GENETIC VARIATIONS OF TWO EGYPTIAN GOAT BREEDS USING MICROSATELLITE MARKERS

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SUMMARY

Two native Egyptian goat breeds: Baladi and Zaraibi were genetically analyzed using three microsatellite markers: INRA005; ILSTS005 and ILSTS087. The results showed that all the microsatellites studied were polymorphic and gave 6, 5 and 8 alleles respectively. The overall heterozygosity and polymorphism information content (PIC) values were 0.9 and 0.755 indicating the presence of high genetic diversity. In the two breeds, low inbreeding rates was observed (mean FIS= -0.114) within the breeds. Genetic differentiation between breeds was moderate with a mean FST value of (4.593). Deviations from Hardy-Weinberg equilibrium were noted for most of the loci. The clusters obtained on the phylogenetic tree generated from Nei's genetic distance matrix agreed with the geographic origin of the breed. The time of divergence in Zaraibi and Baladi breeds was estimated to be 71 generations (284 years). The two breeds showed high degree of admixture. The study analyzed the population structure of these two breeds and contributed to the knowledge and genetic characterization of the Egyptian native goat breeds (Baladi and Zaraibi). In addition, the microsatellites recommended by ISAG proved to be useful for the biodiversity studies in Egyptian goat breeds. Due to the polymorphism observed, the three microsatellites studied could be fruitfully used in paternity tests. Moreover, they could be employed for further researches on mapping quantitative trait loci (QTL) detection and subsequently marker assisted selection (MAS) breeding programs.

Keywords: Genetic variation, Egyptian goats, Baladi and Zaraibi, Microsatellites

INTRODUCTION

The goats are hollow-horned ruminants belonging to the mammalian order Artiodactyla, sub- order Ruminantia, family Bovidae and either of the genera Capra or Hemitragus (Herre and Rohrs, 1973). Together with sheep they constitute the tribe Caprini, but the differentiation between goats and sheep is well established.

The Egyptian goats are believed to be domesticated after migration from Asia along the present Iran–Iraq borders then to Africa (Mason, 1981). Rock drawings of goats have been found in Aswan, dated to the old or the Middle Kingdom of Egypt. Those goats were characterized by scimitar-shaped horns, erect ears, a convex facial profile and absence of a beard (Mason and Maule, 1960; and Epstein, 1971). Domestic goats can be traced to Egypt as far back as the Badarian age when goats

were used extensively for meat and their skins were quite often used to wrap the dead. The origin of domestic animals in Africa, including goats has been described and about 70 different breeds and varieties were recognized (Epstein, 1953; Mason and Maule, 1960; and Epstein, 1971).

In Egypt, 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. Goats are usually found in small holdings as mixed flocks with sheep and other farm animals like cattle and buffaloes, and are mainly kept as household dairy animals. 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 (Galal *et al.*, 2005). 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.

During recent years, a great interest is focused towards the use of molecular markers in understanding the animal genome and genetic diversity analysis. Molecular markers have been widely used to assess genetic variation since they provide information on every region of the genome. Among the molecular markers, microsatellites are currently most used markers. Microsatellites have been used in studying genetic variability in all domestic species of 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. Microsatellites, segments of the nuclear genome composed of tandem repeat of short-sequence motifs, have become excellent candidate markers for genetic studies, since they are numerous, highly variable and easy to score.

Best to our knowledge, only one study conducted by Agha *et al.* (2008) dealt with the microsatellite typing for assessment of the genetic diversity between Egyptian and Italian goat breeds.

The aim of the present study was to analyze the genetic variations within and between Baladi and Zaraibi goats, moreover to evaluate the genetic relationships among them.

MATERIALS AND METHODS

Blood samples:

Individual blood samples were drawn from 20 non-relative goats of each breed with a total number of 40 animals, the sample were collected from both sexes. The samples were collected from Baladi breed located in the research farm of the Department of Animal Production, Faculty of Agriculture. Fayoum University, El-Fayoum, and from Zaraibi breed located in the Agriculture research station (El-Serow, Domiatta) of the Animal Production Research Institute, Agriculture Research Center, Ministry of Agriculture.

