Genetic Diversity in Egyptian Goat Breeds Using Microsatellite Markers

Abdel-Samee, A. M.*; M. E. Mohamed; H. Alatreby***; M. Sherif****; M. G. Abdel-Fadiel* and M. S. Hassanane*****

* Faculty of Agriculture and environmental Science, El Arish- Suez Canal University
** Sinai University, Al-Arish, Egypt
***National Gene Bank, Agriculture Research Center, Egyptian Ministry of Agriculture
****National Cancer Institute, Cairo University
*****Department of Cell Biology, National Research Center, Dokki. Giza, Egypt

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Abstract: Eight microsatellite markers were used to investigate genetic variations among and within three Egyptian Goat breeds, Baladi, Zaraibi, and Sinawi. The Eight tested microsatellites were: (SR-CRSP5, OarFCB20, INRA063, SR-CRSP8, ILSTS87, INRA023, McM527 and ILSTS19). All markers tested were found to be polymorphic. The total observed numbers of alleles (bands) in the three breeds were 19, 16, 14, 18, 21, 17, 17 and 18 for the eight markers respectively, and polymorphism information content (PIC) was 0.873, 0.902, 0.878, 0.902, 0.876, 0.861, 0.885 and 0.881, respectively. The three breeds showed significant deviation from Hardy -Weinberg equilibrium. The genetic distance test showed that the Baladi and Zaraibi individuals had considerable mixture together while Sinawi forms a discrete group. The average gene diversity was 0.907 for all studied breeds.

Keywords: Egyptian Goat breeds; genetic variations; microsatellite markers; genetic distance; polymorphism.

INTRODUCTION

Animal breeders have been effectively using animal genetic diversity to develop breeds suitable for local environmental conditions and have animal products to meet human needs and demands. The total diversity of animal genetic resources available to farmers, and the resulting diverse products, makes it possible for animals to survive in a wide range of production environments. Genetic diversity also makes possible livestock adaptation to diseases, parasites and quality of food, water and other limiting factors. Goats are characterized by their high ability to survive and produce under variable environmental conditions as well as wide climatic zones. Although goats provide meat, hair, leather and soil manures for millions of people, they have been neglected in the past. The goat is among the earliest livestock species to have been domesticated approximately 9000 BP in Southeast Asia along the present Iran–Iraq borders (Mason, 1981). The domestic goat (*Capra hircus*) is known for its ability to thrive on paltry fodder and to withstand harsh environments. From an agricultural standpoint, the world's 700 million goats provide reliable access to meat, milk, skin, and fiber for small farmers particularly in developing countries like Egypt. Egypt is bestowed with 15% of total Egyptian animal production population; they are distributed across the country, especially dense in the Nile valley and delta and with lower concentration in the north-western coastal region and at oases (Galal *et al.,* 2005). Goats viability of living in the desert land, and its ability to climb the mountain peaks to search of food, and its ability to digest fiber, ease of care, and high production of twins they also play a role in the of development nomadic communities. Goats which live under Egyptian condition are Zaraibi (Which we are afraid of its extinction), Barki, Baladi, Wahati, and Saidi. Goats are characterized by higher reproductive efficiency compared with other farm animals, they reach puberty about 4 to 5 months for males and 5 to 6 months for females, fertility rate is very high, from the other hand, the production of twins is very high , and its pregnancy period last approximately five months. Characterization is the first step for the conservation of any genetic resource. The few well defined breeds in Egypt have been only characterized at the phenotypic level. Relationships within and between breeds can be understood only after a thorough characterization at the molecular genetic level has been undertaken. Analysis of genetic diversity as well as relationships between or within different genera, species, or even individuals is a central task for many branches of biological sciences. During the last three decades, classical strategies for evaluating genetic variability such as comparative anatomy, morphology, and embryology have been increased. In the recent years, rapid advanced development in the molecular genetic techniques have made it possible to identify differences between individuals at the DNA level and using genomic variation for the genetic improvement of livestock. The assessment of genetic variation is especially important in highly specialized livestock breeds since the use of assisted reproduction techniques, such as artificial insemination and embryo transfer can rapidly reduce the genetic variation of the population. Molecular methods have provided new markers for the study of genetic variation, even to the level of analysis at the DNA sequences itself. Molecular markers have been widely used to access this variability since they provide information on every region of the genome. Among these molecular markers, Microsatellites (highly polymorphic simple sequence repeats) are currently the most widely used molecular markers. Microsatellites have been used in studying genetic variability in all domestic species either animals, birds and even fish. Genetic variability within and among populations is often of importance and may contribute to the selection and preservation of genetic resources. Molecular genetic markers and determination of genetic differences between breeds will be helpful in the genetic breeding

programs for the improvement of productive traits such as milk and meat (Amills *et al.*, 1995). The aim of the present study is to use eight microsatellite markers for characterization and studying the genetic diversity between and within three breeds of goats raised in Egypt. These breeds are: Baladi, Nubian and Sinawi, the relationship and the purity of these breeds will be also evaluated.

