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Genetic Diversity Assessment of Two Goat Populations and Their Crossbred Using Microsatellite Markers

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Abstract

GOATS play an important economic role in developing countries. Moreover, their donation in boosting economic returns in developed nations has also been steadily increasing. Mating between pure breeds of goats is a suitable breeding approach to develop crossbred characterized by heavy weights and high yield of milk, compared with the unimproved local goats. This study analyzed 36 goats from three different populations using eight microsatellite markers. The crossbreeding scheme included two pure goat breeds that are highly productive (Boer and Damascus),where mating was performed between Boer males and Damascus females to produce the crossbred population. The analysis of microsatellite markers revealed that the total allele count ranged from 71 to 82, with an average of 78.7 alleles per locus. The crossbred group showed the highest number of alleles at the SRCRSP3 locus, with 18 alleles, while the Damascus population had the lowest at the SRCRSP7 locus, with only 4 alleles. Across all goat populations studied, the number of observed alleles exceeded the expected values, suggesting the introduction of new alleles through gene flow. The difference between observed (No) and effective (Ne) allele numbers was most pronounced in the crossbred goats (2.38), attributed to the effects of crossbreeding. Furthermore, observed heterozygosity (Ho) was consistently higher than expected heterozygosity (He), pointing to an excess of heterozygotes within these populations under study. The high heterozygosity within breeds reflects the multi-allelic nature of the loci and the ability of these microsatellite loci to differentiate between goat populations. The Polymorphic Information Content (PIC) was in general high, and was 0.86, 0.81and 0.83 in Boar, Damascus, and crossbred populations, respectively. The results in general reveal the genetic power of crossing in increasing the population fitness.

Keywords: Goats, Genetic Diversity, Crossbred, Microsatellite Markers.

Introduction

Local and regional goat varieties of the Mediterranean region play a vital role in transforming large areas of marginal land into valuable animal products that support human livelihoods. Goats were among the first animals to be domesticated by humans, with their domestication beginning around 10,000 years ago [1]. Goats (*Capra aegagrus hircus*) are globally distributed and comprise more than 500 breeds selected for the production of meat, milk, skin, and fiber. In addition to their economic importance, goats are also used to manage vegetation, help sustain rural communities, and take part in cultural and social traditions [2].

Among domestic ruminants, goats stand out for their ability to survive in a wide range of climates [3,4]. Realizing the importance of preserving livestock genetic resources, scientists have conducted numerous studies on the diversity and variation of local goat breeds across Asia, Europe, and Africa. However, such research remains limited in Middle Eastern countries, even though the region maintains approximately 54 goat breeds [5]. Genetic diversity in livestock provides a valuable pool of traits that helps farmers enhance their herds and supports animal adaptation to changing environments [6]. For this reason, understanding the genetic makeup of goat breeds and populations in Egypt is crucial, both for guiding conservation efforts and for improving the genetic quality of these important animals [7, 8].

The advances in molecular genetics techniques enabled animal geneticists to study the genetic specificity and genetic diversity of livestock using different approaches. In turn, different breeding approaches have become available [9]. In this

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context, molecular markers can detect genetic variation in both coding and non-coding DNA sequences. As a result, advances at the DNA level have made it possible to identify a wide range of genetic polymorphisms. These discoveries have opened up new opportunities in the genetic characterization, improvement, conservation, and molecular evolution studies of various farm animal species [10]. The molecular characterization of a population also forms the basis of genetic conservation [11].

Microsatellites represent one of the most highly variable DNA sequences found within the genome. They are tandem repeats of short DNA sequences with high polymorphism and co-dominant in inheritance [12]. They are scattered throughout the genomes of eukaryotes. Distinct from unique DNA sequences, microsatellite polymorphisms arise primarily from differences in the number of repeat units rather than variations in the primary nucleotide sequence. Moreover, genetic variation at numerous microsatellite loci is marked by high heterozygosity and the presence of multiple alleles, further distinguishing them from unique DNA regions [13].

Microsatellites are widely used markers for genetic characterization in different livestock species. They rely on variations in DNA sequences and are detected by designing PCR primers that target the regions surrounding the microsatellite segments [14]. In animal breeding, estimation of genetic variation within and among the breeds is a basic tool for selection and crossbreeding [15]. Microsatellite markers allow the estimation of genetic diversity within and between breeds and provide additional information for the design and interpretation of breeding programs [16]. This study aimed to assess the genetic diversity of Boer, Damascus, and their crossbred goat populations using microsatellite markers to evaluate allele diversity, heterozygosity, and polymorphic information content. It seeks to investigate the impact of crossbreeding on genetic variation and population fitness.

