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# Microsatellite panels for parentage testing of Kilis goats reared in Turkey

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**Abstract:** The aim of this study was to develop PCR-based suitable microsatellite marker panels for paternity testing and to define pedigree errors in Kilis goats. A total of 137 head of goats were used, consisting of 118 head of kids and 19 head of possible candidate sires. A total of 392 alleles were observed in 22 microsatellite markers. Allele numbers ranged between 12 (SRCRSP7) and 24 (BM1818, INRA0023, and SRCRSP15) with an average of 17.82. The mean value of the effective allele numbers was obtained as 9.44. The overall polymorphic information content value was quite high (0.88). The overall observed (Ho) and expected heterozygosity (He) values for all studied loci were 0.89 and 0.89, respectively. Paternity test panels for the Kilis goat population studied were created based on individual probability of exclusion of microsatellites in multiplex groups. Combined probability of exclusion (CPE) values for different panels ranged between 0.745 (Panel-1) and 0.9999 (Panel-22), while the combined identification probability (CPI) values were obtained in the range of $9.81 \times 10^{-3}$ (Panel-1) to $6.96 \times 10^{-21}$ (Panel-22). As a result of this study, it can be stated that panels with 0.999 CPE values can be used at the most reasonable cost and with high reliability in paternity tests to be performed in Kilis goats, which can be a reference for other populations.

**Key words:** Kilis goats, microsatellite, parentage testing, probability of exclusion

## 1. Introduction

Identification and validation of the biological father of a living thing by methods such as blood group, hemoglobin typing, transferrin typing, or DNA analysis is defined as a paternity test. Pedigree records in animal production farms can be misrecognized for many reasons. Here, paternity tests are used to identify and verify this type of information (1). Because they contain a high level of information, microsatellite markers are used widely in paternity tests to control pedigree records. The high information content of microsatellite markers depends on the number of alleles given by the marker and the frequencies in the corresponding populations (2).

The accuracy of pedigree information in many animal species is one of the most important steps for breeding programs. Pedigree errors have great influence on the answer to the selection in the breeding programs (3). Incorrect selection of male stock candidates in animal breeding programs will result in lower genetic progress than expected (1,4).

In countries such as Turkey, keeping accurate yield and reproductive records in breeding programs for goat populations raised under extensive condition will increase the degree of precision in the breeding value estimation. In addition, the correct use of paternity tests will contribute to the creation of this information for an unknown population of pedigree information. It will also allow for checking the accuracy of existing pedigree information and correcting the incorrectly recorded information (5). Although paternity test studies are carried out on Turkish native sheep breeds (5,6), there are few studies on paternity testing for Turkish native goat breeds, except in a study carried out in Hair goat (7,8).

The National Sheep and Goat Breeding Project is being implemented in Turkey by the Republic of Turkey Ministry of Food, Agriculture, and Livestock with the cooperation of different universities, research institutes, and sheep and goat breeder associations under the condition of breeders. The Kilis Goat Breeding Project is a subproject of this national project and it has been executed in the Kilis and Gaziantep provinces of Turkey for 7 years. During this project, mating records have been recording by breeders in elite flocks.

The aims of this study are to confirm the pedigree information obtained from mating records in the Kilis

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Goat Breeding Project by paternity tests based on DNA analyses and to develop a panel that can be used with the most reasonable cost and high reliability from 22 microsatellites used in this study since the use of many microsatellite loci in paternity tests is expensive and time-consuming.

## 2. Materials and methods

### 2.1. Animal material and DNA isolation

The animal material of this study consisted of 19 head of bucks that were probable candidate sires with 118 head of kids born from hand-mating in the Kilis Goat Breeding Project from 5 different farms with the approval of the Mustafa Kemal University Ethics Committee (MKÜHADYEK-2015/10-1). Two months before the date of the mating, the does and bucks were separated from each other and managed separately in farmer conditions. At the time of mating, teaser bucks were used for estrus detection. After this detection, it was recorded which doe was mated by which buck. The numbers of bucks and kids in these 5 farms are given in Table 1.

Using vacutainer tubes containing the anticoagulant $K_3$-EDTA, blood samples were collected from bucks during the breeding season and from their kids at birth. Genomic DNA was extracted from the blood samples (9,10). Afterward, quality and quantity of DNA was measured using NanoDrop (ND2000, Thermo Scientific, USA).