MATERIALS AND METHODS

Blood sampling and DNA isolation:

Forty four blood samples were colleted from two different regions representing the three breeds under study. All blood samples were collected from unrelated animals (unknown relationship coefficient), moreover the sampled animals were phenotypically normal and healthy.

From each animal 10 ml from peripheral blood was collected from Jugular vein on a tube containing 0.5 ml from EDTA (0.5 M) as an anti-coagulant matter. The samples were transferred to the laboratory in a shadow and kept away from the direct sunlight. The samples were kept at 4 °C and processed for DNA extraction in a period not exceeds 3 days from its arrival to the laboratory. DNA was extracted from whole blood using a modified salting out procedure described by **(Boodram, 2004)**.

Microsatellites used:

The microsatellites markers used in this study were chosen according to the recommendation of International Society of Animal Genetics (ISAG) and FAO (1998) for genetic diversity studies.

PCR conditions

For conducting the PCR reaction, 20 µl was sufficient for the analysis. For facilitating the work a master mix was usually prepared first, and 18 µl from this mix were putted in the eppendorf tube and the template DNA is added then. The standard PCR run cycle was usually as: Primary denaturation: 95 °C for 3 min. then: 35 cycles as: 95 °C for 15 sec.; 55-60 °C for 30-60 sec.; 72°C for 30 sec. Final extension: 72 °C for 5 min., Storage: 15 °C forever. For optimization the PCR the temperature and the time of the annealing temperature were changed. The success of the PCR was detected by running horizontally 5 µl of the PCR product on 1.5% agarose gel electrophoresis and stained by ethidium bromide for viewing the bands on the UV transilluminator. The PCR product size was measured according to a size length DNA marker ØX174/HAE III run at the same time with the samples. A 10-12 % acrylamide is usually used; it is prepared after the methodology described in (Sambrook *et al.*, 1989). The polyacrylamide gels were stained with ethidium bromide and the images were captured using gel documentation system. The alleles sizes were determined using free software named Lab. image V2.7. It is dispersed free from Proland company (Germany) from the internet through the web page: http://www.labimaging.com/servlet/engine/home/start.html

Table (1): Details of the animal sampled and their locations

Area	Breed	No. of Samples
Sakha station in Nile Delta belongs to the Animal Production Research Institute (APRI) of Agriculture Research Center at the Egyptian Ministry of Agriculture.	**Zaraibi**	**15**
	Baladi	**16**
North of Sinai belongs to Faculty of Agricultural and Environmental science in Al Arish – Suez Canal University	**Sinawi**	**13**

Table (2): Details of The microsatellites markers used in this study

Marker name	Primer sequence	Reference
SR-CRSP05	GGA CTC TAC CAA CTG AGC TAC AAG TGA AAT GAA GCT AAA GCA ATG C	Arevalo *et al.* (1994)
OarFCB20	GGA AAA CCC CCA TAT ATA CCT ATA C AAA TGT GTT TAA GAT TCC ATA CAT GTG	Buchanan *et al.* (1994)
INRA063	GAC CAC AAA GGG ATT TGC ACA AGC AAA CCA CAG AAA TGC TTG GAA G	Vaiman *et al.*, (1994)
SR-CRSP8	TGC GGT CTG GTT CTG ATT TCA C CCT GCA TGA GAA AGT CGA TGC TTA G	Bhebhe *et al.* (1994)
ILST S87	AGC AGA CAT GAT GAC TCA GC CTG CCT CTT TTC TTG AGA G	Kemp et al. (1995)
INRA023	GAG TAG AGC TAC AAG ATA AAC TTC TAA CTA CAG GGT GTT AGA TGA ACT	Vaiman *et al.*, (1994)
McM527	GTC CAT TGC CTC AAA TCA ATT C AAA CCA CTT GAC TAC TCC CCA A	Hulme *et al.* (1994)
ILSTS19	AGG GAC CTC ATG TAG AAG C ACT TTT GGA CCC TGT AGT GC	Kemp *et al.* (1993)