Material and Methods

Animals and management

Two goat breeds were used in this study. The breeds were distinctively different in their genetic compositions. The breeds were Boer goats (Boer males are frequently utilized as sires in crossbreeding programs with dairy goat breeds to enhance the meat quality of the resulting offspring), which were probably bred from South Africa [17] and Damascus goats (dairy goats that are mainly used for milk production) which spread in Syria and Cyprus [18]. The Experiment was designed to produce dual-purpose hybrid goats by mating between Boar males and Damascus females. The crossbreds are characterized by their adaptation to the local environmental conditions and the high production of meat and milk as well.

Samples and genotyping

A sample of five mL blood was taken from the jugular vein of each animal in both the parent and crossbred groups. The samples were placed in clean tubes containing ethylene diamine tetra acetic acid to prevent clotting and were immediately stored at −20°C to keep them preserved.

Upon use, samples were thawed and used for the genomic DNA extraction using the phenol/chloroform extraction procedure [19]. To extract DNA, 200 µL of blood was placed into a 1.5 mL Eppendorf tube. Then, 20 µL of proteinase K (10 mg/mL) and 50 µL of 10% SDS were added. The mixture was thoroughly blended using a vortex mixer and incubated in a water bath at 56°C for two hours. After digestion, an equal volume (270 µL) of a phenol/chloroform/isoamyl alcohol (25:24:1) solution was added and mixed well. The sample was then centrifuged at 12,000×g for five minutes. The clear upper layer was transferred to a new tube, and this step was repeated using chloroform/isoamyl alcohol (24: 1) to purify the solution. DNA was then precipitated by adding 2.5 volumes of absolute ethanol and 1/10 volume of 3 M sodium acetate (pH 5.2), followed by thorough mixing and overnight incubation at −20°C. The next day, the sample was centrifuged again at 12,000×g for 15 minutes at 4°C. The resulting DNA pellet was washed with 70% ethanol, air-dried, dissolved in 100 µL of TE buffer, and stored at −20°C for later use. After DNA extraction, the concentration and purity of the genomic DNA were determined using a NanoDrop spectrophotometer (Thermo Scientific, USA). DNA concentration was quantified by measuring absorbance at 260 nm, and purity was assessed by calculating the A260/A280 ratio, with values between 1.8 and 2.0 indicating high-quality DNA suitable for PCR amplification.

The individual samples were screened by 8 microsatellite primers through the polymerase chain reaction (PCR) procedures. The molecular information of the microsatellite primers is presented in (Table 1). A total volume of 12.5 µl mixture was prepared for PCR, including 4.0 µl of DNA (75 ng), 1.0 µl of each of the forward and reverse primers (25 pmol), 6.0 µl master mix, and 0.5 µl PCR-grade water. Amplification was carried out in a thermal cycler (Techne, UK) under the following conditions: an initial denaturation at 95°C for 2 minutes; 35 cycles of denaturation at 95°C for 30 seconds, annealing at 50–55°C for 60 seconds, and extension at 70°C for 60 seconds; followed by a final extension at 70°C for 5 minutes.

Electrophoresis of a DNA fragment

The PCR products were first separated by electrophoresis on 2% agarose gel (w/v) prepared in 1X TBE buffer stained with ethidium bromide (0.5 µg/mL), and run at 100 V for 45 minutes. If DNA fragments were detected on the agarose gel, the PCR products were further separated on 8% non–denaturing polyacrylamide gel (29:1 acrylamide:bisacrylamide) in 1X TBE buffer, electrophoresed at 150 V for 2 hours.. The electrophoresis results were visualized and photographed using the WGD-30 WiseDoc Gel Documentation (Daihan Scientific, South Korea). DNA bands were then analyzed for allele identification, band intensity, and fragment size (in base pairs) using Total Lab software (Total Lab Ltd, UK).

Data analysis

The data generated from the microsatellite-genotyping of the goat breeds were used to calculate the number of alleles (*No*) per locus per breed and the observed heterozygosity (*Ho*) and effective number of alleles (*Ne*). The expected heterozygosity (*He*) within-breed was estimated according to Ott [20] polymorphic information content (*PIC*) was estimated according to Botstein et al. 21], the neutrality D value was estimated according to Tajima [22], and genetic distance was estimated by Nei [23].