### 2.2. Polymerase chain reaction and fragment analysis

In this study, 22 microsatellites loci labeled with fluorescent dye (D2, D3, and D4), as recommended by the FAO (11), were used. PCR amplification was performed for two multiplex groups. The first (M1) and second (M2) multiplex groups consisted of 10 (OarFCB20, INRA0005, INRA0023, ILSTS011, SRCRSP9, SRCRSP15, TCRVB6, OarAE54, INRA0132, and BM1818) and 12 (SRCRSP7, McM0527, CSRD0247, INRABERN185, SRCRSP0023, ILSTS0087, SRCRSP0005, DRBP1, INRABERN172, HSC (OLADRB), SRCRSP3, and BM1329) microsatellite markers, respectively. PCR mixtures containing 1X PCR buffer, 2.0 mM $MgCl_2$, 0.2 mM dNTPs, 0.1 μM of primers (forward and reverse), 1 U of Taq DNA polymerase (Applied Biological Materials Inc., USA), ~50 ng genomic DNA, and sterile dd$H_2O$ with total volume of 20 μL were prepared for amplification of primer-specific sites in the PCR steps. The touchdown PCR technique, as reported by Hecker and Roux (12), was applied in order to achieve more efficient and rapid DNA amplification in the study (Table 2).

Capillary electrophoresis was performed with a Beckman Coulter GeXP fragment analyzer (Beckman Coulter, Inc., USA) for this separation of fragments.

### 2.3. Formation of paternity test panels

The microsatellites in each multiplex group were ranked according to their individual probability of exclusion (PE) values and 22 paternity test panels were created according to this procedure in this study (Table 3).

### 2.4. Statistical analysis

The numbers of alleles (Na), effective alleles (Ne), observed (Ho) and expected (He) heterozygosities, and their mean values for the microsatellite loci used in this study were calculated using the GenAlEx genetic analysis program (13). The Cervus 3.0.3 (14) program was used to calculate polymorphic information content (PIC), probability of exclusion (PE), probability of identity (PI), probability of combined exclusion (CPE), combined probability of identity (CPI), mean proportion of the genotyping individuals (GR), and null allele frequency (F(Null)). The discrimination power of the microsatellites (PD) was determined by the PowerStats v.1.2. program (15).

## 3. Results

Microsatellite-based genetic polymorphism and paternity analysis statistics for Kilis goats constituting the animal material of this study are given in Table 4. A total of 392 alleles were observed in the 22 microsatellite loci examined. Alleles numbers ranged from 12 (SRCRSP7) to 24 (BM1818, INRA0023, and SRCRSP15) with an average number of 17.82. The mean value of the number of effective alleles was obtained as 9.44.

When the Na, Ne, MNa (the mean number of alleles), and PIC values obtained in this study are examined, it is noteworthy that the microsatellites used have very high polymorphism. The average PIC value, which is an important criterion in the selection of microsatellites, was quite high (0.88). The high PIC value suggests that the microsatellites used in the study can be used effectively in paternity tests. The mean of the expected (He) and observed heterozygosity (Ho) values for all studied locus were 0.89 and 0.89, respectively.

The lowest and the highest values of PE, which is defined as the probability to exclude a random parent pair that is unrelated to the individual, were observed in ILSTS011

**Table 1.** Distribution of animal material by farms.

| Farms | Number of kids | Number of bucks |
|---|---|---|
| Farm-1 | 21 | 4 |
| Farm-2 | 30 | 4 |
| Farm-3 | 21 | 4 |
| Farm-4 | 27 | 4 |
| Farm-5 | 19 | 3 |
| Total | 118 | 19 |

**Table 2.** Thermal cycling conditions according to touchdown PCR method.

| Multiplex group | First denaturation | Denaturation | Annealing | Extension | Cycle | Final extension |
|---|---|---|---|---|---|---|
| M1 and M2 | 95 °C (5 min) | 95 °C (40 s) | 50–60 °C (40 s) | 72 °C (60 s) | 30 | 72 °C (10 min) |

(0.384) and DRBP1 (0.750) loci, respectively. The higher the PE value, the more non-fathers are excluded.

