Turkish Journal of Veterinary & Animal Sciences

Volume 49 | Number 5 Article 4

10-16-2025

Design of a SNP panel for highly accurate paternity identification in Eşme sheep

ONUR YILMAZ

İBRAHİM CEMAL

ORHAN KARACA

CENGİZ ELMACI

NEZİH ATA

Follow this and additional works at: https://journals.tubitak.gov.tr/veterinary

 Part of the Animal Sciences Commons, and the Veterinary Medicine Commons

Recommended Citation

YILMAZ, O, CEMAL, İ, KARACA, O, ELMACI, C, & ATA, N (2025). Design of a SNP panel for highly accurate paternity identification in Eşme sheep. *Turkish Journal of Veterinary & Animal Sciences 49* (5): 207-220. https://doi.org/10.55730/1300-0128.4392



This work is licensed under a Creative Commons Attribution 4.0 International License.
This Research Article is brought to you for free and open access by TÜBİTAK Academic Journals. It has been accepted for inclusion in Turkish Journal of Veterinary & Animal Sciences by an authorized editor of TÜBİTAK Academic Journals. For more information, please contact academic.publications@tubitak.gov.tr.

TÜBİTAK

Turkish Journal of Veterinary and Animal Sciences

http://journals.tubitak.gov.tr/veterinary/

Research Article

Turk J Vet Anim Sci
(2025) 49: 207-220
© TÜBİTAK
doi:10.55730/1300-0128.4392

Design of a SNP panel for highly accurate paternity identification in Eşme sheep

Onur YILMAZ[1,*], **İbrahim CEMAL**[1], **Orhan KARACA**[1], **Cengiz ELMACI**[2], **Nezih ATA**[1]

[1]Department of Animal Science, Faculty of Agriculture, Aydın Adnan Menderes, Aydın University, Turkiye

[2]Department of Animal Science, Faculty of Agriculture, Bursa Uludağ University, Bursa, Turkiye

Received: 25.02.2025 • **Accepted/Published Online:** 09.07.2025 • **Final Version:** 16.10.2025

Abstract: SNP paternity testing panels offer high-resolution capabilities for determining livestock paternity, thereby enhancing the reliability of genetic verification and ensuring pedigree record accuracy. In this study, we aimed to develop a SNP-based paternity test panel utilizing a 50K SNP chip for paternity testing and pedigree verification in the Eşme sheep breed. Additionally, the study sought to validate the paternity test panel. Based on data from 26 rams and 524 lambs of the Eşme sheep breed, the results indicated that the 50K SNP chip used demonstrated a very high genotyping rate, with the majority of its 53,738 SNPs exhibiting significant polymorphism. After filtering, the most suitable 144 SNP markers were identified for the paternity test panel. The minor allele frequency (MAF) values of the 144 selected SNPs ranged from 0.48 to 0.50. The combined probability of exclusion (CPE) and the combined probability of identification (CPI) values for the panel containing these 144 SNP markers were 0.999999995 and 4.9×10^{-62}, respectively. Using this SNP paternity test panel, the pedigree error rate was remarkably low—only 3.44%—in paternity tests conducted across 11 breeders' flocks that utilized hand mating. In this study, a 50K SNP chip developed from DNA samples of various sheep breeds worldwide, including indigenous breeds from Türkiye, was utilized. This suggests that the SNP-based paternity test panel presented in this research may also be applicable to other indigenous sheep breeds in Türkiye. The widespread implementation of this test panel will not only reduce pedigree errors but also yield more accurate estimates of genetic parameters within the population.

Key words: Parentage, small ruminants, probability of exclusion

1. Introduction

The existence and accuracy of pedigree information, as well as performance data, are crucial in studies conducted for the breeding and conservation of livestock as genetic resources [1]. The availability of pedigree information is essential for determining genetic parameters such as the heritability of the population, genetic correlations between traits, and breeding value estimates for selection purposes [2–6]. Furthermore, mating programs designed to minimize inbreeding should be implemented to effectively conserve genetic resources. To achieve this, it is necessary to understand the kinship relationships among the individuals within the population [7–8].

In Türkiye, as in many parts of the world, small ruminant breeding is a significant sector within livestock production due to its cultural significance and its role as a vital source of income for rural breeders [9–10]. In breeding studies conducted in the field of small ruminant husbandry, it is essential to maintain performance records to achieve breeding objectives, as well as to obtain pedigree records that have been verified for accuracy [11,12].

Most indigenous sheep breeds raised in Türkiye have been subjected to unsystematic crossbreeding by breeders for centuries and have naturally adapted to various environmental conditions [13]. There is a significant level of genetic variation among these indigenous sheep breeds due to Türkiye's multicultural and intercontinental location. Consequently, 45 sheep breeds have been recognized as national breeds in Türkiye [14]. Additionally, Türkiye is home to many local ecotypes that differ from the 45 recognized national breeds in certain characteristics. Sheep account for 80% of the approximately 57 million small ruminants in Türkiye[1]. The Eşme sheep breed, one of the indigenous breeds of western Anatolia, was developed through unsystematic crossbreeding of various local breeds by breeders [15,16]. In response to breeder demands and expectations, a modern breeding organization was established in 2007, focusing on improving the reproductive and lamb development characteristics of the Eşme sheep population. Scientific findings on the production characteristics of the Eşme breed—along with its genetic parameters, population structure determined

[1] FAO, https://www.fao.org/faostat/en/#data/QCL, [Access date: 07 January 2025].

* Correspondence: oyilmaz@adu.edu.tr

This work is licensed under a Creative Commons Attribution 4.0 International License.

via molecular markers, and genome-wide association studies identifying unique gene regions—facilitated its official registration as a national breed in 2020 [16].

The "National Genetic Improvement Project for Small Ruminants at Breeders' Conditions", which has been underway in Türkiye since 2005 under the coordination of the General Directorate of Agricultural Research and Policies of the Ministry of Agriculture and Forestry (GDAR), aims to maintain performance and pedigree records for breeding purposes and to advance breeding studies based on these records. Through the subprojects initiated as part of this initiative, the necessary infrastructure for performance recording under breeders' conditions has been established in numerous provinces [17–19]. However, these subprojects face several challenges in verifying the accuracy of the parentage information for lambs or kids resulting from controlled hand mating activities. These activities have been implemented—or at least attempted—in a limited segment of the population (elite and multiplier flocks), with significant effort particularly focused on the establishment of a pedigree register [20–22].

