MOLECULAR GENETIC FINGERPRINTING FOR NEW SELECTED EGYPTIAN SHEEP STRAINS IN RELATION TO OSSIMI BREED

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Sheep spread in different parts of the world, and represent one of the most important resources of animal protein, sheep also considered as income source in several countries. There are many types of sheep breeds such as: meat type, dairy type and wool type...etc, about four million heads of sheep found in Egypt (Mervidel, 2007). The major breeds of sheep in Egypt are; Ossimi, Rhmani and Barki. In addition to minor sheep breeds; Abidi, Abudelek, Farafra, Maenit, kanzy, Saidy, Sanabawi and Sohagy and other strains as El-Adely. In Egypt several trials have been carried out to improve their production by selection or crossing with European breeds or using good management.

El-Adely sheep was developed from selected local sheep and selected ones of Ossimi breed followed by selection for many generations. Inbreeding was also used to fix some favorable genes in the animals of the basic flock. Two strains were produced from this breed, high ovulation rate strain (HORS) and high milk yield strain (HMYS) for higher meat and milk production, respectively. The two strains (El-Adely sheep, HORS and HMYS) had many feature like the Ossimi breed. It is hoped to expand the base of this breed to be raised in a vast scale, and to be used as an enhancer breed to be crossed to other local Egyptian sheep breeds under intensive and semi-intensive systems of production aiming to increase mutton in the local meat market and milking ewes to make favorable sheep cheese that is actually imported from abroad. The breed was developed by Adel Said in his farm, and the name of the breed "El-Adely" goes after the name of its founder (Mourad, 2008).

Based on the established fact that proteins are the other face of genetics, the biochemical assays of genetic variation at the protein molecular level can provide rich insights into the genetic structure of biological organisms. (Houle, 1989) used protein banding pattern variations in the main local Egyptian sheep breeds (Rahmany, Ossimi and Barki) and considered SDS-PAGE, as a useful tool for the detection of homogeneity within each breed and generation of specific biochemical markers to identify and differentiate between the three breeds. (Elmaci and Asal, 2000) studied transferrin, post-transferrin, albumin and post-albumin in the blood plasma of cattle by horizontal

polyacrylamide gel electrophoresis. New protein polymorphism in the post-transferrin region was detected through two new clearly separated alleles. During the last few years, some molecular studies were carried out using RAPD-PCR technique to detect the diversity in the local and/or adapted sheep and goat breeds in Egypt. The results of these studies demonstrated the usefulness of the RAPD-PCR technique for detecting DNA polymorphism and establishing the relationships among different breeds; Rahmany, Ossimi and Barki sheep breeds (Ali, 2003).

MATERIALS AND METHODS

1. Materials

In the present study, samples from Oissim breed and El-Adely sheep, high ovulation rate strain (HORS) and El-Adely sheep high milk yield strain (HMYS) were collected from two different stations. The blood samples of Ossimi sheep were collected from the flock present in the farm of the Faculty of Agric, Ain Shams Univ. While the blood samples of El-Adely sheep were collected from El-Adely sheep farm, owned by Mr Adel Said at El-Khatatba area, Egypt. These samples were taken from 30 ewes, 10 from the Ossimi sheep, 10 from the HORS and 10 from the HMYS, which all are phonotypically normal, healthy and fertile. The animals were at the same age and same physiological status to avoid the effects of environmental factors.

Blood plasma was then obtained by centrifugation at 10000 rpm for 10 minutes at 4°C, and the plasma protein was transferred to clean plastic vials and stored at -20°C until electrophoretic analysis of protein. Protein fractionations were performed exclusively on vertical slab (19.8 cm x 26.8 cm x 0.2 cm) gel using the electrophoresis apparatus manufactured by Aplex.

2. Expereimental Methods

2.1. Protein Electrophoresis

Protein samples were applied to 14% polyacrylamid gel for using (SDS-PAGE) technique, according to (Bollag and Edestein, 1994). While protein samples were run on 10% polyacrylamid gel for using Native-PAGE technique, according to (Hames *et al*., 1981).