The PI value, also known as matching probability, which is the probability of two independent samples having the same identical genotype, ranged from 9.34E-03 to 8.75E-02 in this study. The PD, known as the probability that two randomly selected individuals have identical phenotypes or genotypes by chance alone, ranged from 0.890 to 0.981. The higher the discrimination power of a locus, the more efficient it is in discriminating between members of the population. The null allele, which was first introduced by Paetkau and Strobeck (16), causes misreading of the microsatellite peaks. The lowest and highest null allele frequencies were –0.0428 (OarAE54) and 0.0617 (SRCRSP7), respectively.

Information on the correct and incorrect pedigree records according to the results of the paternity tests performed by the microsatellite markers in this study is given in Table 5. As can be seen from Table 5, the average pedigree error rate for five farms was calculated as 3.40%. It can be said that pedigree errors detected are negligible in the population studied.

Paternity test panel statistics, which included the mean number of alleles (MNa), mean polymorphic information content (MPIC), mean expected heterozygosity (MHe), combined probability of exclusion (CPE), combined probability of identity (CPI), and mean proportion of the genotyping individuals (GR), are given in Table 6.

The MNa values ranged between Panel-22 (16.75) and Panel-1 (24.00). The highest and lowest MHe values were observed to be 0.93 (Panel-1, 2, 3, and 11) and 0.88 (Panel-10), respectively. Obtained PIC values from paternity test panels formed varied from 0.87 (Panel-10) to 0.93 (Panel-11). The highest CPE values were obtained from Panel-10 and Panel-22, which were formed by considering the individual PE values of the microsatellites in the multiplex groups. In addition, the CPI values obtained (<0.01) across all the paternity test panels indicated that these panels have high power of individual identification. Mean proportion of the genotyped individuals' value was 97.28% in across all panels studied.

## 4. Discussion

Obtained MNa and PIC values were significantly higher than those of some other Turkish goat breeds and other goat breeds raised in different countries (17,18), while these values were lower than those of goat breeds raised in North Africa (19). The findings related to allele numbers indicated a high level of allelic richness in the breed studied. On the other hand, values obtained for PIC showed that the microsatellites used in this study are highly polymorphic. The overall He and Ho were higher than in past studies conducted in different goat breeds (20,21).

Although the obtained average PE value (0.635), which is known as a measure of efficiency in paternity testing, was in the probability of exclusion with some literature (20,22), it was higher than values obtained from other studies (19). This may have been due to the differences in microsatellite loci used in these studies. The high PD value (>0.85) obtained from the loci used in the study is a natural consequence of the high number of alleles obtained from the microsatellite loci. Null alleles, defined as nonamplifiable alleles due to mutations in the PCR binding site, cause only a single allele to peak like a homozygote, thus cause erroneous readings. It was reported by Dakin and Avise (23) that null allele frequencies below 0.20 have no significant effect on paternity tests. When the null allele frequencies obtained are examined, it is seen that the null allele frequency values of 22 microsatellites to be studied are below 0.20. Taking this value into consideration, it has been demonstrated that the studied loci can be safely used in paternity tests.

The obtained low level of pedigree errors does not pose any risk for genetic parameters to be calculated in populations. In addition, the obtained findings from the present study showed that the errors in the pedigree records can be corrected with high accuracy by the paternity tests to be performed by the microsatellite markers. A total of four kid's sires were recorded incorrectly in the pedigree record. These errors may have occurred due to many factors such as paddock overturning, writing the wrong number during mating, and mistyping of lambs at birth.

The mean number of alleles (MNa), mean expected heterozygosity (MHe), and mean polymorphic information content (MPIC) values obtained from the generated paternity test panels were higher than the values in Brazilian goat breeds reported by da Da Silva et al. (18).

The minimum CPE recommended for accurate identification of the true father is 0.999 (24,25). As can be seen from Table 6, the CPE values obtained for the 22

