# Choosing markers for genome scanning of local and trotter horse breeds

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In order to solve tasks of managing genetic resources of local and trotter horse breeds it is necessary to choose genetic elements which are convenient for polyloci genotyping and "gene pool standard" estimating on the level of breeds, crosses and improved animal groups. Thereupon ISSR (Inter-Simple Sequence Repeat) and IRAP (Inter-Retrotransposon Amplified Polymorphism) markers have become broadly used in polyloci genotyping ("genome scanning"). In current paper we performed a comparative analysis of different markers used for revealing genetic differentiation of several horses of Karachay breed versus other horse breeds: Altai, American standardbred, Orlov trotter and Russian trotter.

We used as PCR primers the following sequences: parts of microsatellites $(AG)_9C$, $(GA)_9C$, $(GAG)_6C$; and terminal flanks of retrotransposons LTR SIRE-1 and PawS 5. The latter primer didn't produce any amplicons in individuals surveyed in spite of presence of some fragments with high homology to it in sequenced horse genome regions. Every group produced fragments which were not observed in other groups. We found a unique 490 bp fragment by using primer $(CTC)_6C$ in Karachay breed. For Altai breed we found unique fragments 980, 900 and 450 bp by using primer $(AG)_9C$; 740 bp by using primer $(GA)_9C$; 1180, 920 and 360 bp by using primer $(GAG)_6C$; 1500, 1430 and 1200 bp by using primer $(CTC)_6C$. For trotter breeds these DNA fragments were 300, 250 and 180 bp in spectra of primer $(GAG)_6C$. Dinucleotide primers produced the lowest share of polymorphic loci (28.6%) in horses of Karachay breed surveyed, while primer $(CTC)_6C$ gave the highest one (77.8%) compared to other horse breeds.

We applied Nei's method (1972, 1978) to calculate genetic distances between breeds studied. That made available creation of dendrogram in TFPGA software (Miller, 1997). Trotter breeds build common cluster while local Altai and Karachay breeds build separate branches. This correlated well with the history of breed development. We found breed specific combinations of DNA fragments of different length in ISSR and IRAP amplicon spectra. These combinations are proposed to be used for estimating "gene pool standard" of horse breeds studied.