The identification and verification of parentage are crucial for success in animal breeding, particularly in selection processes [20,22]. This is especially true for livestock, such as sheep, where free mating is common and animals are often raised in herds under extensive conditions. Accurate parentage verification enables breeders to preserve genetic diversity, enhance desirable traits, and ensure the integrity of breeding programs, ultimately resulting in healthier and more productive flocks. Various factors can lead to errors in parental information, resulting in incorrect data being recorded in the pedigree [23–25]. Some studies on livestock have demonstrated that pedigree errors can lead to biased estimates of genetic parameters and breeding values, which are crucial for effective breeding planning. For this reason, achieving the desired level of genetic progress becomes challenging [23, 26–29]. Therefore, accurate information can be obtained by implementing parentage control methods, both for managing pedigree records and for completing any missing pedigree information [28,30].

Microsatellites and single nucleotide polymorphisms (SNPs) are the most effective markers used for parentage testing. Traditional parentage tests typically rely on microsatellites. While these tests provide strong discrimination due to their high levels of polymorphism, they are limited in their ability to differentiate between closely related individuals and can be unreliable when analyzing degraded or low-abundance DNA samples [31,32]. In recent years, tests based on single nucleotide polymorphisms (SNPs) have emerged as a promising alternative to address these limitations. SNPs are advantageous in parentage analyses because they are more prevalent throughout the genome, exhibit lower mutation rates, and allow for greater automation [33,34]. This method significantly reduces the cost per SNP, enabling both parentage testing and production traits to be assessed from a single sample. Consequently, the SNP microarray approach offers distinct advantages over traditional microsatellite methods [31,35–37].

The present study aims to identify specific SNPs for paternity testing and pedigree verification in the Eşme breed, which serves as a model for other breeds in Türkiye due to its well-structured breeding organization. Additionally, the study seeks to develop a compact, highly reliable, practical, and cost-effective microarray chip, thereby enhancing the efficiency of genetic assessments in livestock management.

2. Materials and methods

2.1. Sampling and genotyping

A total of 550 Eşme breed sheep—consisting of 524 lambs born across 11 farms in the villages of the Eşme district in Uşak province and 26 rams, which were the probable sires of these lambs—constituted the animal material for the study. Controlled hand mating was employed during the mating season. For DNA extraction, 8–10 mL blood samples were collected from all rams during the mating period, as well as from the lambs born to them during the birthing period. The samples were drawn from the jugular vein into vacuum tubes containing K3-EDTA, following established protocols.

Genomic DNA was isolated from blood samples collected from the research animals using the NucleoSpin blood kit (Macherey-Nagel GmbH & Co. KG, Düren, Germany). The quantity and quality of the DNA were assessed using a NanoDrop 2000 (Thermo Fisher Scientific Inc., Waltham, MA, USA), and the DNA sample concentrations were adjusted to 50 ng/µL. DNA samples were genotyped using the OvineSNP50 BeadChip (Illumina Inc., San Diego, CA, USA), developed by the International Sheep Genomics Consortium (ISGC) [38]. This BeadChip contains 54,241 SNPs derived from haplotypes of sheep genotypes from various countries, including Türkiye. SNP genotyping was conducted using the iScan system (Illumina Inc., San Diego, CA, USA) in the Microarray Laboratory of the Aydın Adnan Menderes University Agricultural Biotechnology and Food Safety Application and Research Centre, following the procedures recommended by the manufacturer.

2.2. Selection of SNP markers for paternity testing

The essential quality control and filtering procedures for selecting SNP markers for paternity testing were systematically conducted using PLINK v1.9 software [39], resulting in the identification of the most suitable SNP marker set for the final analysis. After filtering, a paternity

test panel consisting of 144 SNPs was developed. The criteria used to select the SNPs included in the paternity test panel are outlined in Table 1.

2.3. Statistical analysis

Minor allele frequencies, call rates, and Hardy–Weinberg equilibrium were calculated using GenomeStudio software (version 2016.2; Illumina Inc., San Diego, CA, USA) and PLINK v1.9 software [39]. Polymorphic information content (PIC), probability of exclusion (PE), combined probability of exclusion (CPE), probability of identification (PI), and combined probability of identification (CPI) were calculated using equations implemented in the CERVUS software (Field Genetics Ltd., London, UK) [40].

The formula used to calculate the polymorphic information content (PIC), as described by Botstein et al. [41], is as follows:

$$PIC = 1 - \sum_{i=1}^{n} p_i^2 - 2\left[\sum_{i=1}^{n=1}\sum_{j=i+1}^{n} p_i^2 p_j^2\right]$$

where p_i is the allele frequency at the i-th locus, and n is the number of alleles.

The formulas used to calculate the probability of exclusion (PE) and the combined probability of exclusion (CPE) are based on the work of Jamieson and Taylor [42].

$$PE = 1 - 2\sum_{i=1}^{n} {p_i}^2 + \sum_{i=1}^{n} {p_i}^3 + 2\sum_{i=1}^{n} {p_i}^4 - 3\sum_{i=1}^{n} {p_i}^5 - 2(\sum_{i=1}^{n} {p_i}^2)2 + 3\sum_{i=1}^{n} {p_i}^2 \sum_{i=1}^{n} {p_i}^3$$

$$CPE = 1 - \prod_{i=1}^{n}(1 - PE_i)$$

where p_i is the allele frequency of the i-th SNP, n is the number of alleles, and PE_i is the exclusion probability of the i-th SNP.

The formulas for the probability of identification (PI) and the combined probability of identification (CPI) are derived from the work of Peakall and Sydes [43].

$$PI = 2\left(\sum p_i^2\right)^2 - \sum p_i^4$$

$$CPI = 1 - \prod_{i=1}^{n}(1 - PI_i)$$

where, p_i is the allele frequency of the i-th SNP, n is the number of alleles, and PI_i is the identification probability of the i-th SNP.