**Table 3.** Formation of paterntity test panels.

| Multiplex-1 | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Panels | SRCRSP15 (PE = 0.745) | INRA0132 (PE = 0.7229) | TCRVB6 (PE = 0.7199) | BM1818 (PE = 0.687) | OarFCB20 (PE = 0.647) | SRCRSP9 (PE = 0.622) | INRA0023 (PE = 0.596) | INRA0005 (PE = 0.589) | OarAE54 (PE = 0.574) | ILSTS011 (PE = 0.384) | | |
| Panel-1 | ✓ | | | | | | | | | | | |
| Panel-2 | ✓ | ✓ | | | | | | | | | | |
| Panel-3 | ✓ | ✓ | ✓ | | | | | | | | | |
| Panel-4 | ✓ | ✓ | ✓ | ✓ | | | | | | | | |
| Panel-5 | ✓ | ✓ | ✓ | ✓ | ✓ | | | | | | | |
| Panel-6 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | | | | | |
| Panel-7 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | | | | |
| Panel-8 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | | | |
| Panel-9 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | | |
| Panel-10 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | |
| Multiplex-2 | | | | | | | | | | | | |
| Panels | DRBP1 (PE = 0.750) | INRABERN185 (PE = 0.693) | HSC (PE = 0.690) | INRABERN172 (PE = 0.667) | BM1329 (PE = 0.659) | SRCRSP0023 (PE = 0.652) | SRCRSP0005 (PE = 0.644) | McM0527 (PE = 0.642) | CSRD0247 (PE = 0.600 | SRCRSP7 (PE = 0.572) | ILSTS0087 (PE = 0.566) | SRCRSP3 (PE = 0.556) |
| Panel-11 | ✓ | | | | | | | | | | | |
| Panel-12 | ✓ | ✓ | | | | | | | | | | |
| Panel-13 | ✓ | ✓ | ✓ | | | | | | | | | |
| Panel-14 | ✓ | ✓ | ✓ | ✓ | | | | | | | | |
| Panel-15 | ✓ | ✓ | ✓ | ✓ | ✓ | | | | | | | |
| Panel-16 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | | | | | |
| Panel-17 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | | | | |
| Panel-18 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | | | |
| Panel-19 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | | |
| Panel-20 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | |
| Panel-21 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | |
| Panel-22 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |

**Table 4.** Polymorphism statistics of microsatellite loci.

| Loci | N | Na | Ne | Ho | He | PIC | PE | PI | PD | F(Null) |
|---|---|---|---|---|---|---|---|---|---|---|
| OarAE54 | 134 | 18 | 7.08 | 0.93 | 0.86 | 0.85 | 0.574 | 3.26E-02 | 0.952 | –0.0428 |
| INRA0132 | 133 | 22 | 12.35 | 0.94 | 0.92 | 0.91 | 0.722 | 1.19E-02 | 0.973 | –0.0126 |
| BM1818 | 133 | 24 | 10.78 | 0.94 | 0.91 | 0.90 | 0.687 | 1.57E-02 | 0.970 | –0.0195 |
| OarFCB20 | 132 | 17 | 9.35 | 0.93 | 0.89 | 0.88 | 0.647 | 2.05E-02 | 0.966 | –0.0211 |
| INRA0005 | 132 | 14 | 7.77 | 0.87 | 0.87 | 0.86 | 0.589 | 2.95E-02 | 0.961 | 0.0012 |
| INRA0023 | 137 | 24 | 7.46 | 0.82 | 0.87 | 0.86 | 0.596 | 2.76E-02 | 0.961 | 0.0303 |
| ILSTS011 | 132 | 15 | 4.33 | 0.77 | 0.77 | 0.74 | 0.384 | 8.75E-02 | 0.890 | –0.0049 |
| SRCRSP9 | 136 | 16 | 8.63 | 0.84 | 0.88 | 0.87 | 0.622 | 2.41E-02 | 0.963 | 0.0243 |
| SRCRSP15 | 133 | 24 | 13.84 | 0.95 | 0.93 | 0.92 | 0.745 | 9.82E-03 | 0.981 | –0.0103 |
| TCRVB6 | 137 | 17 | 12.45 | 0.95 | 0.92 | 0.91 | 0.719 | 1.22E-02 | 0.980 | –0.0165 |
| SRCRSP3 | 136 | 16 | 6.83 | 0.88 | 0.85 | 0.84 | 0.556 | 3.55E-02 | 0.945 | –0.0225 |
| BM1329 | 136 | 19 | 9.77 | 0.94 | 0.90 | 0.89 | 0.659 | 1.91E-02 | 0.968 | –0.024 |
| SRCRSP7 | 134 | 12 | 7.43 | 0.77 | 0.87 | 0.85 | 0.572 | 3.27E-02 | 0.959 | 0.0617 |
| McM0527 | 128 | 18 | 9.19 | 0.81 | 0.89 | 0.88 | 0.642 | 2.13E-02 | 0.971 | 0.0481 |
| CSRD0247 | 136 | 17 | 8.06 | 0.81 | 0.88 | 0.86 | 0.600 | 2.76E-02 | 0.965 | 0.0400 |
| INRABERN185 | 130 | 18 | 10.98 | 0.96 | 0.91 | 0.90 | 0.693 | 1.48E-02 | 0.973 | –0.0283 |
| SRCRSP0023 | 135 | 21 | 9.42 | 0.84 | 0.89 | 0.89 | 0.652 | 2.00E-02 | 0.974 | 0.0296 |
| ILSTS0087 | 135 | 13 | 7.18 | 0.86 | 0.86 | 0.85 | 0.566 | 3.40E-02 | 0.951 | –0.0009 |
| SRCRSP0005 | 135 | 16 | 9.26 | 0.91 | 0.89 | 0.88 | 0.644 | 2.09E-02 | 0.972 | –0.0105 |
| DRBP1 | 131 | 19 | 14.25 | 0.99 | 0.93 | 0.93 | 0.750 | 9.34E-03 | 0.981 | –0.0330 |
| INRABERN172 | 134 | 14 | 10.20 | 0.96 | 0.90 | 0.89 | 0.667 | 1.79E-02 | 0.970 | –0.0288 |
| HSC(OLADRB) | 135 | 18 | 11.03 | 0.96 | 0.91 | 0.90 | 0.690 | 1.52E-02 | 0.976 | –0.0297 |
| Mean | | 17.82 | 9.44 | 0.89 | 0.89 | 0.88 | | | | |