Statistical analysis

POPGENE software package (Yeh *et al.,* 1999) was used to calculate allele frequencies, observed number of alleles, effective number of alleles (Kimura and Crow, 1964), observed (H_o) and expected (H_e) heterozygosity at each locus in the five populations under study. Polymorphism information content (PIC) value for each locus was calculated by using the method described by (Bostein *et al.,* 1980). Pair-wise alleles sharing were calculated manually from the raw results. Using the variance-base method of (Weir and Cockerham, 1980), population differentiation by *F*-statistics was computed using FSTAT version 2.9.3.2 computer program (Goudet, 2002). Mean a standard deviations of the *F*-statistics program, F .f, that are analogue to Wright's (1951, 1978) Fis and Fst, were obtained across breeds by the Jackknifing procedure over loci (Weir, 1990).The extent of global inbreeding was further studied with the same software by estimated Fis value. The effect of migration and gene flow on the genetic structure of the analyzed populations was estimated between each pair of populations according to an island model under neutrality and negligible mutation (Slatkin 1993). Genetic distances among populations were estimated using (Ds) standard genetic distance of Nei, 1972 and the DA distance of (Nei *et al.,* 1983).

RESULTS AND DISCUSSION

Microsatellites polymorphism:

All the microsatellites studied showed polymorphism in the three breeds. The numbers of observed alleles were (19, 16, 14, 18, 21, 17, 17 and 18) for microsatellites (SR-CRSP5, OarFCB20, INRA063, SR-CRSP8, ILSTS87, INRA023, McM527 and ILSTS19) respectively. This means that these microsatellites could be used for further studies in mapping quantitative trait loci as well as parentage testing. Details of the observed number, sizes and frequencies of microsatellite alleles are presented in Tables (3, 4, 5, 6, 7, 8, 9 and 10). Higher numbers of alleles were observed for all microsatellite if compared with the foreign breeds.

In the present study, the microsatellite SR-CRSP5 (table 3) showed a total of nineteen alleles in the three breeds under study with sizes ranging from 136 to 176 bp. Higher numbers of alleles were observed for all microsatellite if compared with the foreign breeds,(Luikart and England, 1999) & (Bruzzone *et al.,* 2004). While the microsatellite OarFCB20 (Table 4) showed a total of sixteen alleles in the three breeds under study with sizes ranging from 81 to 113 bp. Higher numbers of alleles were observed for all microsatellite if compared with the foreign breeds, (Luikart and England, 1999), (Bruzzone *et al.,* 2004) & (Martinez *et al.,* 2004). While the microsatellite INRA063 (Table 5) showed a total of fourteen alleles in the three breeds under study with sizes ranging from 143 to 169 bp. Higher numbers of alleles were observed for all microsatellite if compared with the foreign breeds, (Luikart and England, 1999), (Bruzzone *et al.,* 2004) & (Martinez *et al.,* 2004). While the Microsatellite SR-CRSP8 (Table 6) showed a total of eighteen alleles in the three breeds under study with sizes ranging from 201 to 239 bp. Higher numbers of alleles were observed for all microsatellite if compared with the foreign breeds, (Luikart and England, 1999), (Bruzzone *et al.,* 2004) & (Martinez *et al.,* 2004). While the Microsatellite ILSTS87 (Table 7) showed a total of twenty-one alleles in the three breeds under study with sizes ranging from 123 to 167 bp. Higher numbers of alleles were observed for all microsatellite if compared with the foreign breeds, (Bruzzone *et al.,* 2004), (Thilagam *et al.,* 2006) (Shadma *et al.,* 2008) & (Ramamoorthi *et al.,* 2009).

Table (3): The observed allele sizes of the SR-CRSP5 microsatellite marker and their frequencies in each breed.

Allele number	Allele Size (bp)	Allele frequencies			
		Baladi	Zaraibi	Sinawi	All the breeds
1	136	0.21	0.17	0.00	0.13
2	138	0.25	0.21	0.00	0.15
3	140	0.13	0.08	0.00	0.07
4	144	0.00	0.04	0.00	0.01
5	146	0.04	0.14	0.18	0.12
6	148	0.00	0.08	0.08	0.05
7	150	0.00	0.08	0.18	0.09
8	152	0.00	0.08	0.08	0.05
9	154	0.13	0.04	0.04	0.07
10	156	0.08	0.08	0.00	0.05
11	160	0.04	0.00	0.04	0.03
12	162	0.04	0.00	0.00	0.01
13	164	0.00	0.00	0.04	0.01
14	166	0.00	0.00	0.04	0.01
15	168	0.08	0.00	0.00	0.03
16	170	0.00	0.00	0.04	0.01
17	172	0.00	0.00	0.04	0.01
18	174	0.00	0.00	0.12	0.04
19	176	0.00	0.00	0.12	0.04