3. Results

The call rate of the 50K SNPs used in the study was > 95%. Information regarding the SNPs obtained through genotyping is presented in Table 2.

As a result of genotyping, 378 of the 54,241 identified SNPs were located in unrecognized regions of sheep chromosomes (OAR). Additionally, 1450 SNPs were identified on the sex chromosomes. The analysis also revealed 127 monomorphic SNPs. No genotype call could be obtained for 4888 SNPs (no genotype call). Furthermore, allele distributions for 4874 SNPs deviated from Hardy–Weinberg equilibrium ($p < 0.05$). The distributions of minor allele frequencies (MAF) resulting from genotyping are presented in Figure.

Individual statistical values for the 144 SNP markers selected to create the paternity testing panel in this study are presented in Table 3.

The minor allele frequency (MAF) values for the 144 selected SNPs ranged from 0.48 to 0.50. After filtering 54,241 SNP markers obtained from the 50K SNP chip according to the criteria outlined in Table 1, 144 SNP markers were identified as candidate SNPs for paternity testing. The call rate for the selected SNPs was 95%. Paternity test statistics for the panel containing these 144 SNPs are presented in Table 4.

In the paternity test conducted using 144 selected SNPs, the values for CPE, CPI, and MAF were 0.99999999540, 4.91×10^{-62}, and 0.489, respectively. The results of the

Table 1. Criteria for SNP selection in paternity testing.

Criteria	Process
Monomorphic SNPs	Eliminated
Nongenotypable SNPs	Eliminated
SNPs not in Hardy-Weinberg Equilibrium (HWE)	Eliminated
SNPs with a call rate < 95%	Eliminated
SNPs with physical distances < 20 Mbp on the same chromosome	Eliminated

Table 2. Data obtained from 50K SNP chip genotyping.

Oar	No. of SNPs	Distance (bp)	Nongenotypable SNPs (nogenocall)	No. of monomorphic SNPs	No. of polymorphic SNPs
0*	378	-	36	3	339
1	5930	50,529	574	7	5349
2	5474	48,065	484	9	4981
3	5008	48,477	434	24	4550
4	2680	47,463	208	5	2467
5	2363	49,512	193	7	2163
6	2592	49,789	245	8	2339
7	2252	48,367	225	7	2020
8	2057	47,597	192	4	1861
9	2141	47,077	202	2	1937
10	1851	50,852	172	5	1674
11	1180	56,677	85	3	1092
12	1723	50,146	132	2	1589
13	1696	52,514	156	1	1539
14	1174	59,031	118	3	1053
15	1694	53,145	155	6	1533
16	1580	48,848	162	5	1413
17	1420	55,362	125	4	1291
18	1413	51,295	116	3	1294
19	1248	51,926	111	4	1133
20	1148	48,400	122	1	1025
21	898	61,778	92	2	804
22	1097	50,818	102	2	993
23	1128	59,118	93	2	1033
24	741	60,528	64	1	676
25	1001	48,240	86	1	914
26	924	54,160	95	0	829
X	1449	89,093	109	6	1334
Y	1	-	0	0	1
Total	**54,241**		**4888**	**127**	**49,226**

* SNPs not assigned to any Ovis aries chromosome.

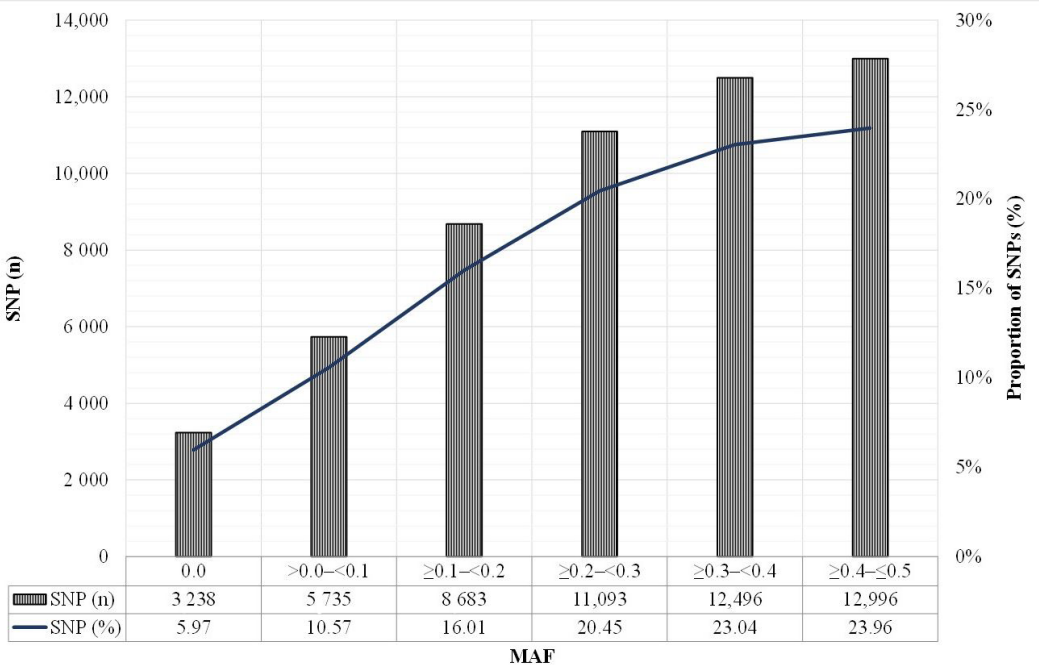


Figure. Distribution of minor allele frequencies (MAF) of 50K SNP markers.

Table 3. Paternity test statistics for the 144 selected SNP markers.

Locus	Chromosome	Position	MAF	PIC	PE	PI	He
DU279054_461.1	25	418585	0.48	0.38	0.125	3.75×10^{-1}	0.500
DU411145_363.1	14	42940921	0.49	0.38	0.125	3.75×10^{-1}	0.500
DU429798_148.1	25	20687490	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR1_104036819.1	1	104036819	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR1_165909318.1	1	165909318	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR1_185953850.1	1	185953850	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR1_21408870.1	1	21408870	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR1_227424908.1	1	227424908	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR1_247832015.1	1	247832015	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR1_289552703.1	1	289552703	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR1_41497208.1	1	41497208	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR1_62521467.1	1	62521467	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR10_43161187.1	10	43161187	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR10_464812.1	10	464812	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR10_63245174_X.1	10	63245175	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR10_86074123.1	10	86074123	0.49	0.38	0.125	3.75×10^{-1}	0.500

Table 3. (Continued).