Na: Number of alleles, Ne: number of effective alleles, Ho: observed heterozygosity, He: expected heterozygosity, PIC: polymorphic information content, PE: probability of exclusion, PI: probability of identification, PD: power of discrimination, F(null): null allele frequency.

**Table 5.** Percentage of sires whose pedigree records are correct and incorrect.

| Farms | Kid number | Mating records | | Error rate (%) |
|---|---|---|---|---|
| | | True | False | |
| Farm-1 | 21 | 21 | - | 0.00 |
| Farm-2 | 30 | 29 | 1 | 3.00 |
| Farm-3 | 21 | 20 | 1 | 4.80 |
| Farm-4 | 27 | 25 | 2 | 7.40 |
| Farm-5 | 19 | 19 | - | 0.00 |
| General | 118 | 114 | 4 | 3.40 |

microsatellites used in this study are within the specified limits. When the CPE values obtained in this study are examined, it is seen that panels formed by six or more microsatellites reached the minimum CPE values reported in the literature. It is an important finding that the CPE values obtained from the paternity test panels formed by six or more microsatellites in the present study are in agreement with the values obtained from paternity test panels formed by eleven microsatellites reported by Luikart et al. (24) and ISAG (26). At the same time, these values were similar to CPE values obtained from paternity test panels consisted of sixteen (18), twelve (27), seventeen (28), and eight (17) microsatellite markers. On the other hand, these values were higher than the values obtained