2.2 RAPD Analysis

DNA was extracted from each individual samples according to (Hillis *et al.*, 1996). PCR reaction mixture was prepared in 5 µl contained 25 ng DNA, 0.3 µM primer, 0.2 mM dNTPs, 25 mM $MgCl_2$ and 0.25 unit Taq polymerase in 1 X buffer. PCR program was adjusted at of one cycle for 4 min at 94°C, 35 cycles for 45 sec at 94°C, 45 sec at 37°C & 1 min at 72°C and one cycle for 10 min at 72°C. Primer codes and their sequences are presented in Table (1).

2.3 Data Analysis

The similarity indexes between individuals of each breed and strains were calculated using the formula: $S_{yx}= 2n_{xy}/(n_x + n_y)$ Where: n_{xy} is the number of bands

shared by individuals x and y, n_x and n_y are the number of bands scored for each individual. S_{yx} is the similarity index between the x and y individuals and the homogeneity ratio was estimated in the following manner: Homogeneity (%) = Number of monomorphic bands/Total number of bands expressed in percentage according Lynch (1990). To construct the dendrogram which describes the phylogenetic relationships between the studied breed and strains , the binary data derived from all protein patterns were combined together and introduced to SPSS software package, the dendrogram was constructed according to Sneath and Sokal (1973), cited in Bardakci and Skibinski (1994), using Unweighted Pair-Group Method of Analysis (UPGMA).

RESULTS AND DISSCUSION

1. Biochemical genetic fingerprinting

1.1. Genetic polymorphism of the tested breed and strains as detected by SDS- PAGE plasma protein

In this study Polyacrylamide gel electrophoresis (PAGE) for the plasma protein was used to assess structure of Ossimi breed and El-Adely sheep strains (HORS and HMYS) and to compare among these groups at the SDS-protein level.

Within each studied group

Figure (1) and Table (2) shows banding pattern of Ossimi breed. The total number of bands was 14 recorded bands with weight ranged from 210 to 5 KDa. There were only five polymorphic bands with molecular weights of 210, 79, 76, 64 and 47 KDa, while the other bands were monomorphic. The band frequencies ranged from 0.1 to 1.0. The similarity values within this breed were calculated and found to range from 1 to 0.81 with an average of 0.93. Figure (1) and Table (3) shows banding pattern of El-Adely sheep (HORS). Where the total number of bands was 15 recorded bands which ranged from 235 to 5 KDa. There were only seven polymorphic bands with molecular weights of 235, 215, 199, 182, 56, 50 and 37 DKa, while the other bands were monomorphic. The band frequencies were ranging from 0.1 to 1.0. The similarity values within this sheep were calculated, where they ranged from 1 to 0.75 with average of 0.91. While Fig. (1) and Table (4) shows banding pattern of El-Adely sheep (HMYS), the maximum number of bands was 14 which ranged from 226 to 5 KDa. There were four polymorphic bands with molecular weights of 226, 59, 37 and 13 KDa. While the other bands were monomorphic. The band frequencies ranged from 0.1 to 1.0. The similarity values within this strain ranged from 1 to 0.83 with average of 0.94.

1.2. Genetic polymorphism of the tested breed and strains as detected by native-PAGE plasma protein

Native-protein of ten blood plasma samples of each studied group was used to characterize and differentiate among Ossimi breed and El-Adely sheep (HOR and HMY) strains.

The electrophortic studies revealed the presence of six zones in each case of the individual samples of Ossimi breed and El-Adely sheep strains (HOR and HMY). These zones are: Immunoglobulin (γ-globulin), post-transferrin, transferrin (β-globulin), α-globulin, albumin and pre-albumin. However, these zones showed some differences among and within the studied groups.

Within each studied group

Results which were illustrated in Fig. (2) and Table (5) shows banding pattern of native protein for Ossimi breed. The total number of bands was 19 with relative fronts ranging from 0.08 to 0.90. There were 9 polymorphic bands. Only one band with relative front of 0.28 was in post-transferrin zone, and one band with relative front of 0.48 was in transferrin zone, six bands with relative fronts of 0.53, 0.55, 0.56, 0.57, 0.72 and 0.74 were in α-globulin zone, and only one band with relative front of 0.80 was in pre-albumin zone.

