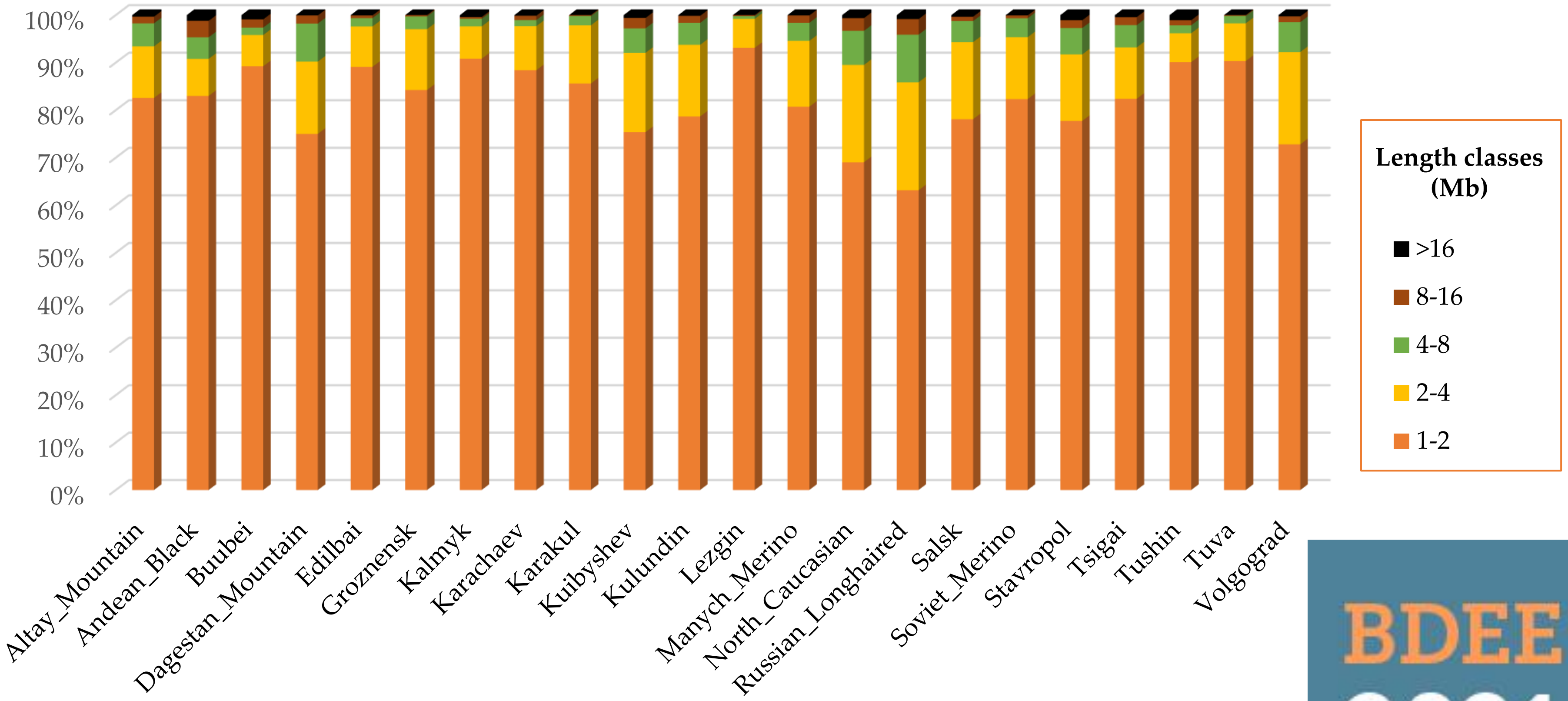

Figure 1. Distribution of the runs of homozygosity in length classes in Russian local sheep breeds

Results and Discussion

The minimum F_{ROH} was calculated in the Lezgin breed ($F_{ROH} = 0.035$) and the maximum was detected in the Russian Longhaired breed ($F_{ROH} = 0.114$).