Results

Genome diversity

In this study, eight microsatellite markers (SRCRSP1, SRCRSP2, SRCRSP3, SRCRSP5, SRCRSP6, SRCRSP7, SRCRSP9, SRCRSP10) were used for the analysis of 36 individuals from three goat populations (Boar, Damascus as parent populations, and crossbred population). Table (2) presents information on the detected microsatellite alleles at the different loci for the two breeds and their crossbreeds. The results revealed that all the studied microsatellite loci were multi-allelic and polymorphic. The breeds varied in the observed number of microsatellite alleles (No) found in different loci. The mean observed number of alleles, overall loci, was 10.38, 8.88 and 10.25 alleles in Boar, Damascus, and crossbred goats, respectively. The locus SRCRSP3 was the richest in alleles; hence, it had up to 17 and 18 microsatellite alleles in different individuals of the Boar and crossbred populations, respectively. The effective number of alleles (Ne) also varied between different populations on different loci, with means of 8.60, 7.24 and 7.88 alleles in Boar, Damascus and crossbred, respectively. The mean number of observed alleles was found to be higher than expected which indicated the immigration of alleles in these goats. The difference between No and Ne monitors the genetic activity of the populations. The differences were larger in the crossbred population (2.38) than the parent breeds because of crossing occurred.

One way to measure genetic variation is by looking at heterozygosity. Table (3) shows both the observed (Ho) and expected (He) heterozygosity values for each genetic marker across the different goat populations.The observed heterozygosity (Ho), estimated at different microsatellite loci in the populations, was generally high. The main parameters used to evaluate genetic diversity within and across populations are He (expected heterozygosity) and gene diversity, as defined by Nei [23]. The expected heterozygosity values were notably high, ranging from 0.84 to 0.87. Heterozygosity is an important indicator of genetic variation at microsatellite loci in livestock [24].The loci SRCRSP3 and SRCRSP6 were in general highly heterozygous in goat populations. These results indicate that inbreeding was low in Boar and Damascus breeds.

Table (4) presents the Polymorphic Information Content (PIC) at the microsatellite loci in different populations. The PIC values were in general high, and accounted for 0.86, 0.81 and 0.83 in Boar, Damascus and crossbred populations, respectively. The results showed that the eight microsatellite markers were highly polymorphic and have been suggested for the analysis of genetic relationships among goat populations. The microsatellite markers were highly informative, with PIC values above 0.50, across all the populations.

Neutrality test values in the different populations at different microsatellite loci are presented in Table (5). The mean D values, overall microsatellite loci, in Boar, Damascus and crossbred were +0.29, -0.01, and -0.12, respectively. The genetic distances between the Boar, Damascus, and Crossed populations were measured across multiple loci are presented in Table (6). The results reveal varying degrees of genetic similarity and divergence, suggesting that the crossbred population inherits genetic material from both parent populations with certain loci indicating closer genetic affinity to either Boar or Damascus. The distances between Boar and Damascus vary from 0.131 to 1.961, indicating different levels of genetic divergence across loci. The Boar-Crossed distances range from 0.328 to 1.577, showing varying genetic similarity, with some loci indicating greater similarity to Boar. Meanwhile, the Damascus-Crossed distances are generally lower for some loci, such as 0.008 at SPCRSP6, suggesting a closer genetic relationship to Damascus at those loci. Overall, the Crossed population shows different levels of genetic similarity to its parent populations across loci, reflecting the diverse genetic contributions from Boar and Damascus.

Discussion

The current study investigated the genetic diversity in two goat breeds, along with their crossbred at microsatellite loci. The obtained results did not largely differ from those obtained previously, as shown by Mahmoud et al. [5] who reported findings consistent with those of the present study, indicating that all examined populations exhibited relatively high genetic diversity, as demonstrated by elevated observed (Ho) and expected (He) heterozygosity values. These results highlight the effectiveness of the selected microsatellite markers for evaluating genetic variation in goat populations. Furthermore, the reported average number of alleles was 9.222 in Ardi goats and 9.722 in Shami goats, closely matching the values obtained in our study. Also, Al-Atiyat et al., [25] found that the average allele numbers were 13, 10, 6, 12, 8, and 10 with an average of 10 alleles for six microsatellites,