Figure (2) and Table (6) illustrate the electrophoretic banding pattern to native protein of El-Adely sheep (HORS). The total number of bands was 19 with relative fronts ranging from 0.05 to 0.80. There were 12 polymorphic bands. Two of these bands with relative front of 0.12 and 0.14 were in Immunoglobulin zone. Three bands with relative front of 0.27, 0.30 and 0.31 were in post-transferrin zone, and three bands with relative front of 0.40, 0.44 and 0.47 were in transferrin zone. Four bands with relative fronts of 0.51, 0.53, 0.56 and 0.62 were in α-globulin zone.

Figure (2) and Table (7) showed the electrophortic banding pattern of native protein of El-Adely sheep (HMYS). The maximum number of bands was 18 with relative fronts ranged from 0.05 to 0.80. There were 8 polymorphic bands. Two bands of them with relative front of 0.18 and 0.21 were in Immunoglobulin zone. Only one band with relative front of 0.28 was in post-transferrin zone. While three bands with relative fronts of 0.40, 0.47 and 0.48 were in transferrin zone and two bands with relative front of 0.50and 0.62 were in α- globulin zone.

The homogeneity percentage of the native-protein banding patterns were summarized to identify the homogeneity percentages within each studied group as shown in Table (8) .This table showed the lowest homogeneity percentage to be 37% in El-Adely sheep HOR strain followed by 53% in Ossimi breed. On the other hand the highest homogenteiy percentage was 55% in the El-Adely sheep HMY strain. In contrast with Awad (2005) who observed that the Homogeneity percentages at Native-PAGE in Ossimi, Rahmani and Barki sheep were 47%, 41% and 29%, respectively. The difference in Homogeneity percentage shows that El-Adely HOR strain had more genetic variation

than either the other El-Adely strain or Ossimi breed.

1.3. Genetic relationships among the studied groups based on SDS-PAGE and native -protein profile

The similarity matrix based on native-protein fractions and SDS-PAGE among the studied groups is shown in Table (9). Similarity was 0.84 between El-Adely sheep HOR strain and El-Adely sheep HMY strain and it was 0.66 between El-Adely sheep HMY strain and Ossimi breed while it was 0.46 between Ossimi breed and El- Adely sheep HOR strain. The high similarity value between El-Adely strains could be attributed to the same origin of these selected strains.

Dendrogram tree as shown in Fig. (3) illustrate the genetic relationships among the Ossimi breed and the two strains of the El-Adely. These two strains of El-Adely sheep were clustered in one group, while Ossimi breed was distant from them. Which mean that there is high relationship between these two strains at protein levels and a low relationship for these strains with Ossimi breed, even though Ossimi was one of the parental origin of these strains which means that selection program caused divergence of both strains from Ossimi breed.

These results are in agreement with the data of (Tapio *et al*., 2002) that differentiated between nine sheep breeds of Finland and North-Western Russia by the same techniques. (Baker and Manwell, 1991) estimated the genetic relationships between European, Asian and African cattle breeds using the same technique. In addition, this technique can also be used for indirect selection in breeding program if there were some relationships between blood proteins and some economically important quantitative traits (Elmaci and Asal, 2000).

2. Molecular genetic fingerprinting

2.1. Genetic polymorphisms of the tested groups as detected by RAPD-PCR analysis

Figure (4) and Table (10) illustrate the PCR products of seven primers used in the studied groups. In Ossimi breed, the total number of bands was 78 bands which ranged from 1665 to 140 bp. 29 bands of them were monomorphic, while the other bands were polymorphic, the highest number of bands was produced with primer A7. In El-Adely sheep (HOR), the total number of bands was 61 bands which ranged from 1422 to 120 bp. 26 bands of them were monomorphic, while the other bands were polymorphic, primer A7 and primer C9 gave the highest number of bands. In El-Adely sheep (HMY), the total number of bands was70 bands which ranged from 1406 to 109 bp. 23 bands of them was monomorphic, while the other bands were polymorphic, the highest number of bands was produced with primer A7.