While The Microsatellite INRA023 (Table 8) showed a total of seventeen alleles in the three breeds under study with sizes ranging from 183 to 215 bp. Higher numbers of alleles were observed for all microsatellite if compared with the foreign breeds, (Bruzzone *et al.*, 2004), (Martinez *et al.*, 2004) & (Traoré *et al.*, 2009). While the microsatellite McM527 (Table 9) showed a total of Seventeen alleles in the three breeds under study with sizes ranging from 125 to 157 bp. Higher numbers of alleles were observed for all microsatellite if compared with the foreign breeds, (Bruzzone *et al.*, 2004) & (Martinez *et al.*, 2004). While the microsatellite ILSTS19 (Table 10) showed a total of eighteen alleles in the three breeds under study with sizes ranging from 131 to 167 bp. Higher numbers of alleles were observed for all microsatellite if compared with the foreign breeds, (Bruzzone *et al.*, 2004), (Thilagam *et al.*, 2006) (Shadma *et al.*, 2008) & (Ramamoorthi *et al.*, 2009).

Observed and expected heterozygosity

The observed average heterozygosity for all populations was higher than the expected heterozygosity, except for the Baladi breed (Table 11). The heterozygosity is an appropriate measure of genetic variability within a population because genetic diversity can be measured as the amount of actual or potential heterozygosity. The observed heterozygosity for the eight microsatellite in the three breeds studied showed a high heterozygosity values. The heterozygosity in Baladi ranged from 0.563 (INRA023) to 0.929 (INRA063). The average observed heterozygosity in Baladi goat breed was 0.768. In Zaraibi goat the observed heterozygosity ranged from 0.800 (OarFCB20) to 1.00 (INRA023), (McM527) and (ILSTS19). The average heterozygosity in Zaraibi goat breed was 0.921. The average heterozygosity in Sinawi goat breed was 0.941. The average heterozygosity across the breeds was found to be 0.876 with maximum heterozygosity observed for OarFCB20, SR-CRSP8, INRA023, McM527 and ILSTS19 (1.00) and minimum heterozygosity observed for locus INRA023 (0.563). The observed and expected heterozygosity obtained in the study are comparable with the earlier studies in Chinese goat breeds, 0.777 to 0.823 (Yang *et al.*, 1999). However, lower heterozygosity values (0.351 and 0.671) were reported for bovine and ovine microsatellite markers in Korean and Chinese goats (Kim *et al.*, 2002). The higher observed heterozygosity values have resulted in instability of the population at the majority of microsatellite loci studied. Because of higher heterozygosity and consequent non-fixation of alleles at these loci, there is further scope for improvement of the breed. The information elucidated through the present study would be useful for the formulation of effective conservation strategies and identification of quantitative trait loci for marker-assisted selection. These values indicate an important level of genetic variability for the breed considering its endangered state. The high values of heterozygosity in the breeds under study which over 0.5 indicates that the breeds evaluated are not pure (Shadma *et al.*, 2008), it is also an indicator for the absence of good selection or breeding programs. The PIC is an expected heterozygosity derived from allele frequencies in a random mating breed. PIC is an indicator of how many alleles a certain marker has how much these alleles divided evenly. For example if a marker has many alleles but only one of them is frequent, the PIC will be low. PIC values were generally high and varied from 0.824 (SR-CRSP5) in Baladi breed to 0.902 (OarFCB20) & (SR-CRSP8) in Sinawi breed.

Table (4): The observed allele sizes of the OarFCB20 microsatellite marker and their frequencies in each breed.

Allele number	Allele Size (bp)	Allele frequencies			
		Baladi	Zaraibi	Sinawi	All the breeds
1	81	0.10	0.00	0.00	0.03
2	83	0.10	0.07	0.14	0.10
3	85	0.30	0.00	0.08	0.13
4	87	0.07	0.10	0.08	0.08
5	89	0.00	0.03	0.08	0.04
6	91	0.03	0.20	0.04	0.09
7	93	0.07	0.13	0.08	0.09
8	95	0.07	0.07	0.08	0.07
9	97	0.17	0.10	0.00	0.09
10	99	0.03	0.07	0.04	0.05
11	101	0.00	0.03	0.14	0.04
12	103	0.00	0.03	0.08	0.04
13	105	0.03	0.07	0.04	0.05
14	107	0.00	0.00	0.04	0.01
15	111	0.03	0.00	0.08	0.04
16	113	0.00	0.10	0.00	0.03

Table (5): The observed allele sizes of the INRA063 microsatellite marker and their frequencies in each breed.