DNA extraction, PCR and electrophoresis:

Genomic DNA was extracted using standard salting out procedure (Miller *et al.*, 1988). Three microsatellite markers were chosen according to a joint meeting

recommendation between the International Society of animal genetics (ISAG) and FAO (1998) for genetic diversity studies. Details of these markers are in the Table 1:

Table 1. Used microsatellites information

Microsatellite	Chromosomal location	Primer sequence	Reference
ILSTS087	6	AGC AGA CAT GAT GAC TCA GC CTG CCT CTT TTC TTG AGA G	*Steffen et al. (1993)*
ILSTS005	10	GGA AGC AAT TGA AAT CTA TAG CC TGT TCT GTG AGT TTG TAA GC	*Steffen et al. (1993)*
INRA05	12	CAATCTGCATGAAGTATAAATAT CTTCAGGCATACCCTACACC	*Vaiman et al. (1994)*

Polymerase chain reaction (PCR) was carried out on 50 ng of genomic DNA in a 25 µl reaction of 50 mM KCl, 10 mM Tris-HCl (pH 8.3), 200 µM dNTP, 1.5 mM $MgCl_2$, 1 mM tetra-ammonium-chloride, 0.1% Triton X-100, 0.01% gelatin, 4.5 pmol of each primer and 0.25 U *Taq* DNA polymerase. The standard PCR run cycle was usually as: primary denaturation at 95°C for 3 min., then: 35 cycles at 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. The success of the PCR was detected on 2% agarose after running in horizontal electrophoresis set and staining with ethidium bromide. For optimization of PCR, the temperature and time of annealing were changed.

The products of the successful PCR were characterized under denaturing conditions on 12% polyacrylamide vertical electrophoresis (Sambrook *et al.*, 1989). By the end of the run, the gel was stained in an ethidium bromide solution (0.5 Πg /ml TBE buffer). The gel image was captured electronically using Biometra gel documentation system. The allele sizes were determined using free software named Lab. image V2.7. It is dispersed free from the web site of Proland company (Germany). http://www.labimaging.com/servlet/engine/home/start.html

Statistical analysis of the results:

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 (Ho) and expected (He) heterozygosity at each locus in both breeds. Polymorphism information content (PIC) value for each locus was calculated using the method of Bostein *et al.* (1980). Pair-wise allele sharing was calculated manually from the raw results.

Using the variance-base method of Weir and Cockerham (1984), population differentiation by *F*-statistics was computed using FSTAT, version 2.9.3.2, computer program (Goudet, 2002). Means and 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, 1985). 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

All the microsatellites studied were shown to be polymorphic and gave many alleles, so they can be used further of mapping quantitative trait loci and subsequently marker assisted selection (MAS) as well as parentage testing.

The microsatellite INRA005 gave 6 alleles with a size range from 114 to 126 bp, the microsatellite ILSTS005 gave 5 alleles with a size range between 164 -188 bp, while the microsatellite ILSTS087 gave 8 alleles with a size range between 136-158 bp. The allele frequencies are presented at Table 2.

Table 2. Different microsatellite results: allele sizes, ranges and frequencies in the two breeds under study

Microsatellite	Allele no.	Allele size range	Allele frequencies		
			Baladi	Zaraibi	All breeds
INRA005	1	114	0.000	0.250	0.125
	2	116	0.125	0.100	0.113
	3	118	0.450	0.150	0.300
	4	122	0.050	0.225	0.138
	5	124	0.250	0.175	0.213
	6	126	0.125	0.100	0.113
ILSTS005	1	164	0.200	0.175	0.188
	2	166	0.175	0.275	0.225
	3	168	0.125	0.225	0.175
	4	186	0.225	0.075	0.150
	5	188	0.275	0.250	0.263
ILSTS087	1	136	0.300	0.200	0.250
	2	138	0.200	0.225	0.213
	3	140	0.050	0.075	0.063
	4	150	0.000	0.025	0.013
	5	152	0.025	0.050	0.038
	6	154	0.125	0.200	0.163
	7	156	0.150	0.150	0.150
	8	158	0.150	0.075	0.113

Hardy- Weinberg equilibrium:

The two breeds under study showed a significant deviation from hardy-Weinberg equilibrium for two of the microsatellite studied (INRA005 and ILSTS005), while the third microsatellite ILSTS087 did not show any significance deviation. The overall result proved that the two breeds are not in equilibrium state. These results are presented at Table (3).