The present study provides evidence that RAPD markers can be used to discriminate among the breeds and strains and have been successfully used to detect the genetic variations among different

sheep breeds. Various studies have been proposed for the same purpose such as El-Seoudy *et al.* (2005) who characterized two local breeds of Egyptian goat (Baladi and Zaraibi) using 10 RAPD primers. (Ali, 2003) used RAPD markers to study the genetic variation among four breeds of sheep (Baladi, Barki, Rahmani and Saffolk). Nineteen random primers were used to amplify DNA fragments in these breeds. However, application of the randomly amplified polymorphic DNA technique has greatly increased the ability to understand the genetic relationships among the studied breeds at the molecular level (Appa Rao *et al*., 1996).

2.2. Genetic relationships among the three tested sheep groups as determined by RAPD-PCR analysis

Similarity values based on RAPD-PCR analysis among Ossimi breed and the two strains of El-Adely sheep are shown in Table (11). The highest similarity 0.82 was observed between the two strains of El-Adely sheep (HOR and HMY), while the lowest 0.50 was between Ossimi breed and El-Adely sheep HOR strain. Moreover, it was 0.57 between Ossimi breed and El-Adely sheep HMY strain. Dendrogram based on RAPD-PCR analysis illustrated that the two strains of El-Adely sheep were clustered together in one group, while Ossimi breed was distant from them. This Dendrogram proved to be similar to that obtained from analysis protein (native-protein fractions and SDS-PAGE).

It can be concluded that biochemical and DNA analyses which were used in the present study succeeded in distinguishing among the tested breed and strains and in detecting genetic variation within each bread and strains. Also, these analyses revealed that Ossimi breed is genetically distant from the two sheep strains of El-Adely, while these two strains are closely related to each other which indicate that they possess similar genetic backgrounds. However, these results could be used in sheep breeding programs in Egypt to assess high milk and meat sheep strains.

SUMMARY

Two strains of El-Adely sheep and Ossimi sheep breed were characterized using biochemical techniques. Protein banding pattern using SDS and native gel electrophoresis were carried out to identify the biochemical genetic fingerprinting of each El-Adely sheep strains and Ossimi breed. The genetic homogeneity percentage based on Native-protein within each of Ossimi, El-Adely (HORS) and El-Adely (HMYS) were 53%, 37% and 55%, respectively. Similarity value based on SDS-PAGE, Native-PAGE and RAPD-PCR analysis was the highest between the two strains of El-Adely sheep (HOR and HMY) strains, while it was the lowest between Ossimi breed and El-Adely sheep HOR strain. Also, similarity value was low between El-Adely sheep HMYstrain and Ossimi breed. The dendrogram was constructed among the studied sheep groups based on SDS-PAGE, Native-PAGE and RAPD analyses showed that

Ossimi breed was distantly related from both the two strains of El-Adely sheep (HOR and HMY strains).

The present study revealed that SDS-PAGE, Native-PAGE and RAPD-PCR techniques could be strongly recommended as useful tools for detecting fingerprint, determination of polymorphism and establishing the genetic relationships among different sheep genotypes.

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Table (1): List of the seven used random primers with their nucleotide sequences.

Primer code	Primer sequence
A19	5'-CAA ACG TCG G-3'
A15	5'-TTC CGA ACC C-3'
A07	5'-GAA ACG GGTG-3'
C18	5'-TGA GTG GGTG-3'
C09	5'-CTC ACC GTCC-3'
C06	5'-GAA CGG ACTC-3'
C04	5'-CCG CAT CTAC-3'

Table (2): Score SDS-protein banding pattern of Ossimi breed individuals.

Band No.	MW(KDa)	BF	1	2	3	4	5	6	7	8	9	10
1	210	0.1	1	0	0	0	0	0	0	0	0	0
2	183	1.0	1	1	1	1	1	1	1	1	1	1
3	163	1.0	1	1	1	1	1	1	1	1	1	1
4	134	1.0	1	1	1	1	1	1	1	1	1	1
5	101	1.0	1	1	1	1	1	1	1	1	1	1
6	79	0.8	1	1	1	1	0	1	1	1	1	0
7	76	0.3	0	0	0	0	1	0	0	0	1	1
8	63	0.2	1	0	0	0	0	0	0	0	0	1
9	57	1.0	1	1	1	1	1	1	1	1	1	1
10	47	0.6	1	1	0	1	1	0	0	1	1	0
11	36	1.0	1	1	1	1	1	1	1	1	1	1
12	24	1.0	1	1	1	1	1	1	1	1	1	1
13	17	1.0	1	1	1	1	1	1	1	1	1	1
14	5	1.0	1	1	1	1	1	1	1	1	1	1

MW: Molecular weight BF: Band frequency.