OAR11_23673049.1	11	23673049	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR11_3642255.1	11	3642255	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR11_63882013.1	11	63882013	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR12_22800650.1	12	22800650	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR12_536075.1	12	536075	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR12_64690849.1	12	64690849	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR12_84938649.1	12	84938649	0.48	0.37	0.124	3.75×10^{-1}	0.499
OAR13_22642702.1	13	22642702	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR13_64415651.1	13	64415651	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR14_2501876.1	14	2501876	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR14_65765891.1	14	65765891	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR15_228181.1	15	228181	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR15_65225287.1	15	65225287	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR15_85650720.1	15	85650720	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR16_21925866.1	16	21925866	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR16_42651043.1	16	42651043	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR16_62937471.1	16	62937471	0.48	0.37	0.124	3.75×10^{-1}	0.499
OAR17_172595.1	17	172595	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR17_20224869.1	17	20224869	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR17_41915634.1	17	41915634	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR17_61988972.1	17	61988972	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR18_24036473.1	18	24036473	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR19_20613783.1	19	20613783	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR2_105587942.1	2	105587942	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR2_125699504.1	2	125699504	0.48	0.37	0.124	3.75×10^{-1}	0.499
OAR2_146111824.1	2	146111824	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR2_186197070.1	2	186197070	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR2_207542754.1	2	207542754	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR2_23295069.1	2	23295069	0.48	0.37	0.124	3.75×10^{-1}	0.499
OAR2_250716720.1	2	250716720	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR2_64445964.1	2	64445964	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR2_85316955.1	2	85316955	0.48	0.38	0.125	3.75×10^{-1}	0.500

Table 3. (Continued).

OAR20_22552509.1	20	22552509	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR20_42731904.1	20	42731904	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR21_22389818.1	21	22389818	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR21_2253887.1	21	2253887	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR21_43118557.1	21	43118557	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR22_1408563.1	22	1408563	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR22_22756887.1	22	22756887	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR22_43552480.1	22	43552480	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR23_41224486.1	23	41224486	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR25_41606769.1	25	41606769	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR26_20397475.1	26	20397475	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR26_353671_X.1	26	353671	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR3_125835006.1	3	125835006	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR3_146751517.1	3	146751517	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR3_166966160.1	3	166966160	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR3_84111819.1	3	84111819	0.48	0.38	0.125	3.75×10^{-1}	0.499
OAR4_123995334.1	4	123995334	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR4_21394967.1	4	21394967	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR4_41623797.1	4	41623797	0.48	0.37	0.124	3.75×10^{-1}	0.499
OAR4_558440.1	4	558440	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR4_62318766.1	4	62318766	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR4_82832865.1	4	82832865	0.48	0.37	0.124	3.75×10^{-1}	0.499
OAR5_43731258.1	5	43731258	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR5_85582355.1	5	85582355	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR6_123771724.1	6	123771724	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR6_20484615.1	6	20484615	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR6_324213.1	6	324213	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR6_41558126.1	6	41558126	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR6_83096006.1	6	83096006	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR7_103728716.1	7	103728716	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR7_40985103.1	7	40985103	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR7_61522228.1	7	61522228	0.49	0.38	0.125	3.75×10^{-1}	0.500

Table 3. (Continued).

OAR8_388402.1	8	388402	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR8_40984723.1	8	40984723	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR8_62425494.1	8	62425494	0.48	0.38	0.125	3.75×10^{-1}	0.500
OAR8_83222049.1	8	83222049	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR9_20964415.1	9	20964415	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR9_42888343.1	9	42888343	0.49	0.38	0.125	3.75×10^{-1}	0.500
OAR9_65555411.1	9	65555411	0.50	0.38	0.125	3.75×10^{-1}	0.500
OAR9_85843210.1	9	85843210	0.48	0.37	0.124	3.75×10^{-1}	0.499
OARX_39477459.1	X	39477459	0.49	0.38	0.125	3.75×10^{-1}	0.500
s00427.1	4	103052535	0.49	0.38	0.125	3.75×10^{-1}	0.500
s01447.1	9	214263	0.48	0.38	0.125	3.75×10^{-1}	0.500
s02536.1	3	63272739	0.49	0.38	0.125	3.75×10^{-1}	0.500
s03197.1	X	3583900	0.48	0.38	0.125	3.75×10^{-1}	0.500
s03382.1	14	22731539	0.49	0.38	0.125	3.75×10^{-1}	0.500
s03639.1	6	103212874	0.50	0.38	0.125	3.75×10^{-1}	0.500
s05093.1	13	84781292	0.48	0.38	0.125	3.75×10^{-1}	0.500
s07742.1	2	230443740	0.50	0.38	0.125	3.75×10^{-1}	0.500
s08511.1	11	43847263	0.50	0.38	0.125	3.75×10^{-1}	0.500
s10452.1	3	228318990	0.49	0.38	0.125	3.75×10^{-1}	0.500
s12482.1	18	1036182	0.48	0.38	0.125	3.75×10^{-1}	0.500
s13817.1	2	44190116	0.48	0.37	0.124	3.75×10^{-1}	0.499
s14389.1	18	65151941	0.48	0.38	0.125	3.75×10^{-1}	0.500
s16840.1	5	64839504	0.49	0.38	0.125	3.75×10^{-1}	0.500
s16899.1	1	145895328	0.50	0.38	0.125	3.75×10^{-1}	0.500
s18643.1	26	40583700	0.50	0.38	0.125	3.75×10^{-1}	0.500
s19141.1	24	21523019	0.49	0.38	0.125	3.75×10^{-1}	0.500
s20865.1	7	81719869	0.48	0.37	0.124	3.75×10^{-1}	0.499
s23457.1	23	20711866	0.48	0.37	0.124	3.75×10^{-1}	0.499
s23717.1	5	2517489	0.48	0.38	0.125	3.75×10^{-1}	0.500
s26418.1	20	1270140	0.50	0.38	0.125	3.75×10^{-1}	0.500
s26580.1	3	21168468	0.48	0.38	0.125	3.75×10^{-1}	0.500
s27908.1	3	104986720	0.50	0.38	0.125	3.75×10^{-1}	0.500

