



CAPACITY OF DNA MICROSATELLITES IN PARENTAGE TESTING OF INDIGENOUS SHEEP POPULATIONS IN THE REPUBLIC OF NORTH MACEDONIA



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SHAPLANINIAN (SHAR)



OVCHEPOLIAN (OVCH)



KARAKACHANIAN (KARA)

Different populations of Pramenka sheep are present in South East Europe, as a result of natural selection, management system, and environmental pressure those sheep populations developed distinctive productive and phenotype characteristics which are sufficient to distinguish between them. This study aimed to determine the capacity of selected microsatellite markers for parentage testing of three autochthonous sheep populations in the country.

	SHAR	OVCH	KARA
MEAN NUMBER ALLELES PER LOCUS	12.13	13.27	11.53
PIC VALUE ACROSS ALL LOCI	0.806	0.852	0.814
COMBINED NON-EXCLUSION PROBABILITY (FIRST PARENT) FOR ALL 15 LOCI	0.00000889	0.00000133	00001259

The sheep genome was analyzed with fifteen microsatellite markers, and 105 collected DNA samples, which means 35 samples per population. Forward primers for the loci: BM 8125, ETH 225, ILSTS 11, OARJMP 58, OARFCB 193, SRCRSP 1, SRCRSP 7, SRCRSP 8, and McM 527 were labeled with IRDyeTM700 will forward primers for loci: ILSTS 28, MAF 214, OARFCB 11, OARFCB 48, SRCRSP 3, and SRCRSP 9 were labeled with IRDyeTM800.

The mean number of detected alleles per locus was 12.13, 13.27, and 11.53, for Shaplaninian, Ovchepolian, and Karakachanian sheep populations, respectively. The average PIC value across all loci was 0.806, 0.852, and 0.814, for Shaplaninian, Ovchepolian, and Karakachanian sheep populations, respectively. Six markers in the genome of Sharplaninian (ETH225, SRCRSP3, OARFCB48, OARFCB193, MAF214) and Ovchepolian (ETH225, SRCRSP3, SRCRSP7, OARFCB193, MAF214, McM527), and three markers in the genome of Karakachanian population (ETH225, SRCRSP3, SRCRSP7) have shown null allele frequencies higher than 0.2. For the above-mentioned markers, higher differences between H_o and H_e were observed. The combined non-exclusion probability (first parent) for all 15 loci was 0.00000889, 0.00000133, and 00001259 for Shaplaninian, Ovchepolian, and Karakachanian sheep populations, respectively.

LOCI	A	n (Sampled alleles)			F (Null)		
		SHAR	OVCH	KARA	SHAR	OVCH	KARA
BM8125	9	7	7	5	+0.0806	+0.1642	-0.0767
ILSTS11	14	10	7	11	-0.0304	+0.0175	+0.1320
ILSTS28	19	14	12	12	+0.0583	0.1278	+0.0166
ETH225	13	9	11	11	+0.2703	+0.3159	+0.5160
SRCRSP1	13	8	12	10	-0.0183	+0.1456	+0.0856
SRCRSP3	16	9	11	11	+0.2285	+0.4565	+0.3838
SRCRSP7	20	14	15	14	+0.1604	+0.2657	+0.2381
SRCRSP8	24	15	15	17	-0.0322	-0.0282	+0.0067
SRCRSP9	9	5	9	6	-0.0585	+0.0248	+0.1099
OARFCB11	17	13	14	13	+0.0218	+0.0490	-0.0147
OARFCB48	17	12	12	10	+0.3785	+0.0483	+0.0284
OARFCB193	23	13	20	11	+0.2736	+0.3269	+0.0266
OARJMP58	23	15	15	16	-0.0326	+0.0760	-0.0401
MAF214	32	19	20	7	+0.2450	+0.3967	+0.0715
McM527	32	19	19	19	+0.1506	+0.2344	+0.1266

Management of genetic diversity in livestock species requires recognition and development of breed conservation priorities and the development of specific breeding programs. Data gained from different types of molecular studies can be used as the foundation for the further sustainable use of indigenous breeds. The application of microsatellite markers provides appropriate information to determine the pedigree relationships, but also provides an opportunity for the development of selective breeding programs and successful management of endangered populations.