Table 3. Estimation of Hardy Weinberg test for microsatellites in the two goat breeds understudy

Breed	Microsatellite		
	INRA005	ILSTS087	ILSTS005
Baladi	26.364**	20.713 ns	25.669**
Zaraibi	37.393**	38.500 ns	28.953**

** Significant at 1% level, ns: non significant

This deviation from HW equilibrium could be ascribed to the presence of linkage disequilibrium which in turn due to population stratification (ie. selection, migration, mutation and genetic drift). Similar HW un-equilibrium results for these microsatellites were reported by Araújo *et al.* (2006), who indicated that breeds showed breeds HW un-equilibrium status, may be they did not been subjected for any of the systematic (selection, migration and mutation) and dispersive forces (genetic drift and inbreeding). This microsatellite may be away or not-linked with an economic trait, so no selections for its alleles were occurred.

Genetic variation measurements:

Data of measuring of genetic variation for each breed (observed and effective number of alleles); (observed and expected heterozygosity) as well as polymorphism information content (PIC) are presented in Table (4):

Table 4. Microsatellite alleles (No, observed number of alleles; Ne, effective number of alleles), heterozygosity (Ho, observed; He, expected) and polymorphism information content (PIC) at each locus in the different breeds under study

Breed	Locus		INRA005	ILSTS087	ILSTS005	Mean
Baladi	Alleles	No	5	7	5	5.667
		Ne	3.344	5.161	4.706	4.404
	Het.	Ho	**0.850**	**0.900**	**1.000**	0.917
		He	0.719	0.827	0.808	0.785
	PIC		0.657	0.780	0.753	0.730
Zaraibi	Alleles	No	6	8	5	6.333
		Ne	5.369	5.970	4.444	5.261
	Het.	Ho	**1.000**	**1.000**	**0.650**	0.883
		He	0.835	0.854	0.795	0.828
	PIC		0.787	0.812	0.738	0.779

The values of observed heterozygosity were higher than the expected for the three microsatellites that indicated much variability. The lowest value of heterozygosity was 0.650, using ILSTS005 microsatellite in Zaraibi breed, while the highest value was 1.000, using ILSTS005 microsatellite in Baladi breed and using INRA05 and ILSTS087 microsatellites in Zaraibi breed. The difference between the observed and expected values (Chi- square) was significant at ($P < 0.05$) for all the microsatellites in both breeds. Similar results were observed by Agha *et al.* (2008), who assessed the genetic polymorphism in Egyptian and Italian goats.

The observed high values of heterozygosity in the breeds understudy may be due to the absence of good breeding programs for goats in Egypt. Many scientists reported a correlation between the observed high number of alleles and the absence of selection (Gregorius, 2009). It may also be due to the selection of animals included in the study which were selected as unrelated animals, which may gives more variations (FAO, 1998). The results of heterozygosity confirms this result which usually higher than 0.5. The observed high heterozygosity values are correlated with

of high heterozygosity and consequent non-fixation of alleles at these loci, there is a further scope for improvement of the breed.

The polymorphism information content (PIC) is an expected heterozygosity derived from allele frequencies in a random mating population. PIC is an indicator of how many alleles a certain marker has or 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 0.657 (INRA005) in Baladi breed to 0.812 (ILSTS087) in Zaraibi breed. PIC indicates the genetic variation; microsatellites with high PIC value are considered highly informative microsatellites (Arora *et al.*, 2003). So the three microsatellites were highly informative since the PIC value was more than 0.5. The results agreed with the report of Agha *et al.* (2008).

Concerning the gene diversity for the three microsatellites in the two breeds, the results are presented in Table (5).

Table 5. Average gene diversity for the microsatellites and breeds

Breed	Microsatellite			Mean estimate
	INRA05	ILSTS087	ILSTS005	
Baladi	1.376	1.754	1.578	1.569
Zaraibi	1.732	1.895	1.537	1.721
The two breeds	1.715	1.853	1.590	1.719

Average gene diversity overall loci was 1.719, while for individual loci the average gene diversity ranged between 1.376 (INRA005) in Baladi breed and 1.895 (ILSTS087) in Zaraibi breed. Since the microsatellite INRA005 had only six alleles, the lowest values of gene diversity were noticed.