in Jabali, Dhaiwi, Shami and Sahrawi goat breeds. On the other hand, Ernie-Muneerah et al. [8] reported that the overall mean of the observed number of alleles was 7.24 ± 2.24, while the mean effective number of alleles (Ne) was lower, at 4.20 ±1.8 in Katjang goat. According to Gholizadeh et al. [26], the average numbers of observed and effective alleles were 4.88 and 3.84 in Sarbisheh, 6.88 and 3.16 in Azerbaijan, 5.44 and 3.27 in Busher, and 8.55 and 3.76 across the entire population, respectively. It is generally recommended that microsatellite markers possess at least four alleles to be effective for evaluating genetic diversity and to ensure accuracy in estimating genetic distances among populations [27, 28]. Elevated heterozygosity values reflect substantial genetic diversity and a high level of genetic variation within the populations. The observed heterozygosity (Ho) values exceeded those of the expected heterozygosity (He), suggesting an excess of heterozygotes in these populations.

The high variability and heterozygosity within breeds reflect the multi-allelic nature of the loci and the ability of these microsatellite loci to differentiate between goat populations. The results in general reveal the genetic power of crossing in increasing the population fitness. As claimed by the classification of Botstein et al. [21], a microsatellite locus is considered highly polymorphic when the polymorphic information content (PIC) exceeds 0.5, moderately polymorphic when PIC ranges between 0.25 and 0.5, and lowly polymorphic when PIC is below 0.25. In a study on Anatolian Hair goats, Demiray et al. [29] reported expected heterozygosity (He) values ranging from 0.85 at locus ILSTS011 to 0.94 at loci BM1818, SRCRSP15, and DRBP1. Similarly, Kawęcka et al. [30] found that Carpathian goats in Poland exhibited considerable genetic diversity, with an average of 9.143 alleles per locus, high heterozygosity (0.764), a PIC value of 0.727 at locus SRCRSP5, and a low inbreeding coefficient. Pakpahan et al. [31] noted that the Gembrong goat population displayed moderate levels of observed allele numbers, expected heterozygosity, and PIC. The observed and expected heterozygosity values obtained in our study closely align with those reported in Taiwan Black goats [32],

Egyptian goats [33], and Spanish Guadarrama goats [34]. High heterozygosity values are indicative of substantial genetic diversity and variability within populations. Gholizadeh et al. [26] reported observed heterozygosity values ranging from 57% to 67% in Azerbaijan and Sarbisheh goat populations, respectively. The relatively high Ho values across most loci could be attributed to factors such as large population sizes and low selection pressure. These findings suggest considerable genetic polymorphism among populations, as reflected by allele numbers per locus and heterozygosity measures [28]. In Taiwan Black goats, Lai et al. [32] reported an average PIC of 0.747 ± 0.103. Ramamoorthi et al. [35] found that PIC values in Barbari goats ranged from 0.5563 to 0.8348 using 21 microsatellite markers. Likewise, El-Sayed et al. [7] recorded a high PIC of 0.791 for SRCRSP8 and a low of 0.375 for SRCRSP23, with most markers exceeding 0.5, except MAF70 and SPS113, in both Siwa and Farafra goat populations, findings that are in agreement with our results. Sah and Dixit [28] emphasized the importance of PIC values in assessing the informativeness of markers in genetic diversity studies. Based on the criteria established by Botstein et al. [21], 84% of the markers evaluated in their study were classified as highly informative (PIC > 0.5), 12% as moderately informative (0.25 < PIC < 0.5), and only 4% as slightly informative (PIC < 0.25), underscoring their suitability for genetic diversity assessments and linkage mapping in goat populations.

Despite the comprehensive assessment of genetic diversity using microsatellite markers, this study is limited by its relatively small sample size. Future research incorporating a larger population size and high-throughput genotyping platforms such as SNP arrays or whole-genome sequencing would provide deeper insights into the genetic architecture of these goat populations.

Conclusion

This study demonstrates that microsatellite markers are highly effective for assessing genetic diversity in Boer, Damascus, and their crossbred goat populations, revealing substantial polymorphism and high heterozygosity across all examined loci. Crossbreeding between Boer and Damascus goats enhances genetic variation and population fitness, supporting its use as a strategy for improving meat and milk production. These findings provide a foundation for future research to link genetic diversity with phenotypic traits, aiding in the

development of targeted breeding and conservation programs for goat populations.