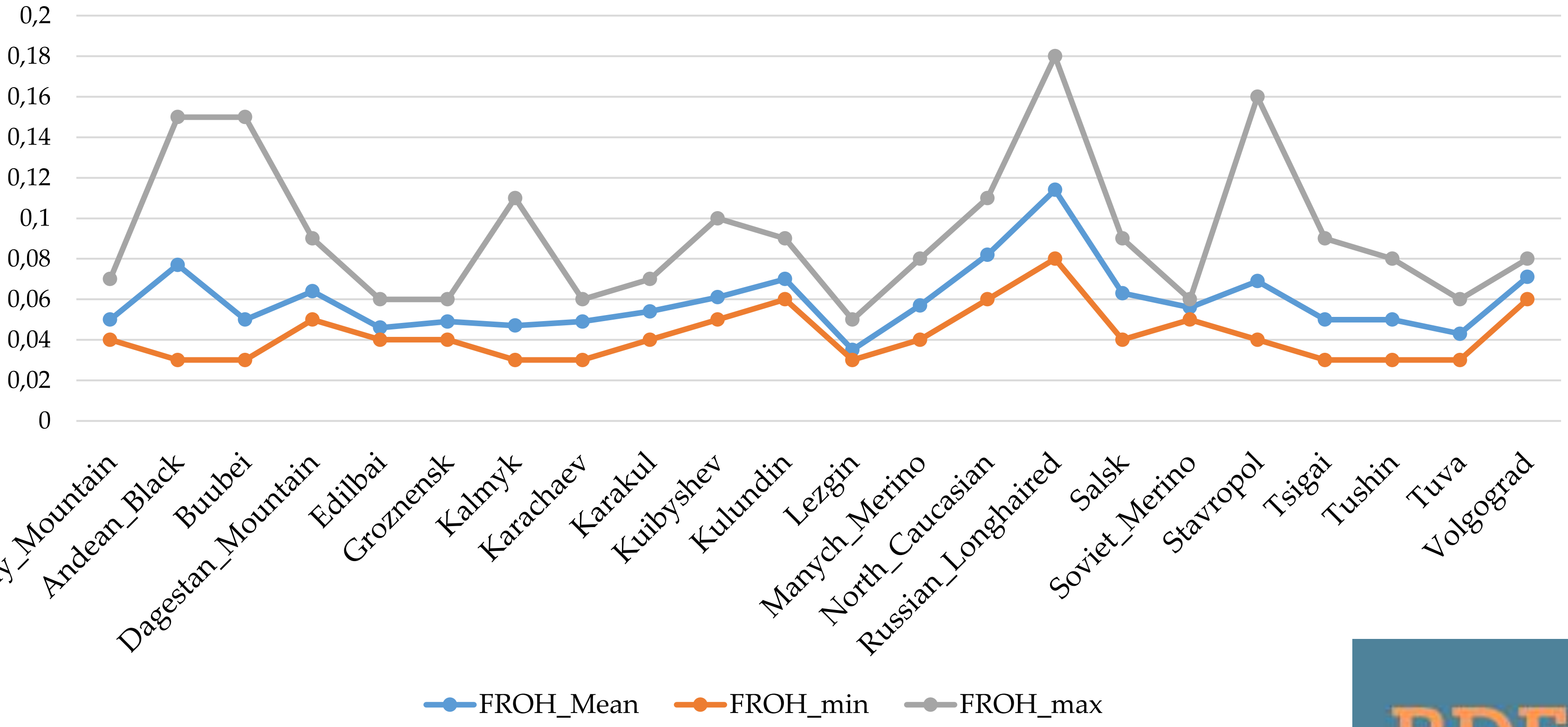

Figure 2. Values of inbreeding coefficient calculated based on ROH (F_{ROH}) in Russian local breeds

Results and Discussion


Present study

Russian

Mean ROH length from 93.7 to 301.7 Mb. Max. ind. ROH length – 470 Mb.

F_{ROH} from oт 0.035 to 0.114 Mb.

Short ROH segments predominant


Al-Mamun et al., 2015

Border Leicester, Merino, and Poll Dorset

Mean ROH length from 94.9 to 126.1 Mb. Max. ind. ROH length - 427, 410 and 396 Mb.
Short ROH segments predominant


Signer-Hasler et al., 2019

Swiss local

Mean F_{ROH} from 0.022 to 0.153.

ROH segments with length classes from 1 to 10 Mb were the most frequent in all breeds using 50k data.


Mastrangelo et al, 2018

Italian local

Mean F_{ROH} varied from 0.016 to 0.099.

Short ROH segments predominant.


Purfield et al., 2017

Charollais, Suffolk, and Texel

Mean ROH length from 92.61 to 128.31 Mb.
Short ROH segments predominant.

Conclusions

- Our findings based on 50k data provide an evidence of a low genomic inbreeding in Russian local sheep populations.
- The study results provide useful information to design conservation programs for local genetic recourses of sheep.

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2021

Supplementary Materials

The details on the relevant dataset including the sampling locations for each breed, the SNP quality control and the phylogenetic links between the breeds are available online at https://gsejournal.biomedcentral.com/articles/10.1186/s12711-018-0399-5.

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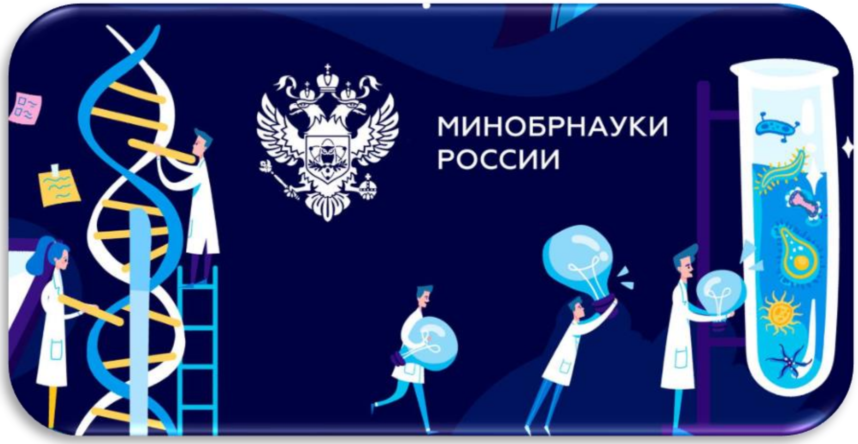

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Thank you for your attention!

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