

Tracing the historical genetic components in Turano-Mongolian cattle breeds based on the microsatellite analysis of modern and museum samples.

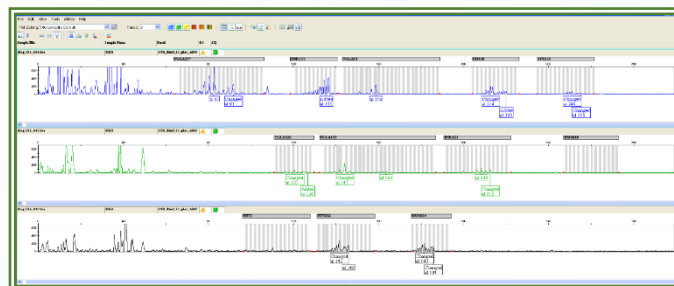
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The beginning of the XX century



PCR
x5



Consensus genotypes

Eleven microsatellite loci
(TGLA227, BM2113, TGLA53,
ETH10, SPS115, TGLA122, INRA23,
TGLA126, BM1818, ETH225,
BM1824)

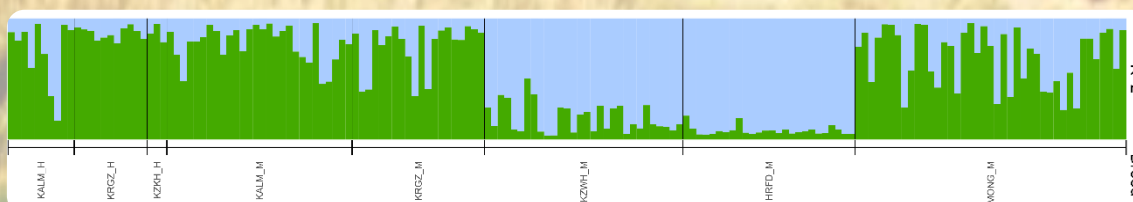
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The intensive cross breeding with high-producing transboundary breeds had been practiced

Historical samples were derived from the craniological collection of the Museum of Livestock named after E.F. Liskun (Moscow)

The aim of our study was to trace the historical genetic components in modern populations of local cattle breeds of the turano-mongolian origin.



Museum populations: KALM_H – Kalmyk, KRGZ_H – Kyrgyz, KZKH_H – Kazakh;
Modern populations: KALM_M – Kalmyk, KRGZ_M – Kyrgyz, KZWH_M – Kazakh White-Headed,
HRFD_M – Hereford, MONG_M – Mongolian cattle

The beginning of the XXI century



Modern samples were derived from the Bioresource collection «Bank of genetic materials of domestic and wild animals and birds» of the L.K. Ernst Federal Research Center for Animal Husbandry.

Results. In total, 132 alleles were identified, including 97 alleles in historical samples and 124 alleles in modern samples. The values of unbiased expected heterozygosity were 0.767–0.776 and 0.653–0.778 for the historical and modern samples, respectively. The STRUCTURE clustering showed the visible differences in genetic structure between the historical and modern populations of Kalmyk, Kyrgyz and Kazakh cattle breeds, however the historical genetic components were still maintained in modern representatives of all of studied breeds. The research results will be useful for the sustainable breeding and conservation of valuable local genetic resources.

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