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Some Genetic Variation Parameters of Iraqi Sheep Population Using SSR Markers in Babylon City

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Abstract: This study focuses on designing a conservation indigenous Awassi sheep breeding program based on the analysis of genetic variation using the simple sequence repeat markers (SSR). The allele frequency distribution of six SSR markers distributed on three different chromosomes was used to determine the genetic variation among 50 Awassi sheep (15 from the north, 20 from the middle, and 15 from the south of Babylon city) that were collected from the private herds. The results showed that the RM32 marker exhibited high frequency and the most genotypes existed compared to other markers. The mean number of alleles (NA), the effective number of alleles (NE), the Shannon index (I), and the polymorphism information content (PIC) values per loci were 2.66 ± 0.81, 2.05 ± 0.87, 0.73 ± 0.42, and 0.37± 0.26 respectively. Also, the average observed (Obs_Hom), expected (Exp_Hom) homozygosity, observed (Obs_Het), expected (Exp_Het) heterozygosity, Nei's expected heterozygosity, and inbreeding coefficient (FIS) were 0.77± 0.18, 0.56 ±0.25, 0.23 ± 0.18, 0.44 ±0.25, 0.43± 0.24, and 0.41± 0.12, respectively. The results of the Bayesian analysis revealed that all populations were homogenous there was a clear overlap between the individuals of the three distinct clusters were formed. On this basis, we conclude that the indigenous Awassi sheep in Babylon city have reasonable genetic variation.

Keywords: Genetic variation, Indigenous Awassi sheep, Number of alleles, Shannon index, SSR marker

Introduction

All nation's native sheep breeds are valued as crucial resources and national capital that contribute to the nation's economic growth and food security (Gizaw *et al.,* 2011). The genetic conservation of these valuable resources should be a priority of the statesmen and the general public of that country (Taberlet *et al*., 2011; Faraj *et al*., 2020). Due to its strategic geographical location, the country of Iraq is considered one of the richest countries in terms of the variation of its genetic resources (Ajmone-Marsan *et al*., 2023). The native livestock breed is the result of mutation processes, genetic drift, and individual adaptation that have been achieved over many years (Naskar *et al*., 2012). This native sheep breed is the result of natural selection in a specific climate under the challenges of diseases, environmental stresses, and favorable criteria for the human societies of that region, and in fact, each breed is a unique pool of valuable genes according to its area (Kristensen *et al*., 2015).

In Iraq, there are three main breeds of sheep, including Awassi, Arabi, and Karadi (Iniguez, 2005; Fadhil & Al-Shuhaib, 2022). Some of the second breeds of sheep, such as Naimi belonging to Awassi, Hamdani belonging to Karadi, and Shefali belonging to Arabi sheep (Alkass & Juma, 2005). These sheep breeds are characterized by their low productivity due to genotypes ability, poor nutrition and health care (Alkass *et al.,* 2021; Aljubouri & Al-Shuhaib, 2023). Studying the genetic variation of these breeds is important to improve their production characteristics and increase their resistance to infectious diseases, as well as to help supply livestock products to the market, including meat, milk, and wool (Alwan *et al.,* 2023).

A level of biological diversity, genetic variation describes the condition of a species' genes and genetic makeup and serves as a breed's primary defense against harsh environmental conditions (Hoban *et al.,* 2022). Understanding the germplasm organization, the inbreeding index in populations, the selection of parents with high heterozygosity to form the initial nucleus of animal breeding, the proper management of genetic resources, and the molecular indicators of genetic variation in indigenous sheep breeds are the first steps in designing genetic conservation programs (Tapio *et al.,* 2005, Asmare *et al.,* 2023).

The principle of simple sequence repeats (SSR) markers, initially introduced by Jeffreys *et al*. (1985), refers to short repeating sequences found in the genomes of organisms and is one of the methods for genetic diversity at the genome level. The majority of vertebrate species have simple sequence repeats (SSRs), with the genomes of mammals including humans, cows, sheep, and goats having the highest frequency of repetitions (Li *et al.,* 2022).

In order to maintain the genetic diversity of the native Awassi sheep of Babylon City, Iraq, this study intends to gather data and markers of population genetic variation, and the data will then be interpreted to inform management choices.