Table 3. (Continued).

s28800.1	1	83573304	0.50	0.38	0.125	3.75×10^{-1}	0.500
s31046.1	15	42620232	0.50	0.38	0.125	3.75×10^{-1}	0.500
s31610.1	7	20629388	0.48	0.38	0.125	3.75×10^{-1}	0.500
s31612.1	13	44012818	0.49	0.38	0.125	3.75×10^{-1}	0.500
s32443.1	1	124412557	0.48	0.38	0.125	3.75×10^{-1}	0.500
s33701.1	7	350358	0.50	0.38	0.125	3.75×10^{-1}	0.500
s33746.1	23	64193563	0.49	0.38	0.125	3.75×10^{-1}	0.500
s34622.1	2	934816	0.49	0.38	0.125	3.75×10^{-1}	0.500
s35547.1	19	62257142	0.49	0.38	0.125	3.75×10^{-1}	0.500
s36729.1	2	166172059	0.50	0.38	0.125	3.75×10^{-1}	0.500
s39822.1	16	344084	0.50	0.38	0.125	3.75×10^{-1}	0.500
s42732.1	18	44842263	0.48	0.38	0.125	3.75×10^{-1}	0.500
s42985.1	1	207255695	0.50	0.38	0.125	3.75×10^{-1}	0.500
s43712.1	3	207981934	0.49	0.38	0.125	3.75×10^{-1}	0.500
s44105.1	19	42112257	0.50	0.38	0.125	3.75×10^{-1}	0.500
s46222.1	1	928512	0.48	0.38	0.125	3.75×10^{-1}	0.500
s47996.1	6	61922422	0.49	0.38	0.125	3.75×10^{-1}	0.500
s48008.1	8	20449630	0.50	0.38	0.125	3.75×10^{-1}	0.500
s48775.1	12	43369502	0.50	0.38	0.125	3.75×10^{-1}	0.500
s49197.1	10	22019546	0.49	0.38	0.125	3.75×10^{-1}	0.500
s53061.1	3	41806864	0.49	0.38	0.125	3.75×10^{-1}	0.500
s54815.1	15	21311981	0.49	0.38	0.125	3.75×10^{-1}	0.500
s56532.1	24	1006379	0.49	0.38	0.125	3.75×10^{-1}	0.500
s59367.1	1	268862655	0.49	0.38	0.125	3.75×10^{-1}	0.500
s60019.1	19	243514	0.49	0.38	0.125	3.75×10^{-1}	0.500
s62475.1	3	187261164	0.49	0.38	0.125	3.75×10^{-1}	0.500
s64535.1	23	621912	0.48	0.37	0.124	3.75×10^{-1}	0.499
s69462.1	24	42641753	0.48	0.37	0.124	3.75×10^{-1}	0.499
s72109.1	13	1604096	0.49	0.38	0.125	3.75×10^{-1}	0.500
s72365.1	5	22638706	0.49	0.38	0.125	3.75×10^{-1}	0.500
s72862.1	3	994657	0.48	0.38	0.125	3.75×10^{-1}	0.500
s73045.1	5	106571513	0.49	0.38	0.125	3.75×10^{-1}	0.500

MAF: minor allele frequency; PIC: polymorphic information content; PE: probability of exclusion; PI: probability of identity; He: expected heterozygosity.

Table 4. Paternity test statistics for the core panel of 144 SNPs.

No. of SNP	CPE	CPI	MAF (Mean)
144	0.99999999540	4.91×10^{-62}	0.489

CPE: combined probability of exclusion; CPI: combined probability of identity; MAF: minor allele frequency.

paternity tests conducted using 144 SNPs on the farms included in the study are presented in Table 5.

Paternity test results conducted on 524 lambs using 144 selected SNPs showed that 96.56% of the lambs were accurately assigned to their sires with 95% confidence. The logarithm of the odds (LOD) scores for the assigned sires were all greater than zero. In addition, based on the results of the paternity tests, sires that were inaccurately recorded in the pedigree records were corrected, thereby preventing errors in genetic parameter estimates.

4. Discussion

With the efforts of the International Sheep Genomics Consortium (ISGC), of which we are a member, chips containing 54,241 SNPs (OvineSNP50 BeadChip) were developed and commercialized in collaboration with Illumina. The design of SNP microarray chips has resulted in numerous studies focused on developing paternity test panels for the determination and verification of parentage [12, 44–47].

It is an expected finding that the SNP chip, created using DNA samples from nearly all breeds worldwide, including domestic sheep breeds from Türkiye, exhibited a high level of polymorphism in the Eşme breed and demonstrated a high genotyping rate. The MAF values of the developed panel were higher than those of the test panels created using varying numbers of SNPs in different breeds [12,45,48,49]. Given that markers with high MAF values offer greater differentiation among individuals and are more effective in paternity testing, it can be concluded that the paternity test panel established in this study demonstrates a significant level of discriminatory power.

The CPE value obtained from the paternity test panel developed in this study was lower than that derived from the panel consisting of 249 SNPs for French sheep breeds [48]. However, it was higher than the CPE values obtained from the panel with 84 SNPs for New Zealand sheep breeds [50] and the panel using 109 SNPs for global sheep breeds [51]. These discrepancies between the present study and the existing literature may be attributed to variations in breed. The minimum CPE value recommended for accurate identification of the true sire is reported to be 0.999 [52,53]. The CPE value obtained in the present study was considerably higher than the specified threshold. This suggests that SNP-based paternity tests can be used with high reliability in native sheep breeds. The results also indicate that the developed panel can effectively distinguish between closely related individuals. This is supported by a CPI value of 4.91×10^{-62} obtained for the 144 SNPs. This value indicates that the probability of two individuals having the same genotype across the 144 SNP loci is virtually zero. Similar CPI values have also been reported in previous studies on SNP paternity test panels [50,51,54,55].