Table (3): Score SDS-protein banding pattern of El-Adely sheep HOR strain individuals.

Band No.	MW(KDa)	BF	1	2	3	4	5	6	7	8	9	10
1	235	0.1	1	0	0	0	0	0	0	0	0	0
2	215	0.4	1	1	0	1	0	0	0	0	0	1
3	199	0.4	0	1	0	0	1	0	0	0	1	1
4	182	0.8	1	0	1	1	1	1	1	0	1	1
5	163	1.0	1	1	1	1	1	1	1	1	1	1
6	134	1.0	1	1	1	1	1	1	1	1	1	1
7	101	1.0	1	1	1	1	1	1	1	1	1	1
8	87	1.0	1	1	1	1	1	1	1	1	1	1
9	63	1.0	1	1	1	1	1	1	1	1	1	1
10	56	0.2	1	1	0	0	0	0	0	0	0	0
11	50	0.8	0	1	1	1	1	1	0	1	1	1
12	37	0.9	1	1	1	1	0	1	1	1	1	1
13	24	1.0	1	1	1	1	1	1	1	1	1	1
14	17	1.0	1	1	1	1	1	1	1	1	1	1
15	5	1.0	1	1	1	1	1	1	1	1	1	1

MW: Molecular weight BF: Band frequency

Table (4): Score SDS-protein banding pattern of El-Adely sheep HMY strain individuals.

Band No.	MW(KDa)	BF	1	2	3	4	5	6	7	8	9	10
1	226	0.3	0	0	0	0	0	0	1	1	1	0
2	200	1.0	1	1	1	1	1	1	1	1	1	1
3	163	1.0	1	1	1	1	1	1	1	1	1	1
4	134	1.0	1	1	1	1	1	1	1	1	1	1
5	101	1.0	1	1	1	1	1	1	1	1	1	1
6	87	1.0	1	1	1	1	1	1	1	1	1	1
7	63	1.0	1	1	1	1	1	1	1	1	1	1
8	59	0.1	1	0	0	0	0	0	0	0	0	0
9	48	1.0	1	1	1	1	1	1	1	1	1	1
10	37	0.4	0	0	0	0	0	0	1	1	1	1
11	24	1.0	1	1	1	1	1	1	1	1	1	1
12	17	1.0	1	1	1	1	1	1	1	1	1	1
13	13	0.4	0	1	1	1	0	0	0	1	0	0
14	5	1.0	1	1	1	1	1	1	1	1	1	1

MW: Molecular weight BF: Band frequency

Table (5): Score of native- protein banding pattern of Ossimi breed individuals.

Band No.	Fraction	RF	1	2	3	4	5	6	7	8	9	10
1	Immunoglobulin (γ-globulin)	0.08	1	1	1	1	1	1	1	1	1	1
2		0.14	1	1	1	1	1	1	1	1	1	1
3	Post- transferrin	0.24	1	1	1	1	1	1	1	1	1	1
4		0.28	1	1	1	0	0	0	1	1	0	1
5		0.31	1	1	1	1	1	1	1	1	1	1
6	Transferring (β-globulin)	0.37	1	1	1	1	1	1	1	1	1	1
7		0.46	1	1	1	1	1	1	1	1	1	1
8		0.48	0	0	0	1	0	0	0	0	0	1
9	α-globulin	0.50	1	1	1	1	1	1	1	1	1	1
10		0.53	0	1	0	0	0	1	0	0	0	1
11		0.54	1	1	1	1	1	1	1	1	1	1
12		0.55	0	0	0	0	0	1	1	0	0	0
13		0.56	1	1	0	0	0	1	0	0	0	0
14		0.58	1	0	0	1	0	0	0	1	1	0
15		0.72	1	0	0	1	1	0	1	0	0	0
16		0.74	0	1	0	1	1	0	0	1	1	1
17	Albumin	0.75	1	1	1	1	1	1	1	1	1	1
18	Pre-albumin	0.80	0	0	0	1	0	1	1	0	0	0
19		0.90	1	1	1	1	1	1	1	1	1	1

RF: relative front

Table (6): Score of native-protein banding pattern of El-Adely sheep HOR strain individuals.

