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Genetic Diversity in Egyptian Goats Based on Microsatellite Markers

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Abstract

Genetic characterization of goat breeds and populations in Egypt is essential for conservation strategy as well as for genetic improvement. The aim of this study was to determine the genetic diversity of goat breeds and population in Egypt using microsatellite markers for proper utilization in breeding program. Six microsatellite markers (TCRVB6, BM6444, ETH10, TGLA53, McM527 and CSRD247) were used for the analysis of 56 goat individuals from four local goat genotypes. The number of alleles per locus ranged from 3 (loci TGLA53 and CSRD247) to 8 (locus ETH10). Allele size of the six loci (TCRVB6, BM6444, ETH10, TGLA53, McM527 and CSRD247) ranged from 210-294, 130-262, 148-239, 128-160, 152-203 and 210-244 bp in Baladi, Zaraibi, Demusces and Farafra goats breeds, respectively. The average values of observed heterozygosity were 0.155, 0.211, 0.100 and 0.222 in Baladi, Zaraibi, Demusces and Farafra goats, respectively. The average values of expected heterozygosity were 0.619, 0.658, 0.431 and 0.632 in Baladi, Zaraibi, Demusces and Farafra goats, respectively. Population fixation indices were Fst = 0.2148 referring to the highest variation among individuals within populations while, Fit = 0.754 referring to differences the lowest in variation of within individuals. A pair wise difference among Baladi, Zaraibi, Demusces and Farafra goats was recorded (0.6863) among populations F index (Fis). Moreover, five specific alleles were observed in Baladi goat breed and Farafra goat population. The suggesting alleles as genotype fingerprint (even it was one allele for one locus) could be used for the differentiation between the goats.

Keywords: genetic diversity, Egyptian goat breeds, populations, microsatellite markers

1. Introduction

Egypt has predominantly Desert and arid and semi-arid rangelands and can be divided into 4 major physical regions; the Nile Valley and Delta, Western Desert, Eastern Desert and Sinai Peninsula. The New Valley Oases (El-Kharga, El-Dakhla, El-Farafra and Siwa) in the Western Desert are geographically isolated regions.

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There are 3.13 million goats raised mainly in three regions: the Nile Delta, Upper Egypt and in the desert rangelands, particularly in the north-west coastal zone. Production systems and breeds in the three zones are different. There are about 700,000 goats in the Nile Delta, where agriculture is very intensive. In Upper Egypt, which is characterized by mild, dry winters and very hot summers, agriculture is less intense. There are about 1.7 million goats, mainly in mixed flocks, with some goats kept as household animals. In the desert rangelands, 1.4 million sheep and goats are kept in extensive systems [1]. In 2007 there are 3.920 million goats in Egypt [2]. The Egyptian goats are classified into several breeds differing in color, size, and other morphological features, such as Zaraibi, Baladi, Sinawi or Bedouin, Barki and Saidi [3].

The majority of Egyptian goats belong to the Baladi breed, which is distributed all over the Nile valley and Delta region. Barki goats are found throughout the coastal zone of the Western Desert. Zaraibi goats are a prolific breed with dairy potential and they have shown encouraging response to selection for dairy production while maintaining their high prolificacy. Their milk production is, on average, 249 kg in a lactation period of 210 days. Saidi and Wahati goats are concentrated in the southern region. Black Sinai goats can be found only in the Negev and Sinai deserts. In 2012 there are 4,207,400 goats in Egypt [4].

One of the most important of them is the Zaraibi or Egyptian Nubian breed that reared mainly for milk production. It is characterized based on a good prolificacy, i.e. litter size [1, 5]. The Damascus goat, also known as Shami, is a native breed of Syria and other Near East countries. The Damascus goat has a reddish brown coat colour consisting mostly of long hair, the ears are long and an adult live weight of about 65±5 kg for the female and 75±5 kg for the male [6]. Goat genetic improvement schemes in Egypt have involved crossbreeding trials with examples Damascus goats and the development of local breeds, in which the Zaraibi breed has been a recent target of joint work with the Food and Agriculture Organization of the United Nations (FAO**)** [7].