Total numbers of alleles observed across all the breeds were found to be 19 alleles. In Baladi 17 and in Zaraibi 19 alleles were observed. The highest number of alleles observed across the breeds was 8 for ILSTS087. The mean observed allele numbers across the breeds for all 3 loci was 6.333, indicating the high level of polymorphism of the selected microsatellites. The maximum numbers of alleles observed were 8 for ILSTS087 in Zaraibi. The mean number of the observed alleles in Zaraibi breed was 6.333, where as in Baladi breed was 5.667. The mean number of alleles and the expected heterozygosities detected are good indicators of the genetic polymorphism within the breed. Generally the mean number of alleles is highly dependent on the sample size because of the presence of unique alleles in the populations, which occur in low frequencies and also because the number of the observed alleles tends to increase with increases in breed size. The number of alleles scored for each microsatellite is an invaluable indicator of the future usefulness of the microsatellite for genetic screening (Luikart *et al.*, 1999).

Inbreeding measurements (F-statistics):

Fixation indexes most currently referred to as F statistics were proposed by Wright (1951) to describe the properties of a subdivided population (inbreeding). Parameters FIT and FIS are the correlation between two uniting gametes with respect to the whole population and to gametes of subpopulations, respectively. Parameter FST is the correlation between random gametes from different individuals within subpopulations with respect to the total breeds and is a measure of the differentiation

of subpopulations. If there is no significant selective advantage of different alleles, FIS can be interpreted as a measure of inbreeding within the breed.

To assess genetic differentiation within the breeds, Fis is a measure of the within breed heterozygote defect (inbreeding). Table (6) is showing within the breeds inbreeding estimates {Fixation index statistics (FIS = *f*)} in the two breeds under study.

Table 6. Inbreeding estimates (FIS = *f*) within breeds under study

Microsatellite	Breed		Total
	Baladi	Zaraibi	
INRA05	-0.2121	0.2289	-0.1491
ILSTS087	-0.1163	-0.2012	-0.1511
ILSTS005	-0.2698	0.1613	-0.0414

All the inbreeding values within the two breeds studied were either below zero or negative meaning the complete absence of the inbreeding within the same breed (Wright, 1931). Inbreeding is the mating of individuals that have higher relationship coefficient than the breed average. Inbreeding coefficient was developed as the correlation between uniting gametes also called coefficient of consanguinity (Lush, 1994).

Inbreeding between breeds under study:

Table (7) indicates pair-wise values of genetic differentiation between breeds measured by fixation index (Fst), which varies between zero (meaning no genetic differentiation) and one (meaning complete genetic differentiation). The observed (Fst) is usually much smaller than 1.To help interpreting (Fst), Wright (1978) divided the value of (Fst) into four intervals: (1) from 0 to 0.05, indicating little genetic differentiation; (2) from 0.05 to 0.15, indicating moderate genetic differentiation; (3) from 0.15 to 0.25, indicating great genetic differentiation; (4) from 0.25 to 1, indicating very great genetic differentiation.

Table 7. FST (Fisher statistics) estimate (below diagonal) and effective migration rate *(Nm)* (above diagonal) (FST=1/4*N* m+1) (Wright 1951)

Breed	Baladi	Zaraibi
Baladi	****	9.158
Zaraibi	0.027	****

Gene flow:

To quantify the effects of breeds of migration on the genetic structure the gene flow was estimated by converting Fst to amount of gene flow *(Nm)*. *Nm* indicates the average number of effective migrants exchanged per generation.

Gene flow was estimated according to Nei (1987) as Nm indicating the ratio of the migrants exchanged from one generation to another. It was estimated using the equation: Gene flow estimated from Nm = 0.25 (1 - Fst)/Fst. The lowest value of genetic differentiation between the breeds is confirmed by the high level of gene flow between each two breeds

The gene flow was also calculated for each microsatellite separately. The results of this analysis are presented at Table (8).

Table 8. Gene flow between the two breeds for each microsatellite

Microsatellite	Gene flow
INRA005	3.987
ILSTS005	17.857
ILSTS087	34.500
Mean	9.158

The values of the gene flow for the 3 microsatellites studied were: 3.987; 17.857 and 34.500 for the microsatellites: INRA005; ILSTS005 and ILSTS087 respectively.

