Analysis of genetic diversity of Kazakh White-headed cattle breed by microsatellites compare with ancestral breeds

Alexandra S. Abdelmanova [1]*, Veronika R. Kharzinova [1], Valeria V. Volkova [1], Arsen V. Dotsev [1], Alexander A. Sermyagin [1], Oxana I. Boronetskaya [1,2], Roman Yu Chinarov [1], Gottfried Brem [1,3], Natalia A. Zinovieva [1]

[1] L.K. Ernst Federal Research Center for Animal Husbandry, Dubrovitsy, Podolsk Municipal District, Moscow Region, Podolsk 142132, Russia;
[2] Timiryazev Russian State Agrarian University—Moscow Agrarian Academy, 49, ul. Timiryazevskaya, 127550 Moscow, Russia;
[3] Institut für Tierzucht und Genetik, University of Veterinary Medicine (VMU), Veterinärplatz, A-1210 Vienna, Austria
* Corresponding author: preevetic@mail.ru

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

L.K. Ernst Federal Research Center for Animal Husbandry

Abstract: Kazakh White-headed is the local beef cattle breed, created in the beginning of 20 century by improving native Kazakh cattle by Hereford breed. The aim of our work was to trace the presence of ancestral genetic components in the modern population of this breed. The samples of modern representatives of Kazakh White-headed (n=29) and Hereford (n=25) breeds as well as historical specimens of native Kazakh breed (n=2), dated by the first quarter of 20th century, were subjected to the study. We genotyped 11 microsatellite loci (BM1818, BM2113, BM1824, ETH10, ETH225, INRA023, SPS115, TGLA53, TGLA122, TGLA126, and TGLA227). For historical samples the PCR reaction were carried out in five replicates to determine the consensus genotypes for each locus. In total, we identified 82 microsatellite alleles. Five alleles, which were found in the historical specimens, were lost in the modern population. We observed the highest level of genetic diversity in historical samples. The modern population of Kazakh White-headed cattle was closer to Hereford breed as was revealed by calculation of pairwise Nei and F_{ST} genetic distances. The STRUCTURE clustering showed the visible presence the historical genetic components in the modern Kazakh White-headed cattle. The research results will be useful for developing the programs of conservation and sustainable use of Kazakh White-headed cattle.

Keywords: local cattle breed, historical DNA, microsatellites, genetic diversity

BDEE
2021

Results and Discussion

Comparing the genotypes of Kazakh White-headed (KZWH_M) breed with their ancestral breeds showed that 4 and 5 alleles, distributed in the Hereford (HRFD_M) and native Kazakh (KZKH_H) breed, respectively, were lost in the Kazakh White-headed population. At the same time, 16 novel alleles that were not observed in ancestral breeds were found in Kazakh White-headed breed.
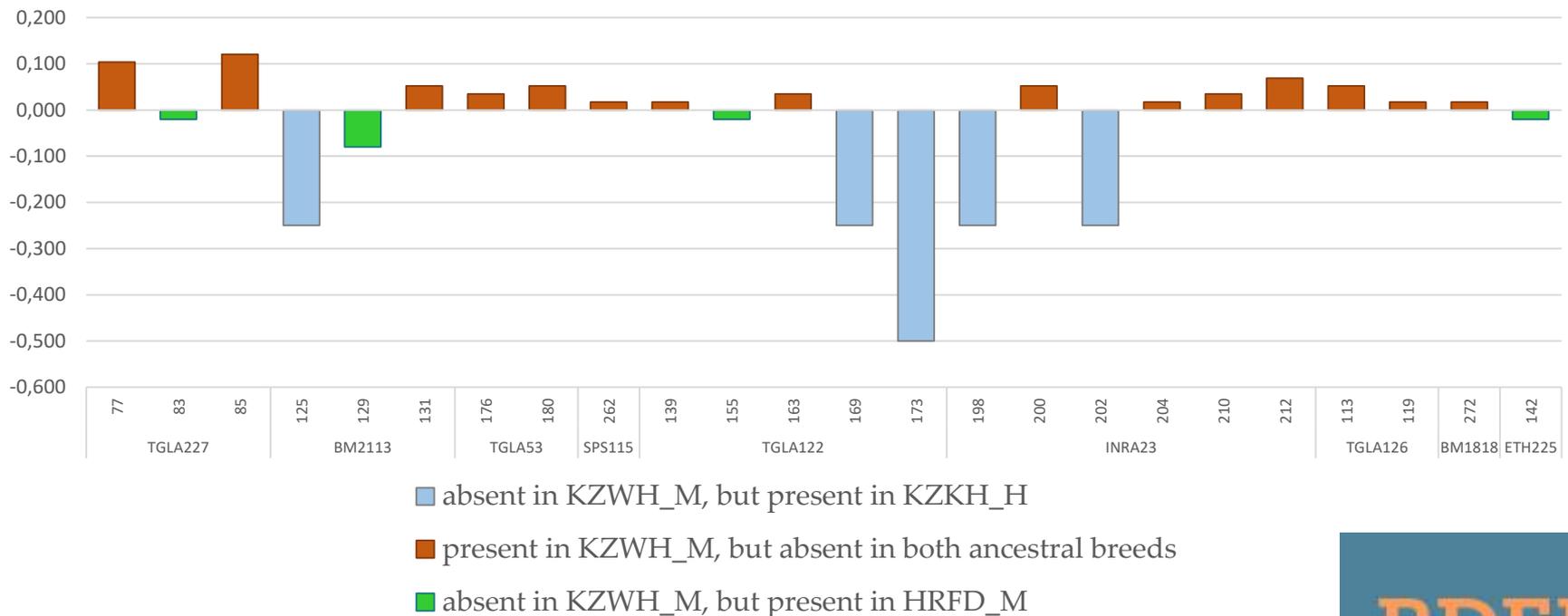
Figure 1. Comparing the genotypes of Kazakh White-headed breed with their ancestral breeds .