Molecular methods have also provided new markers such as microsatellites (i.e. highly polymorphic DNA simple sequence repeats; SSRs) for the study of genetic variation and evolutionary relationships of closely related populations [8-13]. Therefore, they are expected to show a large amount of genetic diversity in adapting to the varying ecosystems. So far, the goat diversity has been studies based on microsatellites because of their high degree of polymorphism, random distribution across the genome and neutrality with respect to selection [14].

The aim of this study was to determine the genetic diversity of some Egyptian goat genotypes (Baladi, Zaraibi, Demusces and Farafra) using microsatellite markers for proper utilization in breeding program.

2. Materials and Methods

2.1 Sample Collection and DNA Extraction

A total of 56 goats of three breeds and one population: Baladi (n=18), Zaraibi (n=13), Damascus (n=5) and Farafra (n=20) were used in the study. Blood samples were collected from Baladi, Zaraibi and Damascus goat breeds located in the Faculty of Agriculture, Al-Azhar University and from Farafra goat population located in El-Farafra oases in the Western Desert of Egypt. DNA isolation was carried out according to the salting out method. The method described by Sambrook *et al.* [15] was used for DNA extraction and purification, the extraction was usually performed in two successive days as follows: DNA was freshly extracted from whole collected EDTA-blood. Two ml of lysis buffer (20 mM Tris-HCl pH 7.6, 640 mM sucrose, 2% Triton X-100, 10 mM MgCl2) was added to the aliquot. The mixture was centrifuged and the pellet suspended in 150 µl Proteinase K, 1.5 ml nuclei lysis buffer and 110 µl SDS 20%. After overnight incubation at 37◦ C, the proteins K were removed by NaCl 6M and the DNA were precipitated by ice cold absolute ethanol. Extracted DNA was diluted with sterilized water in ratio 5:495µl before the optical

density (OD), that is, purity and concentration of each DNA were carried out with the use of ultra violet spectrophotometer.

2.2 Microsatellite Markers and PCR Conditions

Six microsatellite primer pairs were studied and detailed information on these markers is presented in Table 1. The microsatellite primers were selected based on recommended for biodiversity studies by Food and Agriculture Organization [16, 17].

The PCR reaction included: 50 ng template DNA, 10 pmol from each primer, 10µl Master Mix (PCR Master Mix, Takara Bio. Inc. composed of DNA polymerase, optimized reaction buffer, dNTPs and a density reagent. The PCR reactions were carried out under the following conditions: an initial denaturation step for 2 minute at 94°C, followed by 35 cycles of denaturation for 60 seconds at 94°C; annealing temperatures (55-65ºC) for 60 seconds at optimized primer annealing temperatures as shown in Table 1. Extension for 60 seconds at 72°C and final extension step at 72°C for 5 minutes. The samples were mixed with sequencing loading buffer (15µl from the PCR product + 7 µl loading dye). The mixture was loaded on the vertical electrophoresis; a 501 bp DNA size marker (puc19) was loaded and run at the same time. The run lasted for 5 hrs, at 160Volt, 25mA. Amplified fragments were analyzed on a 10% polyacrylamide gel and stained with Ethidium bromide. The gel was photographed and the Image analyzed using Gel Documentation System (Alphaimager TM 2200, Cell Biosciences).

2.3 Statistical analyses

Gels were visualized and scored with Alphaimager 2200 software Version 4.0.1. All scored microsatellite data was first adjusted using a Tandem Repeat Analyzer software package to estimate each allele size according to its number of repeats for each marker. Then, a spread sheet program (Microsoft Excel) was used to arrange the data for each genotypes regarding each locus. Data was analyzed employing the Arlequin 3.11 software package after data conversion using CONVERT program. POPGENE software package [18] was used to calculate allele frequencies; observed, expected heterozygosity, number of alleles and create the phylogenetic tree [19].