Allele number	Allele Size (bp)	Allele frequencies			
		Baladi	Zaraibi	Sinawi	All the breeds
1	143	0.07	0.00	0.11	0.06
2	145	0.15	0.03	0.30	0.16
3	147	0.15	0.10	0.08	0.11
4	149	0.07	0.14	0.04	0.08
5	151	0.10	0.03	0.00	0.04
6	153	0.00	0.14	0.04	0.06
7	155	0.04	0.06	0.15	0.08
8	157	0.00	0.03	0.08	0.04
9	159	0.00	0.00	0.08	0.03
10	161	0.07	0.00	0.04	0.04
11	163	0.17	0.20	0.04	0.14
12	165	0.07	0.06	0.04	0.06
13	167	0.07	0.20	0.00	0.09
14	169	0.04	0.00	0.00	0.01

Table (6): The observed allele sizes of the SR-CRSP8 microsatellite marker and their frequencies in each breed.

Allele number	Allele Size (bp)	Allele frequencies			
		Baladi	Zaraibi	Sinawi	All the breeds
1	201	0.09	0.00	0.00	0.03
2	203	0.09	0.00	0.00	0.03
3	205	0.13	0.00	0.08	0.07
4	207	0.06	0.03	0.00	0.03
5	209	0.06	0.10	0.03	0.06
6	211	0.09	0.23	0.12	0.15
7	213	0.03	0.00	0.00	0.01
8	215	0.09	0.07	0.03	0.06
9	217	0.03	0.07	0.08	0.06
10	219	0.03	0.00	0.12	0.05
11	221	0.17	0.03	0.08	0.09
12	225	0.00	0.00	0.08	0.03
13	227	0.13	0.00	0.03	0.05
14	229	0.00	0.03	0.00	0.01
15	231	0.00	0.10	0.12	0.07
16	235	0.00	0.20	0.08	0.09
17	237	0.00	0.07	0.08	0.05
18	239	0.00	0.07	0.08	0.05

Table (7): The observed allele sizes of the ILSTS87 microsatellite marker and their frequencies in each breed.

Allele number	Allele Size (bp)	Allele frequencies			
		Baladi	Zaraibi	Sinawi	All the breeds
1	123	0.00	0.23	0.00	0.07
2	125	0.00	0.13	0.00	0.04
3	129	0.00	0.06	0.00	0.02
4	131	0.00	0.13	0.19	0.11
5	133	0.00	0.00	0.19	0.06
6	137	0.00	0.10	0.00	0.03
7	139	0.19	0.04	0.09	0.11
8	141	0.11	0.00	0.00	0.04
9	143	0.04	0.00	0.04	0.03
10	145	0.11	0.17	0.04	0.11
11	147	0.00	0.04	0.00	0.01
12	149	0.00	0.04	0.00	0.01
13	151	0.08	0.00	0.09	0.06
14	153	0.04	0.00	0.00	0.01
15	155	0.04	0.06	0.19	0.10
16	157	0.00	0.00	0.04	0.01
17	159	0.08	0.00	0.00	0.03
18	161	0.00	0.00	0.09	0.03
19	163	0.08	0.00	0.04	0.04
20	165	0.15	0.00	0.00	0.05
21	167	0.08	0.00	0.00	0.03

Table (8): The observed allele sizes of the INRA023 microsatellite marker and their frequencies in each breed.

Allele number	Allele Size (bp)	Allele frequencies			
		Baladi	Zaraibi	Sinawi	All the breeds
1	183	0.10	0.00	0.00	0.03
2	185	0.00	0.22	0.00	0.07
3	187	0.22	0.03	0.20	0.15
4	189	0.00	0.00	0.07	0.02
5	191	0.22	0.07	0.04	0.11
6	193	0.03	0.03	0.07	0.04
7	195	0.06	0.07	0.04	0.06
8	197	0.03	0.00	0.07	0.03
9	199	0.03	0.00	0.00	0.01
10	201	0.10	0.14	0.04	0.09
11	203	0.06	0.03	0.04	0.04
12	205	0.06	0.14	0.00	0.06
13	207	0.00	0.03	0.12	0.05
14	209	0.03	0.03	0.00	0.02
15	211	0.06	0.14	0.24	0.15
16	213	0.00	0.00	0.07	0.02
17	215	0.00	0.07	0.00	0.02

Table (9): The observed allele sizes of the McM527 microsatellite marker and their frequencies in each breed.

