

Genotypes database of pedigree cattle population in Kazakhstan and the introduction of a calculating mechanism for livestock parentage verification

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Aim of work: creation a national database and collection of genotyped DNA samples of cattle in Kazakhstan and the introduction of an automated statistical and mathematical calculation of the local pedigree cattle parentage verification.

The research objectives:

- to collect biological samples and information about animals, genotyping the STR DNA loci, to study the distribution of lengths of repeats of microsatellites;
- to create a database of genotypes and implement a mechanism for calculating the reliability of origin.

The object of research is sires and calves of the Auliekol, Kazakh white-headed, Hereford, Aberdeen-Angus breeds and Obrak breed of North Kazakhstan



DNA and STR locus testing have been performed at the University of Queensland's Animal Genetics Laboratory (Australia)

Table 1-List of farms and the amount of DNA studied

Farm	The number of samples (hair), units	DNA tested, samples	Name of breed
Mambetov company	95	95	Aberdeen-Angus
SKSOS LLP	58	58	Kazakh-White-Head
Krymskoe LLP	197	196	Kazakh-White-Head
Pirechnoe-Agro LLP	83	81	Aberdeen-Angus
Alimgaziev-Akylbel LLP	36	36	Auliekol
Adlet-T LLP	53	53	Kazakh-White-Head
Olshanskoe LLP	20	20	Kazakh-White-Head
Moskalevskoe LLP	116	115	Auliekol
Nur-Zhailau NS LLP	93	93	Aberdeen-Angus
Semenovka-AE LLP	60	60	Obrak
Total	811	807	-

Pic.1-Demonstration of the mapping of animal STR genotypes in the IAS system



Pic.2-Animal genetic certificate in the National DB

The number of homozygous alleles in a single DNA sample	Name of breed					For all breeds
	Kazakh-White Head	Aberdin-Angus	Auliekol	Obrak	Hereford	
1	1,23	0,40	-	-	-	0,83
2	4,09	-	1,32	3,33	-	2,82
3	8,17	2,40	2,65	1,67	14,29	5,98
4	13,35	8,40	5,30	5,00	-	10,80
5	16,76	7,20	15,89	21,67	-	14,78
6	18,39	16,40	17,22	25,00	14,29	18,19
7	16,08	15,20	18,54	13,33	42,86	16,20
8	10,76	13,20	20,53	16,67	28,57	12,87
9	7,22	14,80	10,60	10,00	-	9,30
10	2,04	10,80	5,30	1,67	-	4,24
11	1,23	5,60	-	-	-	1,99
12	0,54	4,00	2,65	1,67	-	1,58
14	0,14	1,60	-	-	-	0,42

$$R = \prod_{i=1}^N r_i \quad (1),$$

where r_i are local statistical frequencies for each of the studied loci from their total number N, and is calculated as:

$$r_i = 2p_i - p_i^2, \quad (2),$$

where p_i – the frequency of the corresponding i allele in the population