3. Results and Discussion

In the present study, a set of six microsatellite markers listed in Table 1 was used for the analysis of 56 individuals from four local goat genotypes. The results of microsatellite-markers analysis showed that the total number of alleles was 32, and the largest number of alleles was found at locus ETH10 (8) and the smallest one at loci TGLA53 and CSRD247 (3), with an average of 5.33 alleles per locus (Table 2). The allele numbers of four goat genotypes were lower than those were reported for Farafra and Siwa Egyptian goat populations with 10 microsatellite markers [20], Chinese goats with 30 microsatellite markers [21], Mongolian goat populations with 14 microsatellite markers [22] and Ardi goat with 14 microsatellite markers [23].

Table 1. Information on microsatellite markers used in the study.

Locus Name	Access No[1]	Location[1]	Forward primer[1]	Reverse primer[1]	Repeat type[1]	Ta[2]	STS Size[3] (bp)
TCRVB6	L18953	BTA10	GAGTCCTCAGCAAGCA GGTC	CCAGGAATTGGATCACA CCT	(GT) 12	55	217-255
BM6444	G18444	BTA2	CTCTGGGTACAACACTGA GTCC	TAGAGAGTTTCCCTGTCC ATCC	(GT)22	65	118-200
ETH10	Z22739	CHI5	GTTCAGGACTGGCCCTGC TAACA	CCTCCAGCCCACTTTCTC TTCTC	(TA)13	55	200-210
TGLA53	---	BTA16	GCTTTCAGAAATAGTTTG CATTCA	ATCTTCACATGATATTAC AGCAGA	(TG)16	55	126-160
McM527	L34277	OAR5	GTCCATTGCCTCAAATCA ATTC	AAACCACTTGACTACTCC CCAA	(AT)17	58	165-187
CSRD247	---	OAR14	GGACTTGCCAGAACTCTG CAAT	CACTGTGGTTTGTATTAG TCAGG	(AC)17	58	220-247

1. Gene bank accession number; www.ncbi.nlm.nih.gov/. http://www.ncbi.nlm.nih.gov/genome/sts/sts.cgi?uid=280100
2. Annealing temperature, [16, 17]
3. STS: Sequence tagged site size according to [16, 17]

The number of alleles ranged from 3 (loci TGLA53, McM527 and CSRD247) to 6 (locus BM6444) in Baladi goat breed. While, Zaraibi goat breed ranged from 2 (locus TGLA53) to 5 (locus TCRVB6) and from 1 (locus CSRD247) to 4 (locus ETH10) in Damascus goat breeds and from 2 (loci BM6444 and TGLA53) to 6 (loci TCRVB6 and ETH10) in Farafra goat population (Table 2). The numbers of alleles of the four goat genotypes were lower than those reported for the South African Angora goats [24], Malaysian Goat Breeds [25] and Salem Black goat breed [26].

Table 2. Specific alleles, common alleles and total number of alleles for Baladi, Zaraibi, Damascus and Farafra goat genotypes.

Markers	no. of alleles per genotypes				no. of specific alleles				Common alleles	Total no. of alleles
	Baladi	Zaraibi	Damascus	Farafra	Baladi	Zaraibi	Damascus	Farafra		
TCRVB6	4	5	3	6	0	0	0	0	7	7
BM6444	6	4	2	2	2	0	0	0	5	7
ETH10	4	3	4	6	0	0	0	3	5	8
TGLA53	3	2	2	2	0	0	0	0	3	3
McM527	3	4	2	3	0	0	0	0	4	4
CSRD247	3	3	1	3	0	0	0	0	3	3
Total	23	21	14	22	2	0	0	3	27	32
means	3.83	3.50	2.33	3.67	2	0	0	3	4.50	5.33

The mean number of observed alleles per locus in Baladi (3.83), Zaraibi (3.50), Damascus (2.33) and Farafra (3.67) goatgenotypes was lower compared to the mean number of alleles per locus reported for Katjang (5.43), Jamnapari (5.70), Boer (5.90) and Savanna (5.70) goat breeds and respectively) by Marini *et al.* [27].