Allele number	Allele Size (bp)	Allele frequencies			
		Baladi	Zaraibi	Sinawi	All the breeds
1	125	0.00	0.23	0.00	0.08
2	127	0.00	0.10	0.00	0.03
3	129	0.00	0.13	0.00	0.04
4	131	0.07	0.04	0.08	0.06
5	133	0.25	0.00	0.08	0.11
6	135	0.14	0.00	0.19	0.11
7	137	0.11	0.00	0.08	0.06
8	139	0.00	0.10	0.08	0.06
9	141	0.07	0.13	0.00	0.07
10	143	0.00	0.10	0.00	0.03
11	145	0.00	0.17	0.04	0.07
12	147	0.11	0.00	0.04	0.05
13	149	0.00	0.00	0.04	0.01
14	151	0.14	0.00	0.11	0.08
15	153	0.04	0.00	0.08	0.04
16	155	0.07	0.00	0.14	0.07
17	157	0.00	0.00	0.04	0.01

Table (10): The observed allele sizes of the ILSTS19 microsatellite marker and their frequencies in each breed.

Allele number	Allele Size (bp)	Allele frequencies			
		Baladi	Zaraibi	Sinawi	All the breeds
1	131	0.28	0.20	0.00	0.16
2	133	0.03	0.07	0.00	0.03
3	135	0.06	0.07	0.00	0.04
4	137	0.14	0.10	0.00	0.08
5	139	0.06	0.03	0.00	0.03
6	141	0.19	0.10	0.00	0.10
7	143	0.03	0.00	0.00	0.01
8	145	0.09	0.13	0.15	0.12
9	147	0.03	0.03	0.11	0.06
10	149	0.00	0.03	0.11	0.05
11	151	0.03	0.10	0.08	0.07
12	153	0.06	0.07	0.04	0.06
13	155	0.00	0.07	0.04	0.04
14	159	0.00	0.00	0.08	0.03
15	161	0.00	0.00	0.20	0.07
16	163	0.00	0.00	0.04	0.01
17	165	0.00	0.00	0.04	0.01
18	167	0.00	0.00	0.11	0.04

Table (11): Microsatellite alleles (No, observed number of alleles), heterozygosity (H_o, observed; H_e, expected) and polymorphism information content (PIC) at each locus in the different breeds under study.

Locus Within Breeds			SR-CRSP5	Oar FCB20	INRA 063	SR-CRSP8	ILST S87	INRA 023	McM 527	ILST S19	Mean
Baladi	Alleles	No	11	11	11	12	11	12	9	11	11
	Het.	H_o	0.833	0.694	0.929	0.875	0.846	0.561	0.714	0.688	0.768
		H_e	0.88	0.874	0.921	0.927	0.92	0.895	0.889	0.873	0.897
	PIC		0.823	0.827	0.878	0.886	0.876	0.852	0.843	0.827	0.852
Zaraibi	Alleles	No	12	12	10	11	10	12	8	12	11
	Het.	H_o	0.833	0.8	0.933	0.933	0.867	1	1	1	0.921
		H_e	0.913	0.922	0.892	0.894	0.89	0.903	0.881	0.926	0.903
	PIC		0.859	0.881	0.846	0.851	0.848	0.861	0.836	0.881	0.858
Sinawi	Alleles	No	11	13	11	13	10	11	12	11	12
	Het.	H_o	0.923	1	0.846	1	0.909	0.846	1	1	0.941
		H_e	0.914	0.942	0.877	0.951	0.909	0.902	0.926	0.917	0.917
	PIC		0.873	0.902	0.834	0.902	0.846	0.848	0.885	0.871	0.87

Photo (1): Showing the ethidium bromide stain for the two separated alleles of the marker, run vertically on Polyacrylamide gel electrophoresis of goat DNA microsatellite. Band patterns observed for SR-CRSP5 microsatellite alleles size range between (136-176) bp.

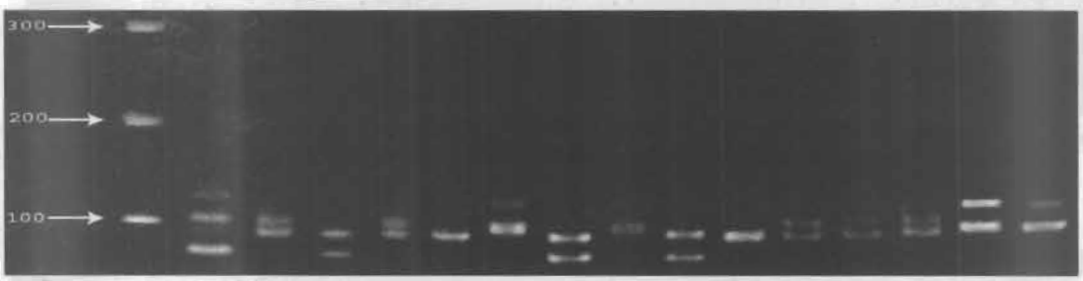

Photo (2): Showing the ethidium bromide stain for the two separated alleles of the marker, run vertically on Polyacrylamide gel electrophoresis of DNA microsatellite. Band patterns observed for OarFCB20 microsatellite alleles size range between (81-113) bp.