Materials & Methods

Sampling and Blood Collection

Fresh blood samples were collected from the jugular veins using 10 ml containing EDTA from 50 unrelated Awassi sheep breed (15 from the north, 20 from the middle, and 15 from the south of Babylon City (Fig. 1). The samples were sent to the Laboratory of Physiology and Genetic Engineering in the Department of Animal Production Techniques at the Al-Musiab Technical College/Al-Furat Al-Awsat Technical University, Babylon, Iraq.

DNA Extraction and Genotyping

DNA was extracted according to the commercial kit method (Geneaid, USA) and by the instructions in the kit. Spectrophotometry and electrophoresis were used to determine the amount and quality of DNA. The gel concentration for loading the genome sample was 1%. The six SSR markers (Table 1), used in this study are recommended by the International Society of Animal Genetics (ISAG)/FAO to study genetic variation in sheep (FAO, 2011).

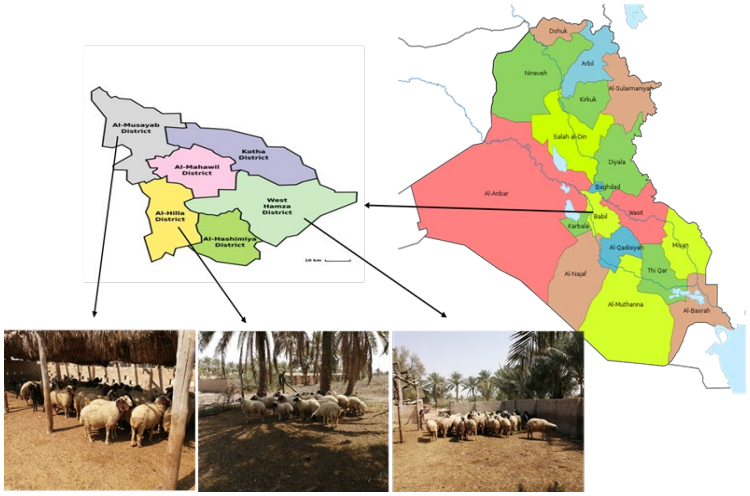


Fig. (1): Geographical distribution of indigenous Awassi sheep populations in Babylon City, Iraq.

Polymerase Chain Reaction (PCR)

PCR specific program, which was designed to simultaneously amplify the loci and minimize nonspecific and starter bands. The "touchdown" PCR protocol included Initial denaturation of 94°C for 10 minutes, 10 cycles containing {denaturation of 95 °C for 1 min, decreasing annealing temperature from 68 to 58C° for 1 min, extension at 72°C for 30 sec, and finally the final amplification temperature was set to 72°C for eight mins. The PCR products were loaded inside after mixing with weighting buffer and loaded inside the 2% Agarose gel and a ladder with 11 lines (25-755 bp) (Life Sciences Corporation) was used to estimate the allele size.

Statistical analysis

POPGENE version 1.31 (Yeh *et al*., 1997), GenAlEX version 6.5 (Excoffier & Lischer, 2010), and STRUCTURE version 2.3.4 (Pritchard *et al*., 2000) were used to calculate indicators and statistics such as genetic variation (similarities and differences) within populations, the genotypes, allele frequency, homozygosity, heterozygosity, Nei, FIS, F-statistics, phylogeny tree, allele admixture, population structure.

Results & Discussion

After confirming the desired SSR markers, electrophoresis was performed on agarose gel of PCR products and then the gels were stained. Fig. (2) showed the samples of banding patterns obtained for the SSR marker's position in the indigenous Awassi sheep populations.

The results of table (2) show the presence of genetic variation for the SSR markers studied within the same local Awassi sheep, as it was noted that the number of alleles found in the sheep reached 16 alleles The number of alleles for studying SSR included three alleles for OarfCB20 and TGLA137, two alleles for OarAE129, ILSTS011, and MCMC527, and four alleles for RM32. The animals carried the alleles 136 or162 for OarfCB20 and OarAE129. Aside from that, the alleles 96 or 94 or 105 for 110RM32, TGLA137, ILSTS011 and the alleles 1161 and 165 for MCMC527 were all present. The allele frequency analysis showed that the dominant alleles for OarAE129, ILSTS011, TGLA were 137, 94, and 145 and alleles 136, 253, and 161, respectively. Whereas, the dominant allele for MCMC527 was 161. The dominant allele for OarfCB20 was 99 and OarAE129 was 136.