Common and specific alleles for Baladi, Zaraibi, Damascus and Farafra were shown in Table 2. A total of 27 common alleles were detected versus six microsatellite loci overall genotypes. Regarding specific alleles, a total of 5 out of 32 alleles (15.63 %) were noticed in overall loci for the two genotypes studied. For Baladi and Farafra goats, 2 specific alleles were observed in Baladi breed while 3 ones were obtained in the case of Farafra goat population. Consequently, these specific alleles would be utilized as breed fingerprint even one allele for one locus. El-sayed *et al.* [20] reported that the total of specific alleles was 20 out of 42 alleles (47.62%) of 10 microsatellite markers in Farafra (8) and Siwa (12) with common alleles were 22.

The mean of observed heterozygosity was lower than the mean of expected

heterozygosity for the four goat genotypes. The means of observed heterozygosities in Baladi, Zaraibi, Damascus and Farafra were 0.155, 0.211, 0.100 and 0.222, respectively. The values were lower than the mean of expected heterozygosity for the four goat genotypes in this study. The Damascus goats showed the lowest observed heterozygosity suggesting higher level of inbreeding in this breed compared with the other breeds. The high level of inbreeding in both populations studied was confirmed by the inbreeding coefficient (IC) which was estimated as (0.75), (0.68), (0.77) and (0.65) in Baladi, Zaraibi, Damascus and Farafra goat genotypes, respectively as shown in Table 3. Similar to the present study, the observed heterozygosities of Farafra and Siwa Egyptian goat populations were lower than the expected heterozygosities [20]. High heterozygosity values indicate high genetic diversity as well as a high degree of genetic variation. The means of expected heterozygosities in Baladi, Zaraibi, Farafra and Damascus were 0.619, 0.658, 0.632 and 0.431, respectively. Similarly, Araújo [28] reported 0.6952 for Alpine, 0.7043 for Saanen and 0.4984 for Moxotó goat populations.

Table 3 showed that all loci found positive FIS values. These positive values indicate heterozygote deficit with a mean Fis value of 0.699. Thus, the results of Fis, together with the low number of alleles indicate the occurrence of inbreeding in all four goat breeds. A positive Fis value indicates an excess of homozygotes, while a negative value shows deficit in homozygotes [27]. The mean Fit and Fst values of 0.767 and 0.225, respectively were measured by the degree of differentiations within and among breeds. The Fst value indicates a lack of genetic differentiation among the goat breeds. The means of Fit and Fst in the present study were higher than those of the Malaysian Goat Breeds with the mean Fit and Fst values of 0.46 and 0.06, respectively [27].

Table 3. Observed heterozygosity (H_o), expected heterozygosities (H_e) and fixation indices and their means, standard deviation estimated for each genotypes.

	Ho				He				Fis	Fit	Fst
	Baladi	**Zarail**	**Damascu**	**Farafra**	**Baladi**	**Zaraib**	**Damascus**	**Farafra**			
TCRVB6	0.0000	0.1429	0.0000	0.0000	0.7273	0.8022	0.6222	0.8205	0.9492	0.9579	0.1717
BM6444	0.0000	0.1667	0.0000	0.0000	0.7632	0.6232	0.4286	0.4762	0.9232	0.9453	0.2878
ETH10	0.6471	0.2000	0.6000	0.6842	0.7362	0.6889	0.6444	0.8122	0.2122	0.3187	0.1352
TGLA53	0.0556	0.0909	0.0000	0.0500	0.6429	0.4545	0.3556	0.4500	0.8919	0.9225	0.2834
McM527	0.1667	0.6667	0.0000	0.6000	0.2556	0.7059	0.5333	0.5731	0.2664	0.4564	0.2590
CSRD247	0.0588	0.0000	0.0000	0.0000	0.5900	0.6737	0.0000	0.6615	0.9683	0.9759	0.2390
Mean	**0.155**	**0.211**	**0.100**	**0.222**	**0.619**	**0.658**	**0.431**	**0.632**	**0.699**	**0.767**	**0.225**
St. Dev	0.2488	0.2338	0.2449	0.3268	0.1896	0.1157	0.2384	0.1611			
IC	**Baladi**	**0.750**									
	Zaraibi	**0.68**									
	Damascus	**0.77**									
	Farafra	**0.65**									