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Declaration of Conflict of Interest

The authors declare that there is no conflict of interest.

Ethical of approval

All experimental protocols were reviewed and approved by the Medical Research Ethics Committee of the National Research Centre under approval number 07420124.

TABLE 1. The molecular information of microsatellite primers.

	Locus	Ch.	Primer sequences (5' - 3')	Melting temperature (○C)
1	**SRCRSP1**	13	F- TGCAAGAAGTTTTTCCAGAGC R- ACCCTGGTTTCACAAAAGG	50
2	**SRCRSP2**	22	F- TGCTGTATCCTGTGTAATATCTT R- GCATAAACAGATTATTGTGATGAT	52
3	**SRCRSP3**	10	F- CGGGGATCTGTTCTATGAAC R- TGATTAGCTGGCTGAATGTCC	55
4	**SRCRSP5**	21	F- GGACTCTACCAACTGAGCTACAAG R- TGAAATGAAGCTAAAGCAATGC	53
5	**SRCRSP6**	19	F- CATAGTTCATTCACAATATGGCA R-CATGGAGTCACAAAGAGTTGAA	52
6	**SRCRSP7**	6	F- TCTCAGCACCTTAATTGCTCT R- GGTCAACACTCCAATGGTGAG	55
7	**SRCRSP9**	12	F- AGAGGATCTGGAAATGGAATC R- GCACTCTTTTCAGCCCTAATG	58 or 50
8	**SRCRSP10**	8	F- ACCAGTTTGAGTATCTTGCTTGGG R- AGGAAGTTTATTGGACAGTGCTGG	

TABLE 2. The allele diversity in different microsatellite loci

	Boar			***Damascus***			***Crossbred***		
locus	N_o	N_e	**diff**	N_o	N_e	**Diff**	N_o	N_e	**Diff**
SRCRSP1	11	9.4	1.6	10	6.9	3.1	13	8.9	4.1
SRCRSP2	6	4.6	1.4	5	4.2	0.8	5	3.5	1.5
SRCRSP3	17	14.3	2.7	13	10.6	2.4	18	13	5.0
SRCRSP5	12	9.8	2.2	11	8.3	2.7	12	9.1	2.9
SRCRSP6	11	9.9	1.1	11	10.7	0.3	11	10.4	0.6
SRCRSP7	8	5.4	2.6	4	2.7	1.3	5	4.4	0.6
SRCRSP9	11	8.9	2.1	10	8.2	1.8	11	7.3	3.7
SRCRSP10	7	6.5	0.5	7	6.3	0.7	7	6.4	0.6
Mean	10.38	8.60	1.78	8.88	7.24	1.64	10.25	7.88	2.38
SE	1.22	1.09	0.27	1.13	1.00	0.36	1.57	1.11	0.63

N_o and N_e indicates number of alleles and effective number of alleles, respectively.

TABLE 3. The observed heterozygote (H_o) and expected heterozygote (H_e) at different microsatellite loci

Locus	Boar		Damascus		Crossbred	
	H_o	H_e	H_o	H_e	H_o	H_e
SRCRSP1	1.00	0.89	1.00	0.86	1.00	0.89
SRCRSP2	1.00	0.78	1.00	0.76	1.00	0.71
SRCRSP3	1.00	0.93	1.00	0.91	1.00	0.92
SRCRSP5	1.00	0.90	1.00	0.88	1.00	0.89
SRCRSP6	1.00	0.90	1.00	0.91	1.00	0.90
SRCRSP7	0.83	0.82	0.83	0.63	0.80	0.78
SRCRSP9	1.00	0.89	1.00	0.88	1.00	0.86
SRCRSP10	1.00	0.85	1.00	0.85	1.00	0.84
Mean	0.98	0.87	0.98	0.84	0.98	0.85
SE	0.02	0.02	0.02	0.03	0.03	0.03

TABLE 4. Polymorphic information content (*PIC*) at different microsatellite loci

locus	Genotype		
	Boar	**Damascus**	**Crossbred**
SRCRSP1	0.88	0.84	0.88
SRCRSP2	0.75	0.72	0.67
SRCRSP3	0.93	0.90	0.92
SRCRSP5	0.89	0.87	0.88
SRCRSP6	0.89	0.90	0.90
SRCRSP7	0.79	0.56	0.75
SRCRSP9	0.88	0.86	0.83
SRCRSP10	0.83	0.82	0.82
Mean	0.86	0.81	0.83
SE	0.02	0.05	0.03