The high combined probability of exclusion (CPE) values obtained from the paternity test panel developed using 144 SNPs are noteworthy for pedigree record management in this study. In the paternity test conducted, pedigree errors in the Eşme sheep population were lower than those observed in the Creole sheep breed (5.88%) [56], Norwegian white sheep (4.9%) [54], Australian sheep breeds (5.4%) [55], French sheep breeds (13.17%) [48], and New Zealand sheep breeds (6%) [50].

As a result, a low-density and cost-effective paternity test panel was developed, enabling high-sensitivity paternity testing through the careful selection of appropriate SNPs. This study, the first of its kind in sheep in Türkiye, demonstrates that paternity tests can be conducted with high accuracy using a chip design incorporating 144 SNPs. The development of low-cost parentage testing chips tailored to local livestock represents a significant advancement for Türkiye, particularly in verifying parentage in lambs produced through hand-mating under breeder conditions.

SNP paternity test panels used for the creation and verification of pedigree records enhance the accuracy of breeding value estimation by minimizing pedigree errors and filling in missing information. This, in turn, accelerates genetic progress. Such advancements provide substantial benefits to breeders by enabling a more effective utilization of the genetic potential within the herd. This is particularly important in large herds or breeding systems that employ free mating, as the elimination of paternity uncertainties significantly improves herd management efficiency. Furthermore, integrating these panels into national breeding programs strengthens the reliability of selection indices by enhancing pedigree accuracy.

50K SNP chips developed using DNA samples from local sheep breeds in Türkiye and from sheep breeds raised in other countries were used. In this context, the paternity test panel derived from this study can be utilized in breeds that contributed to the development of the SNP chips. Furthermore, this research establishes genomic references for paternity testing, making a significant contribution

Table 5. Paternity test results and pedigree errors based on 144 SNPs in farms.

Flock	No. of lambs detected	No. of rejected paternity	Pedigree error rate (%)
Flock-1	32	1	3.13%
Flock-2	55	-	0.00%
Flock-3	35	-	0.00%
Flock-4	58	1	1.72%
Flock-5	86	-	0.00%
Flock-6	60	1	1.67%
Flock-7	44	-	0.00%
Flock-8	18	-	0.00%
Flock-9	56	4	7.14%
Flock-10	55	8	14.55%
Flock-11	25	3	12.00%
Total	**524**	**18**	3.44%

to both the literature and sheep breeding studies in Türkiye, with benefits that extend beyond mere monetary quantification.

Acknowledgment
This research was funded by the General Directorate of Agricultural Research and Policies (TAGEM), grant number TAGEM14/ARGE13.

We would like to express our gratitude to the General Directorate of Agricultural Research and Policies (TAGEM) for providing essential financial support for this research, which enabled the study to be conducted on animal material as part of the "National Genetic Breeding Project in Small Ruminants under Breeders' Conditions." We also extend our thanks to the sheep breeders who permitted this study to take place within their flocks and offered invaluable assistance. Additionally, we would like to acknowledge the Adnan Menderes University Agricultural Biotechnology and Food Safety Application and Research Center (ADU-TARBİYOMER) for supplying the laboratory infrastructure necessary for molecular genetic analysis.

Conflict of interest
The authors declared that there is no conflict of interest.

Informed consent
Permission was obtained from the Aydın Adnan Menderes University Animal Experiments Local Ethics Committee (ADU-HAYDEK) for blood sampling (Permission no: 64583101/2014/038).

References

1. Cortellari M, Negro A, Bionda A, Grande S, Cesarani A et al. Using pedigree and genomic data toward better management of inbreeding in Italian dairy sheep and goat breeds. Animals-Basel 2022; 12 (20): 2828. https://doi.org/10.3390/ani12202828
2. Carolino N, Vitorino A, Carolino I, Pais J, Henriques N et al. Genetic diversity in the Portuguese Mertolenga cattle breed assessed by pedigree analysis. Animals-Basel 2020; 10 (11): 1990. https://doi.org/10.3390/ani10111990
3. Zhang J, Song H, Zhang Q, Ding X. Assessment of relationships between pigs based on pedigree and genomic information. Animal 2020; 14: 697-705. https://doi.org/10.1017/S1751731119002404
4. Cesarani A, Garcia A, Hidalgo J, Degano L, Vicario D et al. Genomic information allows for more accurate breeding values for milkability in dual-purpose Italian Simmental cattle. Journal of Dairy Science 2021; 104: 5719-5727. https://doi.org/10.3168/jds.2020-19838

5. Cortellari M, Negro A, Bionda A, Frattini S, Grande S et al. Inbreeding depression in small ruminants: from pedigree to genomic estimation. Italian Journal of Animal Science 2021; 20 (suppl. 1), 98.

6. Rahim A, Chaudhary R, Rajaravindra KS, Pourouchottamane R, Gowane GR et al. Elucidating population structure and genetic diversity of intercross sheep through pedigree analysis. Small Ruminant Research 2024; 237: 107309. https://doi.org/10.1016/j.smallrumres.2024.107309

7. Demir E, Ceccobelli S, Bilginer U, Pasquini M, Attard G et al. Conservation and selection of genes related to environmental adaptation in native small ruminant breeds: a review. Ruminants 2022; 2(2): 255-270. https://doi.org/10.3390/ruminants2020017

8. Endris M, Hosseini SM, Tadesse Y, Abate M. Genetic management in conservation programs: a review. Global Journal of Animal Scientific Research 2023; 11: 67-88.

9. Ergün OF, Bayram B. Türkiye'de hayvancılık sektöründe yaşanan değişimler. Bahri Dağdaş Hayvancılık Araştırma Dergisi 2021; 10: 158-175 (in Turkish).