Immigration is an important force shaping the social structure, evolution, and genetics of breeds. Multilocus genotypes can be used to identify individuals who are immigrants, or have recent immigrant ancestry. The method given by Rannala and Mountain (1997) is appropriate for use with allozymes, microsatellites, or restriction fragment length polymorphisms (RFLPs) and assumes linkage equilibrium among loci. Potential applications of detecting immigrants include studies of dispersal among natural breeds of animals and plants, human evolutionary studies, and typing zoo animals of unknown origin (for use in captive breeding programs).

Genetic distance and phylogeny evaluations:

Estimation of Nei's standard genetic distances (Ds) and assumed mutation rates of microsatellites loci (α) were used to estimate the time of divergence (t, in generations) Where, $Ds = 2\alpha t$.

The Ds method described by Nei (1972) for determining genetic distances was used. Genetic distance measures the time that has elapsed since breeds were genetically equivalent.

The genetic distance value indicates that the two breeds are evolved from a common ancestor, and this took around 284 years to separate the two breeds from this common ancestor. This is a logical result since the two breeds were evolved and raised from the same area. Moreover the Nei genetic analyses are presented at Table (9).

Table 9. Nei's genetic identity, (above diagonal), and genetic distance (below diagonal)

Breed	Baladi	Zaraibi
Baladi	***	0.1708
Zaraibi	0.8430	***

The relationship among the breeds can be examined using the genetic distances/identities and these are calculated using allele frequencies. In this study three microsatellites were used for the measurement of genetic distances/identities between two goat breeds.

A reliable approach to measure the genetic distances is to estimate the differences in the frequency of different genetic variants (alleles) at the number of microsatellite loci. Breeds which share the same alleles at different frequencies (or different alleles

all together) are farther apart. Distances or relationship between breeds can then be summarized using a phylogenetic tree or by multidimensional scaling. Microsatellite DNA seems to be very useful for clarifying the evolutionary relationships of closely related breeds (Takezaki and Nei, 1996). The majority of mutations that the microsatellite loci exhibits are stepwise in nature, changing allele size by one or a very few number of repeats, and thus distances that are designed specifically to apply to microsatellite generally assume Kimura and Ota, (1975) stepwise mutation model and one of its generalization. However the genetic distances which are based on IAM (Infinite allele model) and purely geometrical and or mathematical considerations perform well for phylogenetic reconstruction. All the genetic distances estimated in the study are those from IAM. This is the major reason for using these distances for phylogenetic reconstruction. In the present study genetic distance estimates viz. proportion of shared alleles (Dps), fuzzy set similarity (Dfs), absolute difference algorithm (Dad), Goldstein distance ($\delta\mu$) 2 Ddm, average square D1 (ASD), Nei's chord distance (1983) (Da), Nei's standard genetic distance (corrected for sample size) (D), Cavalli-Sforza and Edwards (1967) chord distance (Dc) were used to estimate the relationship within Baladi and Zaraibi goat breeds. The estimates of distances measured using proportion of shared alleles, Nei's chord distance; Nei's standard genetic distances Cavalli Sforza and Edwards chord distance are found relative to one another. The standard genetic distance of Nei's (1978) and Cavalli-Sforza and Edwards (1967) chord distance, calculated from the allele frequencies, demonstrated their superior performance in phylogenetic tree construction when the microsatellite markers were used.

Estimated divergence time between the two breeds understudy are were calculated according to Nei standard genetic distance and the mammalian mutation rate are presented in Table 10.

Table 10. Estimated divergence time of the two breeds under study on the basis of the 3 microsatellites loci studied (Nei, 1978)

Breed	Nei's standard genetic distance (Ds)	Mutation rate (α)	Divergence time	
			Generations	Years
Baladi & Zaraibi	0.1708	$1.2 X10^{-3}$	71	284

CONCLUSION

The values obtained for allele diversity, heterozygosity, inbreeding measurements and gene diversity showed that Baladi and Zaraibi goat breeds possessed substantial amount of genetic diversity. This variability can be a good tool for further improvement of goat performance in Egypt. From another side the results from the present study, point to the usefulness of evaluations of diversity using molecular markers for the choice of breeds worthy of conservation.