TABLE 5. Neutrality (D) values in different microsatellite loci in the goat populations

locus	Neutrality (D)		
	Boar	**Damascus**	**Crossbred**
SRCRSP1	+1.310	-0.777	-0.612
SRCRSP2	-0.520	-0.590	-0.950
SRCRSP3	+0.260	+1.642	+1.650
SRCRSP5	-0.764	+0.890	+0.977
SRCRSP6	+0.759	+0.494	-0.550
SRCRSP7	+0.03	-0.92	-0.034
SRCRSP9	+1.116	-0.68	-1.00
SRCRSP10	+0.111	-0.169	-0.433
Mean	0.29	-0.01	-0.12
SE	0.26	0.33	0.34

TABLE 6. Genetic distance values Across Multiple microsatellite loci in the goat populations

Locus	Boar vs. Damascus	Boar vs. Crossed	Damascus vs. Crossed
SPCRSP1	0.636	0.884	0.786
SPCRSP2	0.131	0.426	0.094
SPCRSP3	0.485	0.338	0.364
SPCRSP5	0.701	0.494	0.494
SPCRSP6	0.145	0.328	0.008
SPCRSP7	1.961	1.577	1.203
SPCRSP9	0.491	0.736	0.807
SPCRSP10	1.619	1.061	1.139

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تقييم التنوع الوراثي لسلالتين من الماعز وهجينهما باستخدام علامات الميكروساتلايت

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الملخص

تلعب الماعز دورًا اقتصاديًا هامًا في الدول النامية. علاوة على ذلك، يتزايد دورها في تعزيز العوائد الاقتصادية في الدول المتقدمة باطراد. يُعدّ التزاوج بين سلالات الماعز الأصيلة أسلوبًا تربية مناسبًا لإنتاج سلالات مهجنة تتميز بأوزان ثقيلة وإنتاجية عالية من الحليب، مقارنةً بالماعز المحلي غير المُحسّن. حللت هذه الدراسة ٣٦ ماعزًا من ثلاث سلالات مختلفة باستخدام ثمانية علامات ميكروساتلايت. شمل مخطط التهجين سلالتين نقيتين من الماعز عاليتي الإنتاجية (البوير والدمشق)، حيث تم إجراء التزاوج بين ذكور البوير وإناث الدمشقي لإنتاج السلالة المهجنة. كشف تحليل علامات السواتل الدقيقة أن إجمالي عدد الأليلات يتراوح من ٧١ إلى ٨٢، بمتوسط ٧٨,٧ أليل لكل موضع. أظهرت المجموعة المهجنة أعلى عدد من الأليلات في موضعSRCRSP3 ، بـ ١٨ أليل، بينما كان لدى مجموعة دمشق أقل عدد في موضعSRCRSP7 ، بـ ٤ أليلات فقط. في جميع مجموعات الماعز التي تمت دراستها، تجاوز عدد الأليلات المرصودة القيم المتوقعة، مما يشير إلى إدخال أليلات جديدة من خلال تدفق الجينات. كان الفرق بين أعداد الأليلات المرصودة (لا) والأليلات الفعالة (Ne) أكثر وضوحًا في الماعز المهجنة (٢,٣٨)، ويعزى ذلك إلى تأثيرات التهجين. علاوة على ذلك، كان التغاير الزيجوتي الملحوظ (Ho) أعلى باستمرار من التغاير الزيجوتي المتوقع(He) ، مما يشير إلى وجود فائض من المتغايرين الزيجوتيين ضمن هذه المجموعات المدروسة. يعكس ارتفاع التغاير الزيجوتي ضمن السلالات الطبيعة متعددة الأليلات للمواقع الجينية وقدرة هذه المواقع الجينية الدقيقة على التمييز بين مجموعات الماعز. كان محتوى المعلومات متعدد الأشكال (PIC) مرتفعًا بشكل عام، وبلغ ٠,٨٦ و٠,٨١ و٠,٨٣ في مجموعات الخنزير البري والدمشقي والهجين، على التوالي. تكشف النتائج بشكل عام عن القوة الوراثية للتزاوج في زيادة لياقة المجموعة.

الكلمات الدالة: الماعز، التنوع الجيني، الهجين، علامات التوابع الدقيقة.