Band No.	Fraction	RF	1	2	3	4	5	6	7	8	9	10
1	immunoglobulin (γ-globulin)	0.05	1	1	1	1	1	1	1	1	1	1
2		0.12	0	0	1	1	1	1	1	1	1	1
3		0.14	1	1	0	0	0	0	1	0	0	0
4	Post- transferrin	0.25	1	1	1	1	1	1	1	1	1	1
5		0.27	0	0	0	0	0	0	0	1	1	1
6		0.30	0	0	1	0	1	1	1	0	0	1
7		0.31	1	1	1	1	0	0	0	0	0	0
8	ɣransferrin (β-globulin)	0.40	1	0	0	0	0	1	1	0	1	1
9		0.44	1	0	0	1	0	0	0	0	1	1
10		0.45	1	1	1	1	1	1	1	1	1	1
11		0.47	0	0	0	0	0	0	1	1	0	0
12	α-globulin	0.49	1	1	1	1	1	1	1	1	1	1
13		0.51	0	1	0	1	1	1	0	1	0	0
14		0.53	1	0	1	1	0	0	0	1	0	0
15		0.55	1	1	1	1	1	1	1	1	1	1
16		0.56	0	1	0	0	1	0	0	0	0	0
17		0.62	1	1	0	0	0	0	1	0	0	1
18	Albumin	0.67	1	1	1	1	1	1	1	1	1	1
19	Pre-albumin	0.80	1	1	1	1	1	1	1	1	1	1

RF: relative front

Table (7): Score of native- protein banding pattern of El-Adely sheep HMY strain individuals.

Band No.	Fraction	RF	1	2	3	4	5	6	7	8	9	10
1	immunoglobulin (γ-globulin)	0.05	1	1	1	1	1	1	1	1	1	1
2		0.11	1	1	1	1	1	1	1	1	1	1
3		0.18	1	0	0	0	0	0	0	1	0	0
4		0.21	1	0	0	0	1	0	1	1	1	1
5		0.23	1	1	1	1	1	1	1	1	1	1
6	Post-transferrin	0.25	1	1	1	1	1	1	1	1	1	1
7		0.28	0	1	1	1	1	1	1	1	1	0
8		0.37	1	1	1	1	1	1	1	1	1	1
9	transferrin (β-globulin)	0.40	0	0	0	0	0	0	0	0	1	1
10		0.43	1	1	1	1	1	1	1	1	1	1
11		0.45	1	1	1	1	1	1	1	1	1	1
12		0.47	0	0	0	1	0	1	0	1	0	0
13		0.48	1	1	1	0	1	0	1	1	1	1
14	α-globulin	0.50	1	0	0	0	1	0	1	0	0	0
15		0.59	1	1	1	1	1	1	1	1	1	1
16		0.62	0	1	0	0	0	0	0	0	0	0
17	albumin	0.67	1	1	1	1	1	1	1	1	1	1
18	Pre-albumin	0.80	1	1	1	1	1	1	1	1	1	1

RF: relative front

Table (8): Homogeneity percentage within studied groups based on native-protein banding patterns.

Groups	Total no. of bands	Polymorphic bands	Monomorphic bands	Homogeneity %
Ossimi	19	9	10	53
El-Adely (HORS)	19	12	7	37
El-Adely (HMYS)	18	8	10	55

Table (9): Similarity matrix of studied breed and strains based on SDS-PAGE and Native-PAGE.

Bands	El-Adely (HORS)	El-Adely (HMYS)	Ossimi
El-Adely (HORS)	1.00		
El-Adely (HMYS)	0.84	1.00	
Ossimi	0.46	0.66	1.00

Table (10): Score the total number, rang of fragment size and monomorphic bands produced by using seven random primers (RAPD-PCR) for studied groups.