10. Aydin KB, Bi Y, Brito LF, Ulutas Z, Morota G. Review of sheep breeding and genetic research in Türkiye. Frontiers in Genetics 2024; 15: 1308113. https://doi.org/10.3389/fgene.2024.1308113

11. Kelleher J, Thornton KR, Ashander J, Ralph PL. Efficient pedigree recording for fast population genetics simulation. PLoS Computational Biology 2018; 14 (11): e1006581. https://doi.org/10.1371/journal.pcbi.1006581

12. McClure MC, McCarthy J, Flynn P, McClure JC, Dair E et al. SNP data quality control in a national beef and dairy cattle system and highly accurate SNP based parentage verification and identification. Frontiers in Genetics 2018; 9: 84. https://doi.org/10.3389/fgene.2018.00084

13. Karabaş M, Yilmaz O. Identification of selection signatures and genetic diversity in the sheep. PREPRINT (Version 1) available at Research Square 2024. https://doi.org/10.21203/rs.3.rs-3836943/v1

14. GDAR. Domestic Animal Genetic Resources in Türkiye. 1st ed. General Directorate of Agricultural Research and Policies, Ankara, Türkiye; 2011.

15. Alarslan E, Ata N, Yilmaz O, Öner Y, Kaptan C et al. Genetic identification and characterisation of some Turkish sheep. Small Ruminant Research 2021; 202: 106455. https://doi.org/10.1016/j.smallrumres.2021.106455

16. Yilmaz O, Kizilaslan M, Arzik Y, Behrem S, Ata N et al. Genome-wide association studies of preweaning growth and in vivo carcass composition traits in Esme sheep. Journal of Animal Breeding and Genetics 2022; 139: 26-39. https://doi.org/10.1111/jbg.12640

17. Daskiran I, Ayhan V. National Sheep and Goat Breeding Program and breeder associations' collaboration systems of Türkiye. FAO-CIHEAM Network on Sheep and Goats Sub-Network on Production Systems. 8th International Seminar. Technology creation and transfer in small ruminants: roles of research, development services and farmer associations. FAO-CIHEAM, Tangier, Morocco; 2013 pp. 11-13.

18. Daşkıran İ, Koluman N, Savaş T, Keskin M, Ankaralı B. National genetic improvement project for small ruminants at breeders' conditions and its achievements. In: Proceedings of the 9th National Animal Science Congress; Konya, Türkiye; 2015. pp. 166-175.

19. Cedden F, Cemal I, Daşkıran I, Esenbuğa N, Gül S et al. Türkiye küçükbaş hayvancılığında mevcut durum ve gelecek. Türkiye Ziraat Mühendisliği IX. Teknik Kongresi Ankara, Türkiye; 2020. pp. 133-152 (in Turkish).

20. Yilmaz O. Power of different microsatellite panels for paternity analysis in sheep. Animal Science Papers and Reports 2016; 34: 155-164.

21. Yılmaz O, Cemal I, Coşkun B, Oğrak YZ, Ata N et al. Comparison of different paternity test panels in sheep. Turkish Journal of Veterinary and Animal Sciences 2018; 42: 633-641. https://doi.org/10.3906/vet-1805-80

22. Keskin M, Yılmaz O, Gündüz Z, Ata N, Gül S et al. Microsatellite panels for parentage testing of Kilis goats reared in Türkiye. Turkish Journal of Veterinary and Animal Sciences 2019; 43: 94-101. https://doi.org/10.3906/vet-1809-21

23. Berry DP, Spangler ML. The benefit of a national genomic testing scheme. The Veterinary Clinics of North America: Food Animal Practice 2024; 40 (3): 435-445. https://doi.org/10.1016/j.cvfa.2024.05.008

24. Pimentel ECG, Edel C, Emmerling R, Götz KU. How pedigree errors affect genetic evaluations and validation statistics. Journal of Dairy Science 2024; 107 (6): 3716-3723. https://doi.org/10.3168/jds.2023-24070

25. Vesal SE. Molecular parentage analysis in aquaculture: Principles, applications, and challenges: a review. Asian Journal of Fisheries and Aquatic Research 2024; 26 (3): 62-75. https://doi.org/10.9734/AJFAR/2024/v26i3747

26. Nwogwugwu CP, Kim Y, Chung YJ, Jang SB, Roh SH et al. Effect of errors in pedigree on the accuracy of estimated breeding value for carcass traits in Korean Hanwoo cattle. Asian-Australasian Journal of Animal Science 2020; 33 (7): 1057-1067. https://doi.org/10.5713/ajas.19.0021

27. Chao CH, Yeh YH, Chen YM, Lee KH, Wang SH et al. Sire pedigree error estimation and sire verification of the Taiwan dairy cattle population by using SNP markers. Polish Journal of Veterinary Sciences 2022; 25 (1): 61-65. https://doi.org/10.24425/pjvs.2022.140841

28. Kaseja K, Mucha S, Yates J, Smith E, Banos G et al. Discovery of hidden pedigree errors combining genomic information with the genomic relationship matrix in Texel sheep. Animal 2022; 16 (3): 100468. https://doi.org/10.1016/j.animal.2022.100468

29. Tesema Z, Deribe B, Tilahun M, Lakew M, Getachew T et al. Effect of different types and levels of errors in sire pedigree on the accuracy of genetic evaluation in crossbred goats. Ecological Genetics and Genomics 2023; 26: 100165. https://doi.org/10.1016/j.egg.2023.100165

30. Bradford HL, Masuda Y, Cole JB, Misztal I, VanRaden PM. Modeling pedigree accuracy and uncertain parentage in single-step genomic evaluations of simulated and US Holstein datasets. Journal of Dairy Science 2019; 102 (3): 2308-2318. https://doi.org/10.3168/jds.2018-15419

31. Marina H, Suarez-Vega A, Pelayo R, Gutiérrez-Gil B, Reverter A et al. Accuracy of imputation of microsatellite markers from a 50K SNP chip in Spanish Assaf sheep. Animals-Basel 2021; 11 (1): 86. https://doi.org/10.3390/ani11010086

32. Butler JM. Advanced Topics in Forensic DNA Typing: Interpretation.1st ed. Oxford, England: Academic Press, Elsevier; 2015.