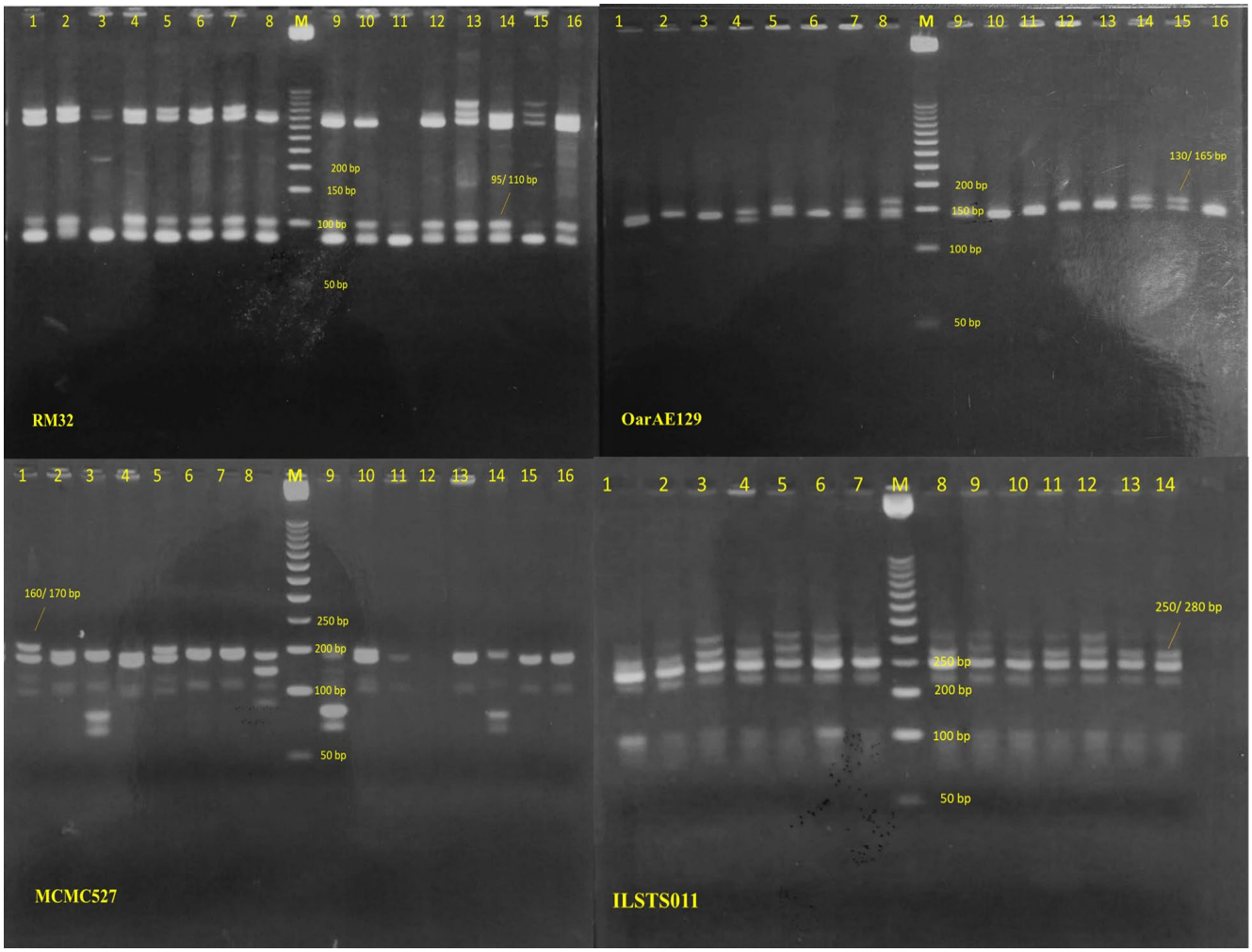


Fig. (2): Agarose gel electrophoresis of SSR markers in indigenous Awassi sheep using 2% agarose gel.

The study of genetic variation plays an important role in developing strategies for breeding and improving animals. The SSR markers in farm animals have been widely used to estimate genetic variations between and within breeds. Our study investigated the genetic variation in indigenous Awassi sheep in Babylon province using 6 SSR genetic markers, as it was noted that all SSR markers are polymorphic. A study was conducted to determine the amount of genetic variation in indigenous Iraqi sheep for a number of SSR markers used. The results of the RM32, OarfCB20, and TGLA137 research indicate differences in the size and number of alleles, which can be used in the study of genetic variation and the relationship between individuals within and between local Awassi sheep breeds. These results are in accordance with that obtained by (Hadi *et al*., 2020; Kirikci *et al*., 2020; Alnajm *et al*., 2021). The SSR markers used in the study contain low allele frequencies, and this is due to the use of a small number of animals. These results were similar to some studies conducted to study genetic variation within Awassi breeds based on SSR markers, which indicated that they contain genetic variation at a certain level when detected using genetic markers (Owaid, 2015; Hadi *et al*., 2020).

