

PSX-18 High-density genomic description of Russian native sheep breed of the Republic of Tyva

Tatiana Deniskova¹, Arsen Dotsev¹, Chechena Sambu-Khoo², Henry Reyer³, Marina Selionova⁴, Margaret Fornara¹, Klaus Wimmers³, Gottfried Brem^{1,5}, Natalia Zinovieva¹

¹ L.K. Ernst Federal Science Center for Animal Husbandry, Russia; ² Tuvan state university, Russia; ³ Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Germany; ⁴ Russian State Agrarian University - Moscow Timiryazev Agricultural Academy, Russia; ⁵ Institute of Animal Breeding and Genetics, VMU, Austria

INTRODUCTION: Tuva breed is the oldest native sheep breed in Russia with more than 2000 year-history and comes in third place by population size among coarse wool sheep. Tuva sheep produce high-quality meat as well as coarse wool to make traditional clothing in the Republic of Tyva.

In present study, we aimed to evaluate genetic diversity and to establish genetic links of the Tuva breed with the other Russian coarse wool sheep to understand the origin and current status of this valuable livestock species.

MATERIALS AND METHODS: Twenty samples of Tuva were genotyped using Ovine Infinium® HD SNP BeadChip (Illumina, USA). SNP-data were processed in R package 'diveRsity' and *SneP* software. High-density SNP-genotypes of six long -fat-tailed, three short-fat-tailed, and two fat-rumped breeds were used as comparison groups.

RESULTS (Table 1): Observed heterozygosity and allelic richness in Tuva breed practically equal to mean values estimated across all analyzed sheep breeds. All coarse wool breeds showed moderate heterozygote excess which was the highest in Tuva breed (1.6%).

Table 1. Comparative analysis of genetic diversity indicators of Tuva breed

Breeds	Heterozygosity				Inbreeding coefficient (Fis)		Allelic richness (Ar)	
	Observed (Ho)		Expected (He)		min	max	min	max
	min	max	min	max				
Long -fat-tailed	0.322	0.337	0.316	0.326	-0.019	-0.042	1.867	1.893
Fat-rumped	0.331	0.336	0.323	0.329	-0.022	-0.024	1.883	1.893
Short-fat-tailed	0.336	0.345	0.325	0.331	-0.033	-0.081	1.872	1.894
Tuva breed	0.336		0.32		-0.047		1.884	
Mean	0.335		0.324				1.884	

RESULTS (Table 2): Effective population sizes estimated for three (Ne3) and five (Ne5) generations ago for Tuva breed were less than those in other breeds but not the lowest. Values of historical effective population size estimated for 60 generations ago for Tuva breed was 1457 that was compatible with those obtained for other breeds (Ne60 from 586 for Buubei to 2634 for Kalmyk).

Table 2. Effective population sizes

Breeds	Ne3	Ne5	Ne60
Long - fat-tailed	127-263	187-379	1259-2511
Fat-rumped	300-314	441-450	2354-2634
Short-fat-tailed	49-245	72-331	586-2285
Tuva breed	118	179	1457

RESULTS (Fig.1): Admixture clustering demonstrated that Tuva breed has common ancestry with other short-fat-tailed and fat-rumped breeds.

CONCLUSION: Despite the obvious decrease in effective population size, levels of genetic diversity are not critical that would allow to develop programs to ensure preservation and sustainable development of Tuva breed.

ACKNOWLEDGMENTS: The study was funded by RSF according project No. 19-16-00070.

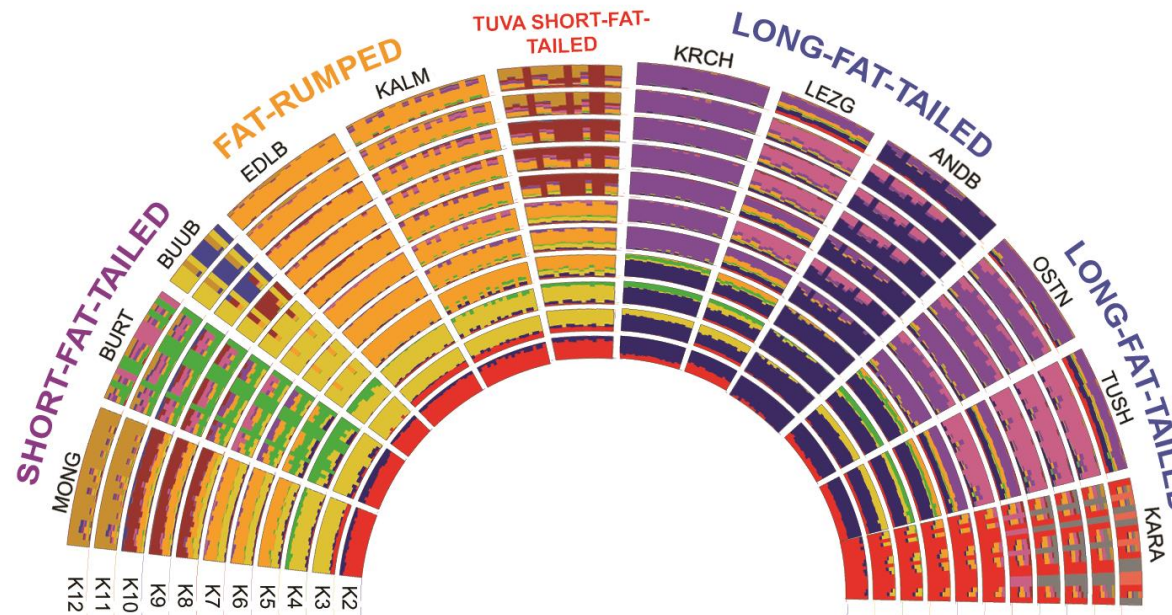


Fig 1. Ancestral links of Tuva breed with the other fat-tailed breeds

CORRESPONDING AUTHOR:
Tatiana Deniskova horarka@yandex.ru