IC: inbreeding coefficient. ($IC= (H_E- H_O)/H_E$)
St. Dev: Standard Deviation

Analysis of molecular variance (AMOVA) of Baladi, Zaraibi, Damascus and Farafra goat genotypes based on microsatellite DNA variation showed that the majority of the genetic diversity presented among individuals within populations (53.88%) and within individuals (24.63%) (Table 4). Population fixation indices give an idea about the genotype structure in terms of inbreeding coefficient and population differentiation. Population fixation indices revealed a 0.7537 of variation referring to differences among individuals versus total variance (Fit). While, the fixation index among population differences versus total variance was the lowest (Fst = 0.2148) indicating low level of population differentiation. A pair wise difference among Baladi, Zaraibi, Damascus and Farafra goat genotypes was 0.6863 based on breeds F index (Fis) as shown in Table 5. Our

results are in agreement with El-sayed *et al.* [20] reported the fixation index values (Fit =0.7063), (Fst = 0.2371) and (Fis = 0.6151) of Farafra and Siw goat populations. Also, our results are higher than the Fis values (0.044, 0.066, 0.032, 0.082, 0.064, 0.034, 0.045 and 0.069) obtained from Zavkhan Buural, Ulgii Red, Bayandelger, Zalaajinst White, Sumber, Erchim Black, Dorgon and Gobi Gurvan Saikhan Mongolian goat populations, respectively as reported by Takahashi *et al.* [22]. Thiruvenkadan *et al.* [26] reported that the value of Fis was 0.233 for Salem Black goat population.

Table 4. ANOVA analysis of Baladi, Zaraibi, Damascus and Farafra goat genotypes on microsatellite DNA variation

Source of variation	d.f.	S .S.	Percentage variation	Fixation indices
Among populations	3	19.020	21.48	Fis = 0.6863
Among individuals within populations	52	62.382	53.88	Fst = 0.2148
Within individuals	56	12.500	24.63	Fit = 0.7537
Total	111	93.902	----	----

F_{IS}: Fixation indices (Among populations)
F_{ST}: Fixation indices (Among individuals within populations)
F_{IT}: Fixation indices (Within individuals)

Allele size in base pair, their frequencies for each locus, average of allele frequencies and polymorphism information content (PIC) values for each locus per genotype as observed are showed in Table 5. Allele sizes of the six loci (TCRVB6, BM6444, ETH10, TGLA53, McM527 and CSRD247) ranged from 210-294, 130-262, 148-239, 128-160, 152-203 and 210-244 bp, respectively in Baladi, Zaraibi, Demusces and Farafra goats breeds and these results were in agreement with the selective standard of the microsatellite loci [17].

The highest allele frequency for overall loci was 1.00 for allele 244 at locus CSRD247 in the case of Damascus goat breed. While, the lowest one was 0.0500 associated with Farafra goat population at locus TCRVB6 (for alleles 210 and 240). The highest average of allele frequency estimated was (1.00) for Damascus goat breed at locus CSRD247. On the other hand, the lowest one was 0.17 in the case of loci TCRVB6 and ETH10 for Farafra goat population and locus BM6444 for Baladi breed. El-sayed *et al.* [20] reported that allele frequency ranged from 0.053 at loci ILSTS029 (for allele 135) and SRCRSP8 (for alleles, 170 and 266) to 0.750 for allele 87 at locus SRCRSP23 in Siwa goat population. Four of the 18 microsatellite markers (MAF65, ILSTS87, ILSTS5 and INRA5) analyzed had an allele with a relatively high frequency (0.64 to 0.82) in South African Angora goats [24].

