

The distribution of runs of homozygosity in nine native Russian sheep breeds

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INTRODUCTION: Native coarse wool fat-tailed sheep breeds are the main producers of mutton in mountainous, steppe and semi-desert regions of Southern Russia (Fig.1). An assessment of homozygosity is required to prevent loss of genetic diversity and inbreeding depression onset.

Our **AIM** is estimation of genomic inbreeding and distribution of the runs of homozygosity (ROH) segments in Russian sheep breeds.

MATERIALS AND METHODS: We collected 165 samples from nine native breeds (Tab.1) which were genotyped using Ovine Infinium® HD SNP BeadChip (Illumina, USA). A consecutive runs method implemented in the R package “detectRUNS” was used for estimation of ROH segments.

RESULTS: We detected the ROH in all breeds with mean length ranging from 0.35 in Lezgin to 11.18 Mb in Karachaev (Fig.2). Andean had the greatest number of the ROH segments (total of 8496), while 3094 ROH segments were found in Buubei.

Table 1. Variation of genomic inbreeding coefficient (FROH) based on ROH

Breed	Code	n	FROH	
			min	max
Andean	ANDB	20	0.052	0.170
Buubei	BUUB	11	0.031	0.077
Buryat	BURT	18	0.039	0.064
Edilbai	EDLB	20	0.039	0.111
Kalmyk	KALM	22	0.042	0.116
Karachaev	KRCH	20	0.051	0.083
Karakul	KARA	20	0.055	0.078
Lezgin	LEZG	15	0.041	0.061
Tushin	TUSH	19	0.044	0.092

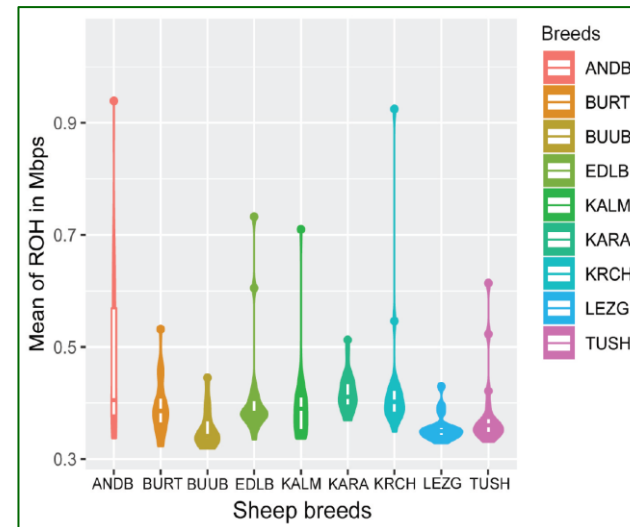


Fig 2. Pattern of ROH distribution

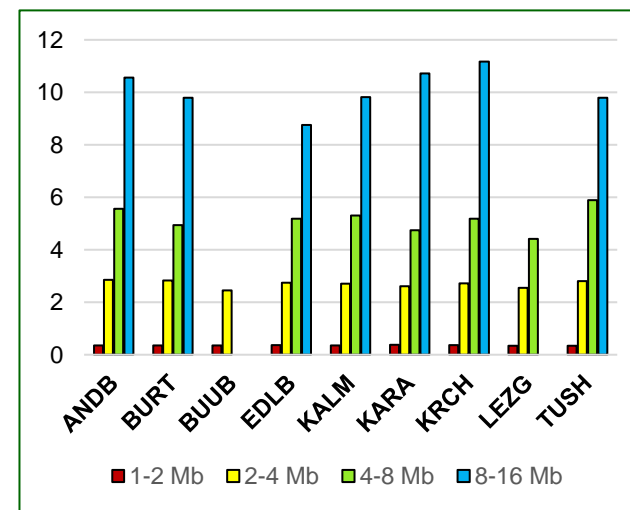


Fig 3. ROH coverage in ROH length classes

RESULTS (CONTINUED): Short ROH segments (<2 Mb) were predominant in all breeds and varied from 96.83% in Andean to 99.87% in Buubei. The frequencies of the ROH segments of 8-16 Mb ranged from 0.03% in Karakul to 0.18% in Andean. ROH segments of 8-16 Mb did not occur in the Buubei and Lezgin breeds. Nonetheless, the ROH coverage was larger in long length classes (Fig.3).

The ROH segments were found on all autosomes. The largest genome coverage in the ROH was identified on OAR1, OAR 12 and OAR 20 and the lowest was accounted for OAR 17, OAR 18 and OAR 19.

The individual values of FROH ranged from 0.031 in Buubei to 0.170 in Andean (Tab.1).

CONCLUSION: Except of Andean, no traces of long-term inbreeding were detected in local breeds. The data is relevant for future sustainable management of native fat-tailed sheep breeds in Russia.

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Fig 1. Native sheep on the pasture