**Table 6.** Paternity test parameters for panels formed with increasing numbers of microsatellites.

| | Panels | NMP | MNa | MHe | MPIC | CPE | CPI | GR |
|---|---|---|---|---|---|---|---|---|
| MG1 | Panel-1 | 1 | 24.00 | 0.93 | 0.92 | 0.745322 | 9.8E-03 | 97.08% |
| | Panel-2 | 2 | 23.00 | 0.93 | 0.92 | 0.929123 | 1.2E-04 | 97.08% |
| | Panel-3 | 3 | 21.00 | 0.93 | 0.92 | 0.980057 | 1.4E-06 | 98.05% |
| | Panel-4 | 4 | 21.75 | 0.92 | 0.91 | 0.993759 | 2.24E-08 | 97.85% |
| | Panel-5 | 5 | 20.80 | 0.92 | 0.91 | 0.997796 | 4.6E-10 | 97.52% |
| | Panel-6 | 6 | 20.00 | 0.91 | 0.90 | 0.999168 | 1.1E-11 | 97.81% |
| | Panel-7 | 7 | 20.57 | 0.91 | 0.90 | 0.999664 | 3.1E-13 | 98.12% |
| | Panel-8 | 8 | 19.75 | 0.90 | 0.89 | 0.999862 | 9.0E-15 | 97.90% |
| | Panel-9 | 9 | 19.56 | 0.90 | 0.89 | 0.999941 | 2.9E-16 | 97.89% |
| | Panel-10 | 10 | 19.10 | 0.88 | 0.87 | 0.999964 | 2.6E-17 | 97.74% |
| MG2 | Panel-11 | 1 | 19.00 | 0.93 | 0.93 | 0.750233 | 9.3E-03 | 95.62% |
| | Panel-12 | 2 | 18.50 | 0.92 | 0.91 | 0.923253 | 1.4E-04 | 95.26% |
| | Panel-13 | 3 | 18.33 | 0.91 | 0.91 | 0.976238 | 2.1E-06 | 96.35% |
| | Panel-14 | 4 | 17.25 | 0.92 | 0.91 | 0.992097 | 3.7E-08 | 96.72% |
| | Panel-15 | 5 | 17.60 | 0.91 | 0.90 | 0.997307 | 7.1E-10 | 97.23% |
| | Panel-16 | 6 | 18.17 | 0.91 | 0.90 | 0.999063 | 1.4E-11 | 97.45% |
| | Panel-17 | 7 | 17.86 | 0.91 | 0.90 | 0.999666 | 3.0E-13 | 97.60% |
| | Panel-18 | 8 | 17.88 | 0.91 | 0.90 | 0.999881 | 6.4E-15 | 97.08% |
| | Panel-19 | 9 | 17.78 | 0.90 | 0.89 | 0.999952 | 1.8E-16 | 97.32% |
| | Panel-20 | 10 | 17.20 | 0.90 | 0.89 | 0.999980 | 5.8E-18 | 97.37% |
| | Panel-21 | 11 | 16.82 | 0.90 | 0.88 | 0.999991 | 2.0E-19 | 97.48% |
| | Panel-22 | 12 | 16.75 | 0.89 | 0.88 | 0.999996 | 7.0E-21 | 97.63% |
| MG1-2 | Panel-23 | 22 | 17.82 | 0.89 | 0.88 | 0.999999 | 1.78E-37 | 97.68% |

NMP: Number of microsatellites in the panel, MG: multiplex group, MNa: mean number of alleles, MHe: mean expected heterozygosity, MPIC: mean polymorphic information content, CPE: combined probability of exclusion, CPI: combined probability of identity, GR: mean proportion of the genotyping individuals.

from paternity test panels reported by the MAPA (29). It is believed that panels with a CPE above 0.999 in the presented study may be suitable for use in other goat breeds.

It is clear that increasing the number of microsatellite loci to be used in the panels increases the value of the CPE. However, working with a smaller number of microsatellite loci and multiplex groups will allow time and cost savings. In this context, it can be said that panels containing six or more microsatellite markers can be used safely in paternity tests to be applied to Kilis goats. This application will be cheaper and more practical than other panels created with more microsatellite markers.

The calculated CPI values (<0.01) for all panels show that the microsatellites used have high individual identification power and are in the confidence interval indicated by Waits et al. (30). Obtained CPI values were in accordance with values reported by Luikart et al. (24).

The national animal breeding project is being carried out successfully by the General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture, and Livestock in coordination with universities and breeders' associations. In this context, the habits of keeping records in small ruminants have been initiated and spread over time. On the other hand, with the numbering of the animals and breeding records, the possibility of obtaining the production potential information of the herds was ensured safely. Besides this possibility, it is important to note that special efficiency records can be kept and the efficiency records can be made continuous on the basis of the pedigree. However, the issue of controlling the correctness of reported outcomes and the problem of correct identification of parents is still being updated. In this context, it has been revealed that hand-mating in this study was recorded in field conditions with high accuracy.

It has also been found that it is possible to prove the validity of the obtained mating results using DNA-based microsatellite markers. On the other hand, the current study has developed cheap, fast, and reliable paternity test panels that can be used for Kilis goat populations. It can be stated that panels with a CPE above 0.999 can be used at the most reasonable cost and with high reliability in paternity tests to be performed in Kilis goats, which can be a reference for other populations. In order to provide more effective and widespread use of these panels, it is possible to test these panels in different breeds in the future and develop easy-to-use kits for them. This can contribute to the solution of the problem about verification of hand-mating in large-area projects under breeder conditions such as the National Sheep and Goat Breeding Project.

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