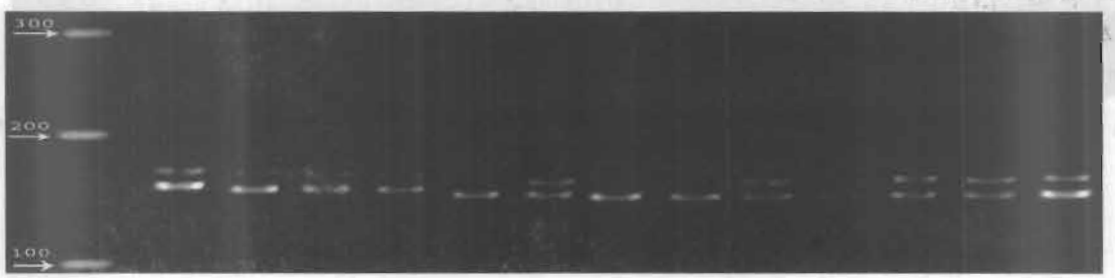

Photo (3): Showing the ethidium bromide stain for the two separated alleles of the marker, run vertically on Polyacrylamide gel electrophoresis of goat DNA microsatellite. Band patterns observed for INRA063 microsatellite alleles size range between (143-169) bp.

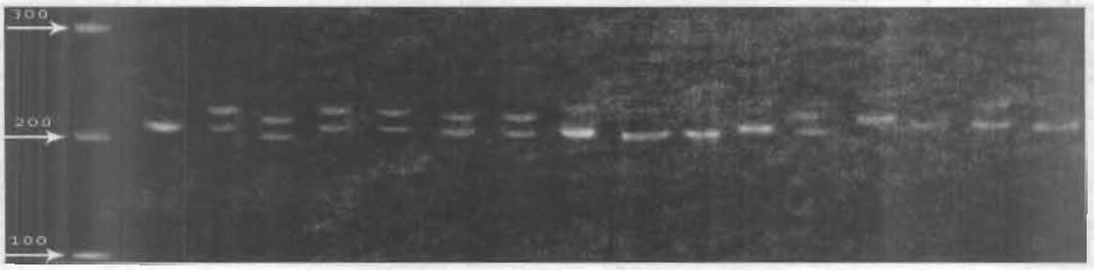

Photo (4): Showing the ethidium bromide stain for the two separated alleles of the marker, run vertically on Polyacrylamide gel electrophoresis of goat DNA microsatellite. Band patterns observed for SR-CRSP8 microsatellite alleles size range between (201-239) bp.

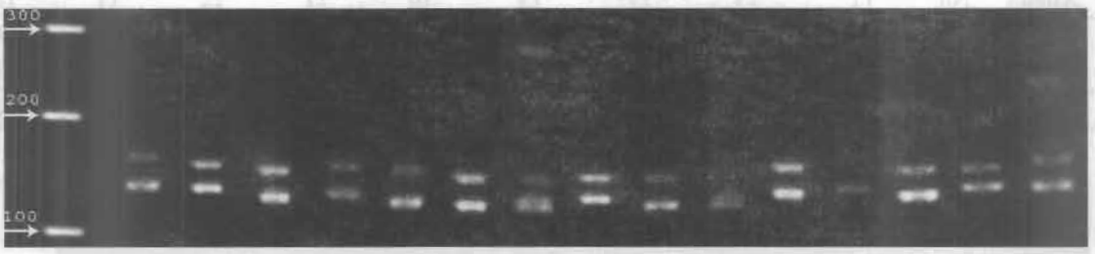

Photo (5): Showing the ethidium bromide stain for the two separated alleles of the marker, run vertically on Polyacrylamide gel electrophoresis of goat DNA microsatellite. Band patterns observed for ILSTS87 microsatellite alleles size range between (123-167) bp.