Bands	Sheep		
	El-Adely (HORS)	El-Adely (HMYS)	Ossimi
Total number	61	70	78
Range (bp)	1422-120	1406-109	1665-140
Monomorphic	26	23	29

Table (11): Similarity matrix among of the three studied sheep groups based on RAPD-PCR analysis.

Bands	El-Adely (HORS)	El-Adely (HMYS)	Ossimi
El-Adely (HORS)	1.00		
El-Adely (HMYS)	0.82	1.00	
Ossimi	0.50	0.57	1.00

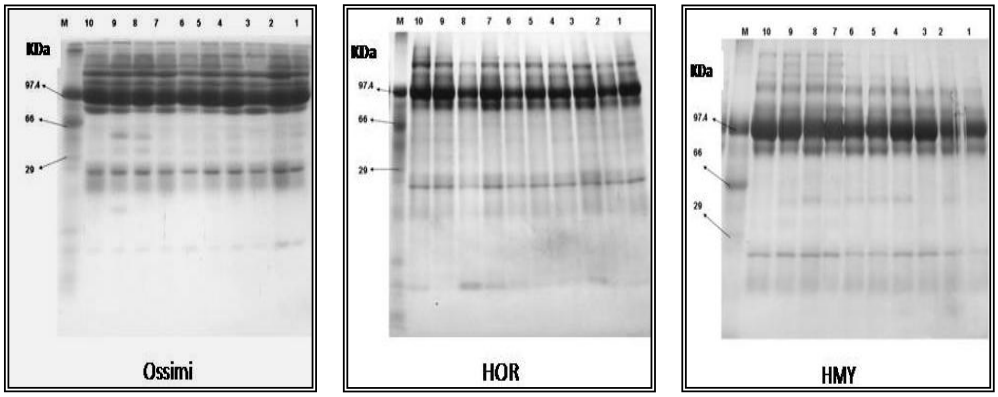

Fig. (1): Plasma protein electrophoretic pattern as revealed by gel electrophoresis of studied sheep groups.

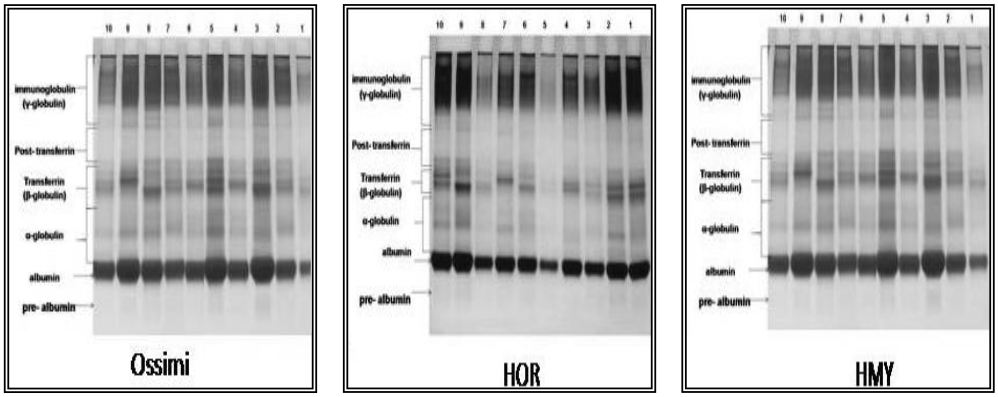

Fig. (2): Plasma protein electrophoretic pattern as revealed by native gel electrophoresis of of studied sheep groups.

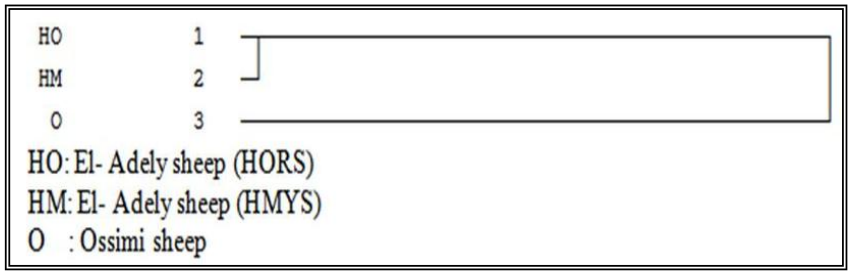

Fig. (3): Dendrogram for the genetic distance for studied breed and strains based on, SDS-PAGE and Native-PAGE.