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الإختلافات الوراثية لسلالتين من الماعز باستخدام التوابع الوراثية الدقيقة

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تناولت هذه الدراسة تحليل التباين الوراثى لسلالتين من سلالات المعز المصرية وهما: البلدى والزرايبى باستخدام ثلاثة من واسمات التتابعات الوراثية الدقيقة هى:
(INRA005, ILSTS005, ILSTS087)

ولإجراء هذا البحث تم تجميع اربعين عينة دم من معز ليس بينها درجة قرابة 20 (عينة لكل سلالة) ثم تم عزل وتنقية المادة الوراثية (DNA) من عينات الدم التى تم جمعها. أجري تفاعل إنزيم البلمرة المتسلسل {Polymerase Chain Reaction (PCR)} للواسمات المراد دراستها وذلك مع بادئات تتابعات دقيقة متخصصة لكل واسم على حدة، هذا وقد تم تفريد ناتج تفاعل انزيم البلمرة المتحصل عليه على جهاز تفريد كهربائى رأسى و علي مادة البولي أكريلميد تحت ظرف denaturing وذلك لفك الاليلين عن بعضهما في وجود مادة وراثية معلومة الطول (DNA size marker). وبعد التفريد تم الصبغ بمادة بروميد الايثيديوم ثم التصوير بكاميرا مخصصة لذلك ثم إدخال الصور المتحصل عليها على برنامج كمبيوتر متخصص لتحليلها و تحديد أطوال الاليلات لهذه الحيوانات. وبعد الحصول على قياسات هذه الأطوال تم جدولة النتائج وتحليلها إحصائيا باستخدام برامج FSTAT & POPGENE و هى برامج متخصصة فى مجال وراثة العشائر.

أظهرت جميع واسمات التتابعات الوراثية الدقيقة التى شملتها الدراسة نتائج عالية فى تعدد الأشكال المظهرية وقد أعطت أكثر من أليل حيث أعطت الواسمات الثلاث عددا من الأليلات يتراوح من 5-8. وعليه فانه يمكن استخدام هذه الواسمات الثلاثة فى اختبار معرفة الأبوية أو النسب وبالإضافة إلى ذلك يمكن استخدامها فى التعرف على المواقع الجينية المرتبطة بالصفات الإنتاجية الكمية واستخدمها فى برامج التربية الحديثة والتى تسمى بالانتخاب بمساعدة الواسمات الوراثية.

أظهرت النتائج أيضا أن السلالتين قيد الدراسة ليستا في حالة اتزان بين هاردي- واينبرج. وقد أظهر اختبار عدم التجانس أن جميع القيم قد تجاوزت 0.5 وهذا يعني ارتفاع نسب الخلط ، و كانت نسبة الخلط الكلية لسلالة المعز البلدى 0.917 بينما كانت 0.833 لسلالة المعز الزرايبى.

وقد أظهرت النتائج أيضا ارتفاعا ملحوظا فى متوسط قيم التنوع الجيني لجميع الواسمات المستخدمة فى السلالتين قيد الدراسة. كما وجد أن قيمة محتوى معلومات تعدد المظاهر الوراثية أو ما يعرف أيضا بالتنوع الوراثى المتحصل عليها تتراوح من (0.730- 0.779) وهى قيم عالية مما يثبت وجود درجة عالية من التنوع الوراثى فى السلالتين.

وفيما يتعلق بنتائج التربية الداخلية (inbreeding) بين السلالتين دلت الدراسة على عدم وجود تربية داخلية بين او داخل السلالتين تحت الدراسة.

وبالإضافة إلى ذلك وجد أن قيمة الهجرة أو التدفق الجيني فى سلالتى المعز المحلية كانت عالية بمتوسط يساوى 9.1578. وهو عالى ويدل على زيادة معدل الهجرة والخلط بين سلالتى المعز تحت الدراسة.

أوضحت الدراسة انبثاق السلالاتان من بعضهما، وأنهما قد نشئوا من سلف مشترك والمسافة الوراثيـــة بينهما هى 284 عاما.

النتائج بشكل عام هي دليل على أن سلالتى المعز تحت الدراسة و التي أثيرت في مصر تشير إلـــى أن هاتين السلالتين ليستا نقيان تماما حتى الان وأن بكل سلالة درجة عالية من التنوع الوراثى يمكن استخدامها فى برامج التحسين الوراثى مستقبلا.