33. Krawczak M. Informativity assessment for biallelic single nucleotide polymorphisms. Electrophoresis: An International Journal 1999; 20 (8): 1676-1681. https://doi.org/10.1002/(SICI)1522-2683(19990101)20:8<1676::AID-ELPS1676>3.0.CO;2-D

34. Pakstis AJ, Speed WC, Fang R, Hyland FC, Furtado MR et al. SNPs for a universal individual identification panel. Human Genetics 2010; 127: 315-324. https://doi.org/10.1007/s00439-009-0771-1

35. Fernández ME, Goszczynski DE, Lirón JP, Villegas-Castagnasso EE, Carino MH et al. Comparison of the effectiveness of microsatellites and SNP panels for genetic identification, traceability and assessment of parentage in an inbred Angus herd. Genetics and Molecular Biology 2013; 36 (2): 185-191. https://doi.org/10.1590/S1415-47572013000200008

36. Flanagan SP, Jones AG. The future of parentage analysis: from microsatellites to SNPs and beyond. Molecular Ecology 2019; 28: 544-567. https://doi.org/10.1111/mec.14988

37. Laoun A, Harkat S, Lafri M, Gaouar SBS, Belabdi I. Inference of breed structure in farm animals: empirical comparison between SNP and microsatellite performance. Genes-Basel 2020; 11 (1): 57. https://doi.org/10.3390/genes11010057

38. Kijas JW, Lenstra JA, Hayes B, Boitard S, Neto LRP et al. Genome-wide analysis of the world's sheep breeds reveals high levels of historic mixture and strong recent selection. PloS Biology 2012; 10 (2): e1001258. https://doi.org/10.1371/journal.pbio.1001258

39. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MAR et al. PLINK: a tool set for whole-genome association and population-based linkage analyses. The American Journal of Human Genetics 2007; 81: 559-575. https://doi.org/10.1086/519795

40. Kalinowski ST, Taper ML, Marshall TC. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. Molecular Ecology 2010; 16: 1099-1106. https://doi.org/10.1111/j.1365-294X.2007.03089.x

41. Botstein D, White RL, Skolnick M, Davis RW. Construction of a genetic linkage map in man using restriction fragment length polymorphism. The American Journal of Human Genetics 1980; 32: 314-331.

42. Jamieson A, Taylor SS. Comparisons of three probability formulae for parentage exclusion. Animal Genetics 1997; 28: 397-400. https://doi.org/10.1111/j.1365-2052.1997.00186.x

43. Peakall R, Sydes MA. Defining priorities for achieving practical outcomes from the genetic studies of rare plants. In: Stephens S, Maxwell S (editors), Back from the Brink: Refining the Threatened Species Recovery Process. Surrey Beatty and Sons, Australia: New South Wales; 1996. pp. 119-129.

44. Talenti A, Palhière I, Tortereau F, Pagnacco G, Stella A et al. Functional SNP panel for parentage assessment and assignment in worldwide goat breeds. Genetics Selection and Evolution 2018; 50-55. https://doi.org/10.1186/s12711-018-0423-9

45. Calvo JH, Serrano M, Tortereau F, Sarto P, Iguacel LP et al. Development of a SNP parentage assignment panel in some North-Eastern Spanish meat sheep breeds. Spanish Journal of Agricultural Research 2020; 18 (4): e0406. https://doi.org/10.5424/sjar/2020184-16805

46. de Deus ARS, Silva GR, Sena LS, Britto FB, de Carvalho DA et al. Comparison of kinship estimates in Santa Inês sheep using microsatellite and genome-wide SNP markers. Small Ruminant Research 2021; 201: 106399. https://doi.org/10.1016/j.smallrumres.2021.106399

47. Ablondi M, Stocco G, Cortellari M, Carta A, Summer A et al. Microsatellite imputation using SNP data for parentage verification in four Italian sheep breeds. Journal of Animal Breeding and Genetics 2024; 141 (3): 278-290. https://doi.org/10.1111/jbg.12839

48. Tortereau F, Moreno CR, Tosser-Klopp G, Servin B, Raoul J. Development of a SNP panel dedicated to parentage assignment in French sheep populations. BMC Genetics 2017; 18: 1-11. https://doi.org/10.1186/s12863-017-0518-2

49. Yang TF, Miller M, Forgacs D, Derr J, Stothard P. Development of SNP-based genomic tools for the Canadian bison industry: parentage verification and subspecies composition. Frontiers in Genetics 2020; 11: 585999. https://doi.org/10.3389/fgene.2020.585999

50. Clarke SM, Henry HM, Dodds KG, Jowett TW, Manley TR et al. A high throughput single nucleotide polymorphism multiplex assay for parentage assignment in New Zealand sheep. PloS one 2014; 9 (4): e93392. https://doi.org/10.1371/journal.pone.0093392

51. Heaton MP, Leymaster KA, Kalbfleisch TS, Kijas JW, Clarke SM et al. SNPs for parentage testing and traceability in globally diverse breeds of sheep. Plos One 2014; 9 (4): e94851. https://doi.org/10.1371/journal.pone.0094851

52. Sherman GB, Kachman SD, Hungerford LL, Rupp GP, Fox CP et al. Impact of candidate sire number and sire relatedness on DNA polymorphism-based measures of exclusion probability and probability of unambiguous parentage. Animal Genetics 2004; 35: 220-226. https://doi.org/10.1111/j.1365-2052.2004.01143.x

53. Van Eenennaam AL, Weaber RL, Drake DJ, Penedo MCT, Quaas RL et al. DNA-based paternity analysis and genetic evaluation in a large, commercial cattle ranch setting. Journal of Animal Science 2007; 85: 3159-3169. https://doi.org/10.2527/jas.2007-0284

54. Belay KT. Development of a SNP markers panel for parentage testing and individual identification in the Norwegian white sheep (NWS) population. MSc, Norwegian University, Norway, 2013.

55. Bell AM, Henshall JM, Gill S, Gore K, Kijas JW. Success rates of commercial SNP based parentage assignment in sheep. In: Villalobos NL (editor), Association for the Advancement of Animal Breeding and Genetics, New Zealand: Napier; 2013. pp. 278-281.

56. Macedo F, Aguilar I, Grasso AN, Pieruccioni F, Ciappesoni G. New parentage testing SNP panel for commercial breeds will be a useful tool for conservation of Creole sheep. In: Proceedings of the 10th World Congress of Genetics Applied to Livestock Production, Vancouver, Canada; 2014. pp.