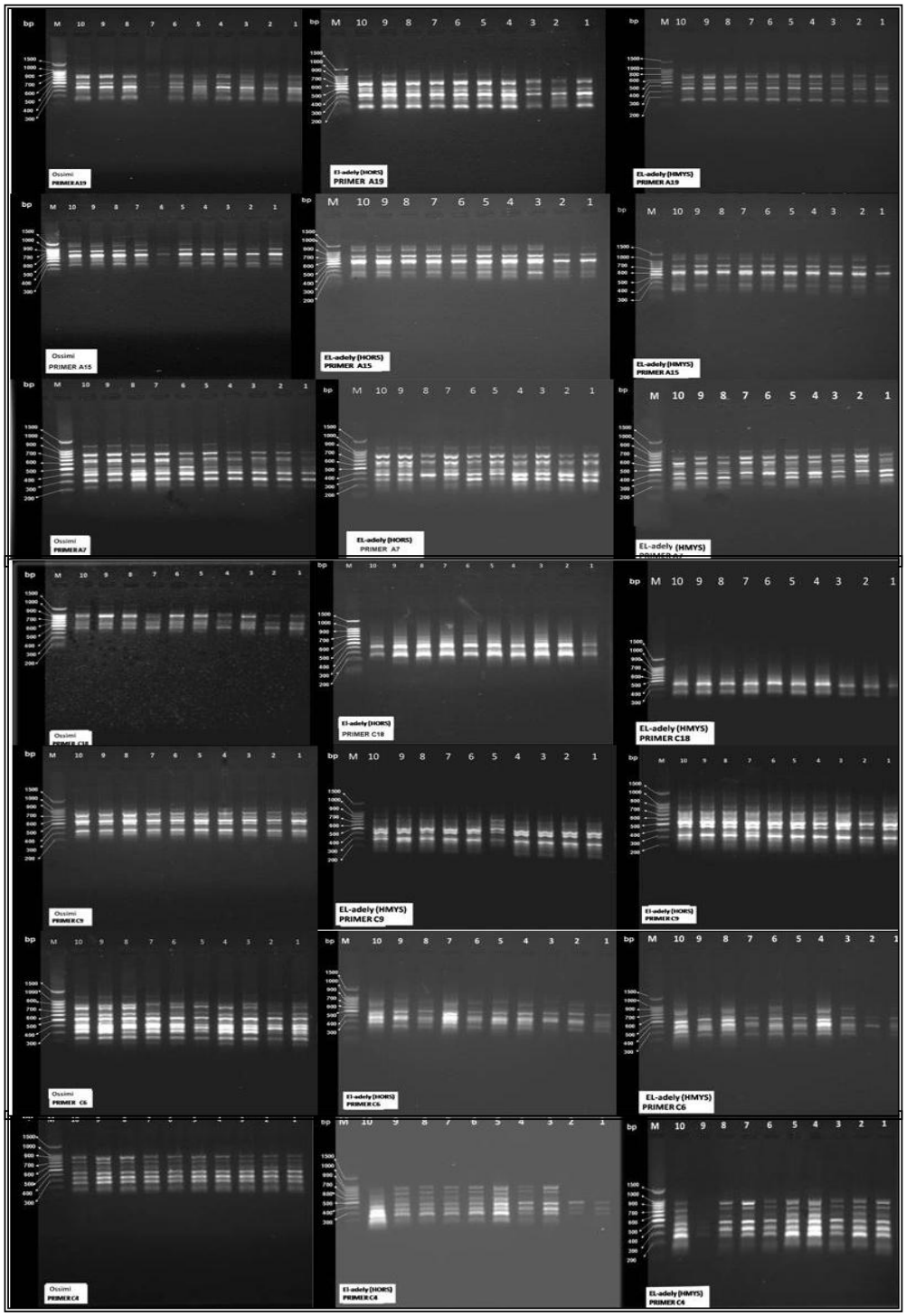

Fig. (4): RAPD-PCR-fragments using seven primers for Ossimi breed, El-Adely HOR strain and El-Adely HMY strain individuals.