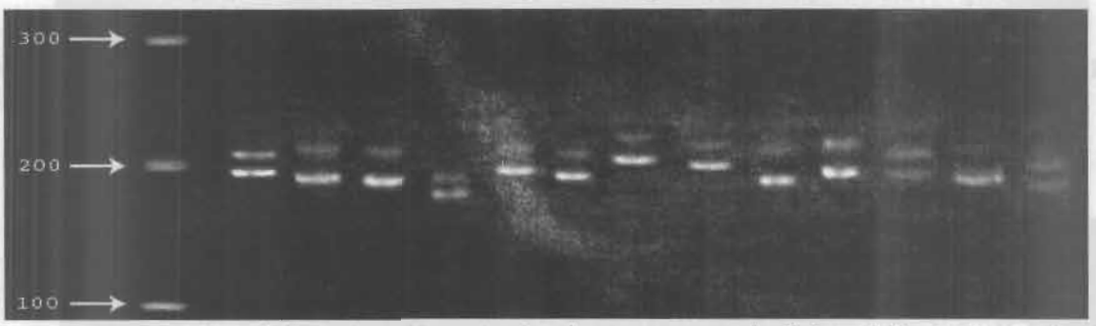

Photo (6): Showing the ethidium bromide stain for the two separated alleles of the marker, run vertically on Polyacrylamide gel electrophoresis of goat DNA microsatellite. Band patterns observed for INRA 023 microsatellite alleles size range between (183-215) bp.

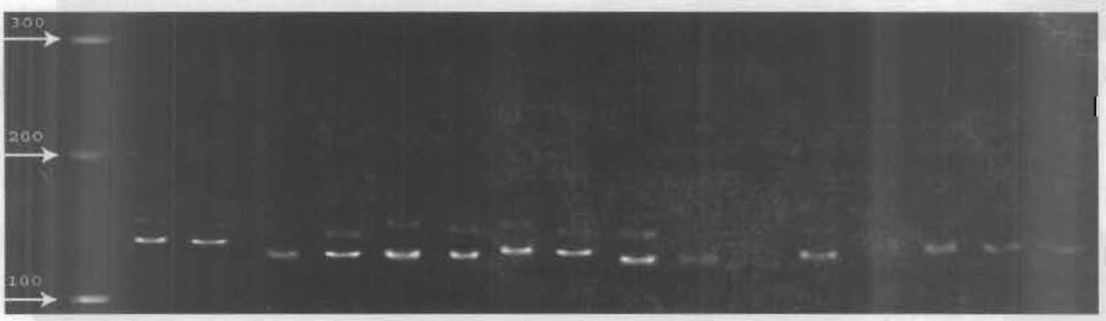

Photo (7): Showing the ethidium bromide stain for the two separated alleles of the marker, run vertically on Polyacrylamide gel electrophoresis of goat DNA microsatellite. Band patterns observed for McM527 microsatellite alleles size range between (125-157) bp.

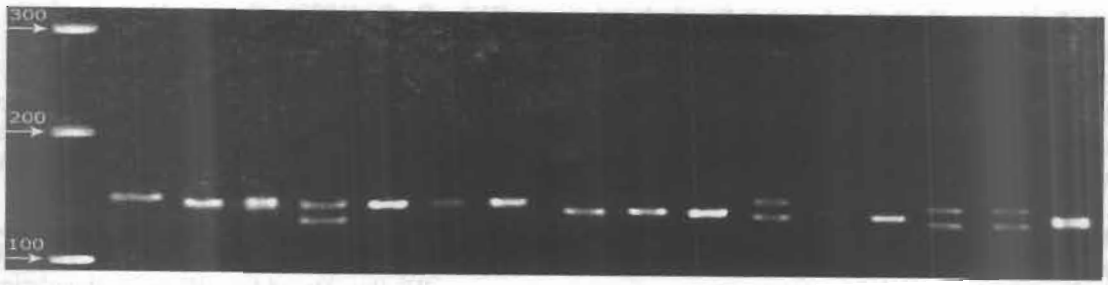

Photo (8): Showing the ethidium bromide stain for the two separated alleles of the marker, run vertically on Polyacrylamide gel electrophoresis of goat DNA microsatellite. Band patterns observed for ILSTS19 microsatellite alleles size range between (131-167) bp.

CONCLUSION

The values obtained for allele diversity, heterozygosity, showed that Baladi, Zaraibi and Sinawi goat breeds possessed substantial amount of genetic diversity. This variability can be a good tool for further improvement of goat performance in Egypt. Due to the large number of alleles and high ratios of heterozygosity, the breeds are no pure enough. From another side results from the present study, therefore, points to the usefulness of evaluations of diversity using molecular markers for the choice of breeds worthy of conservation.

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