The polymorphism information content (PIC) is a parameter indicative of the degree of informativeness of a marker. According to classification of Botstein *et al.* [29], the highly informative markers have PIC values >0.50, the reasonably informative markers have PIC value between 0.25-0.50 and the slightly informative markers have PIC value <0.25. In the present study, the values of PIC of TCRVB6 for Baladi, Zaraibi and Farafra, BM6444 for Baladi and ETH10 for Baladi and Farafra exceeded 0.7 which indicated that these loci could be used as genetic markers for genetic diversity analysis of Baladi, Zaraibi and Farafra goat genotypes. Hassanane *et al.* [3] reported that the PIC of (ILSTS087) exceeded 0.7 in Egyptian Zaraibi breed. Also, El-sayed *et al.* [20] reported that the PIC of loci (SRCRSP8 and OarFCB48) exceeded 0.7 in Farafra and Siwa Egyptian goat populations. The polymorphism information content (PIC) values for all 30 microsatellite loci ranged from 0.424 (MAF 209) to 0.904 (BM6444) in Albanian Capore goat breed [30]. The overall average PIC genotypes of the six markers were 0.60, 0.62, 0.39 and 0.62 for Baladi, Zaraibi, Damascus and Farafra goat genotypes, respectively, which indicated that the six microsatellite markers contained high polymorphic loci in both Egyptian

goat genotypes. In the genetic diversity analysis, microsatellite markers with PIC>0.7 were taken as the most ideal selected markers. The majority of the loci TCRVB6, BM6444 and ETH10 were highly polymorphic information content it could be used to improve the performance of Egyptian goat populations.

Table 5. Allele size in base pair, their frequencies for each locus and genotypes, average allele frequencies and polymorphic information content (PIC) as observed in the present study.

Locus	Alleles (bp)	Frequencies				Locus	Alleles (bp)	Frequencies			
TCRVB6		**Baladi**	**Zaraibi**	**Dam-ascus**	**Farafra**	**BM6444**		**Baladi**	**Zaraibi**	**Dam-ascus**	**Farafra**
	210	0.0000	0.1429	0.6000	0.0500		130	0.0000	0.5833	0.2500	0.6429
	222	0.0000	0.3571	0.2000	0.3000		152	0.1333	0.0000	0.0000	0.3571
	234	0.0000	0.2857	0.2000	0.2000		174	0.0667	0.1667	0.7500	0.0000
	246	0.1176	0.1429	0.0000	0.0500		196	0.0667	0.0000	0.0000	0.0000
	258	0.2353	0.0714	0.0000	0.0000		218	0.2667	0.1667	0.0000	0.0000
	282	0.4118	0.0000	0.0000	0.2000		240	0.0667	0.0000	0.0000	0.0000
	294	0.2353	0.0000	0.0000	0.2000		262	0.4000	0.0833	0.0000	0.0000
Average		0.25	0.20	0.33	0.17	**Average**		0.17	0.25	0.50	0.50
PIC		0.71	0.75	0.56	0.79			0.74	0.60	0.38	0.46
ETH10	148	0.0000	0.0000	0.0000	0.1053	**TGLA53**	128	0.1667	0.0000	0.0000	0.6750
	161	0.0000	0.0000	0.0000	0.1316		144	0.4167	0.3182	0.8000	0.3250
	174	0.0000	0.0000	0.0000	0.0526		160	0.4167	0.6818	0.2000	0.0000
	187	0.0000	0.0000	0.1000	0.2895						
	200	0.2941	0.2000	0.6000	0.2632						
	213	0.3824	0.3000	0.1000	0.1579						
	226	0.1471	0.0000	0.2000	0.0000						
	239	0.1765	0.5000	0.0000	0.0000						
Average		0.25	0.33	0.25	0.17	**Average**		0.33	0.50	0.50	0.50
PIC		0.71	0.62	0.58	0.79			0.63	0.43	0.32	0.44
McM527	152	0.0556	0.1111	0.4000	0.0000	**CSRD247**	210	0.0882	0.2000	0.0000	0.4500
	169	0.8611	0.3333	0.0000	0.6000		227	0.5000	0.4000	0.0000	0.3000
	186	0.0833	0.4444	0.6000	0.2250		244	0.4118	0.4000	1.0000	0.2500
	203	0.0000	0.1111	0.0000	0.1750						
Average		0.33	0.25	0.50	0.33	**Average**		0.33	0.33	1.00	0.33
PIC		0.25	0.67	0.48	0.56			0.57	0.64	0.00	0.65
(PIC)Mean	**Baladi**	0.60									
	Zaraibi	0.62									
	Damas-cus	0.39									
	Farafra	0.62									

PIC, Polymorphic Information Content.