Results and Discussion

We observed the highest level of genetic diversity in the native Kazakh cattle breed, while the Hereford cattle were the least divergent. The significant deviation from the Hardy–Weinberg equilibrium in heterozygote number ($_UF_{IS}$=−0.100, excess of heterozygotes) was observed only for historical population

Table 1. Genetic diversity based on eleven STR markers.

Population	n	H_O (M ± SE)	$_UH_E$ (M ± SE)	A_R (M ± SE)	$_UF_{IS}$ (CI)
KZKH_H	2	0.864±0.097	0.788±0.090	3.091±0.285	-0.100(-0.165;-0.035)
KZWH_M	29	0.740±0.038	0.731±0.029	2.737±0.096	-0.011(-0.062;0.040)
HRFD_M	25	0.662±0.062	0.654±0.051	2.505±0.143	0.004(-0.068;0.076)

n, number of individuals; H_O, observed heterozygosity; $_UH_E$, unbiased expected heterozygosity; A_R, rarefied allele richness; $_UF_{IS}$, unbiased inbreeding coefficient; M, mean value; SE, standard error; CI 95%, range variation coefficient of $_UF_{IS}$ at a confidence interval of 95%

**Table 2.** Genetic distances between the studied populations.

Population	KZKH_H	KZWH_M	HRFD_M
KZKH_H	-	0.638	0.746
KZWH_M	0.115	-	0.157
HRFD_M	0.143	0.034	-

Nei genetic distances values are presented above the diagonal; F_{ST} values are presented below the diagonal

KZKH_H – historical population of native Kazakh cattle; KZWH_M – modern population of Kazakh White-headed breed; HRFD_M – modern population of Hereford breed

BDEE 2021

Resuts and Discussion

Analysis of genetic structure of studied breeds at k = 2 showed the visible presence of the historical Kazakh-specific genetic components in the modern population of Kazakh White-headed breed.
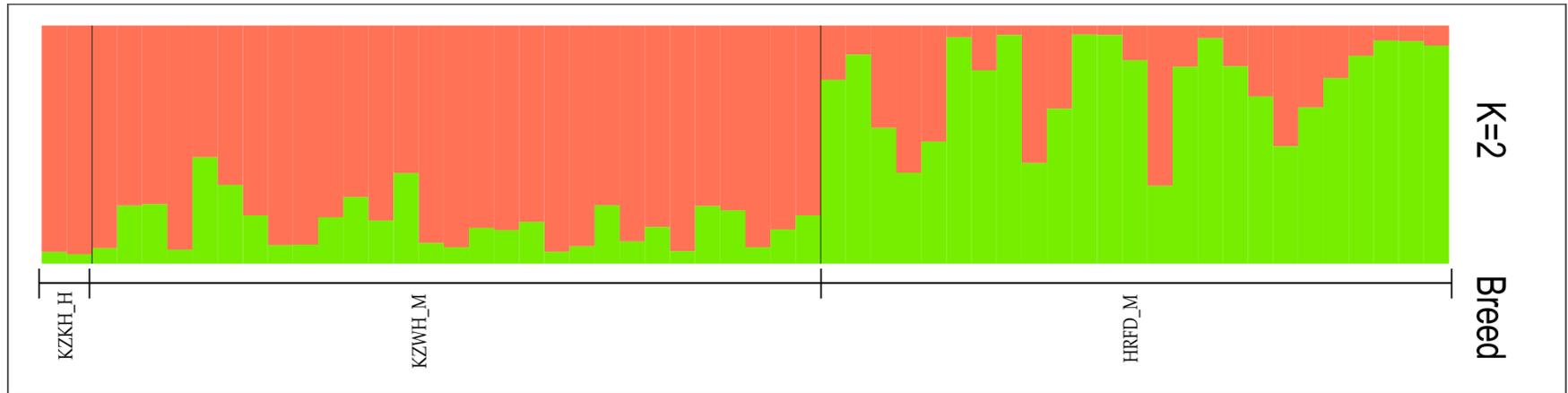
Figure 2. Genetic structure of historical and modern cattle populations. KZKH_H – historical population of native Kazakh cattle; KZWH_M – modern population of Kazakh White-headed breed; HRFD_M – modern population of Hereford breed.

Conclusions

❖ Comparative molecular genetic studies of modern Kazakh White-headed cattle and museum specimences of their ancestor - native Kazakh cattle, dated by the first quarter of 20th century, revealed the maintainance of the historical genetic components in the modern population.

❖ Our results could be useful for developing the programs of conservation and sustainable use of Kazakh White-headed cattle.

BDEE 2021

Acknowledgments

RSF
Russian Science Foundation

Thank you for your attention!

BDEE 2021