The standard genetic distance and the UPGMA dendrogram of the genotypes are shown in Table 6 and in Figure 1, respectively. The highest genetic distance was found between Damascus breed and Farafra population (0.9673). While, the lowest value for genetic distance was found between Baladi and Zaraibi breed (0.4383). High values for genetic identity means low values for genetic distance and vice versa. Mahrous *et al.* [14] reported the high genetic distance was found between Barki and Ardi breeds (0. 3825) and low value was found between Zaraibi and Ardi (0.2075).

Table 6. Genetic identity and genetic distance (31) for all loci and all genotypes. Nei's genetic identity (above diagonal) and genetic distance (below diagonal)

genotypes	Baladi	Zaraibi	Damascus	Farafra
Baladi	****	0.6452	0.4021	0.5940
Zaraibi	0.4383	****	0.5970	0.5836
Damascus	0.9110	0.5158	****	0.3801
Farafra	0.5208	0.5386	0.9673	****

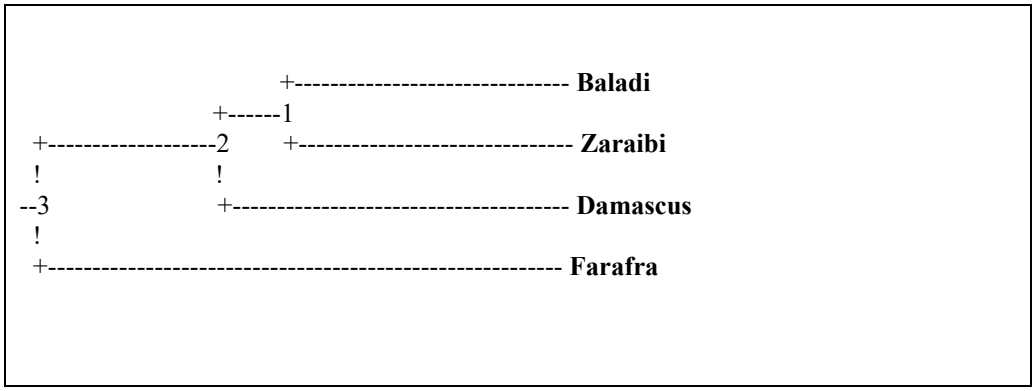

Figure 1. UPGMA dendogram generated from Nei's genetic distances of the four goat genotypes

4. Conclusions

A set of six microsatellite markers used in this study for analysis of 56 individuals from four local goat genotypes were shown as a polymorphic pattern. The primers, which used as a markers were useful for the molecular characterization of Egyptian goats. The information elucidated through the present study would be useful for the formulation of effective conservation strategies. The high level of inbreeding in both genotypes studied was confirmed by the inbreeding coefficient (IC) which was estimated as (0.75), (0.68), (0.77) and (0.65) in Baladi, Zaraibi, Damascus and Farafra goat genotypes, respectively. Among the Baladi, Zaraibi, Damascus and Farafra genotypes, moderate depicting lack of proper management plans, thus it is necessary to consider a national plan for conserving the unique genetic resources of Baladi, Zaraibi, Damascus and Farafra genotypes. The markers TCRVB6, BM6444 and ETH10 could be used in marker assisted selection (MAS) to improve the performance of Egyptian goat genotypes. The present work suggests using wide genome scan analysis based on more recommended microsatellites covering goat genome which could be further employed in MAS (marker assisted selection) and QTL (Quantitative Trait Loci) programs. In addition the present study pointed to the usefulness of evaluations of diversity using molecular markers for the choice of breeds worthy of conservation.

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