Table (2): Locus, Chromosome location (Chr.), Size range S.R. (bp), Genotype (number of individuals), Alleles (A.) and Alleles frequency (A. F.) of studying markers

Locus	Chr.	S. R. (bp)	Genotype	A.	A. F.
OarfCB20	2	94- 105	94/94 bp (20)	94	0. 48
			99/105 bp (1)	105	0.01
			99/99 bp (22)	99	0.51
			94/99 bp (7)		
OarAE129	5	136- 162	136/136bp (43)	136	0.910
			136/ 162 bp (5)		
			162/ 162 bp (2)	162	0.090
ILSTS011	9	253- 279	253/253bp (45)	253	0.950
			279/253 bp (5)	279	0.050
TGLA137	2	135 – 152	135/135 bp (6)	135	0.120
			145/145 bp (30)	145	0.650
			145/152 bp (5)	152	0.230
			152/ 152 bp (9)		
RM32	2	94 – 110	94/94 bp (9)	94	0.210
			96/94 bp (2)	96	0.430
			96/96 bp (20)	105	0.160
			110/ 94 bp (1)	110	0.200
			110/ 96 bp (1)		
			110/105 bp (16)		
			110/ 110 bp (1)		
MCMC527	5	161 – 165	161/ 161 bp (18)	161	0.610
			161/ 165 bp (25)	165	0.390
			165/ 165 bp (7)		

The number of alleles per locus (NA) ranged from 2.00(OarAE129, ILSTS011, and MCMC527) to 4 (RM32), so the observed mean number of alleles per locus was 2.66 ± 0.81 (Table 3). The effective number of alleles (NE) ranged from 1.10 (ILSTS011) to 3.39 (RM32), with a mean of 2.05 ± 0.87 (Table 3). The Shannon index (I) per locus diverse from 0.19 for ILSTS011 to 1.30 for RM32, while the overall mean for SSR markers within animals was 0.73 ± 0.42. Estimates of polymorphic information content (PIC) varied from 0.09 for ILSTS011 to 0.65 for RM32, with a mean of 0.37± 0.26 (Table 3).

The number of alleles at different loci serves as a measure of genetic diversity in all animals. These results are larger than (Ahmed *et al.,* 2022), but lower than (Jehan *et al.,* 2022; Odjakova *et al.,* 2023; Mihailova *et al.,* 2023). In studies of population variation, Shannon's index is the most used, which considers the abundance and evenness of the studied breeds. These results are lower than those by (Oner *et al.,* 2014; Odjakova *et al.,* 2022), but higher than (Nigussie *et al.,* 2019). The low mean PIC value detected across 6 SSR loci indicates that some of these SSR markers have the ability to show genetic variation in Awassi sheep populations. PIC is an important feature for molecular studies and

PIC value is a function of allele number and frequencies. The 2 out of 6 SSR markers display PIC values higher than 0.5, therefore, the means PIC considering all SSR markers showing that the markers panel used was lowly informative. Although the result mean PIC value was lower than (Yilmaz *et al.,* 2015; Karsli *et al.,* 2020).

Table (3): Genetic parameters measured in the local Awassi sheep breed using 6 SSR markers.

Locus	NA	NE	I	PIC
OarfCB20	3.00	2.69	1.04	0.55
OarAE129	2.00	1.19	0.30	0.15
ILSTS011	2.00	1.10	0.19	0.09
TGLA137	3.00	2.04	0.87	0.45
RM32	4.00	3.39	1.30	0.65
MCMC527	2.00	1.92	0.67	0.36
Mean	2.66	2.05	0.73	0.37
St. Dev	0.81	0.87	0.42	0.26

St. Dev.: Standard deviation; Na: number of alleles observed; Ne: effective number of alleles and I: Shannon index; PIC: polymorphic information content

The observed (Obs_ Hom) and expected (Exp_ Hom) homozygosity, observed (Obs_ Het) and expected (Exp_ Het) heterozygosity, Nei's expected heterozygosity, and inbreeding coefficient (F_{IS}) for each locus are indicated in table (4). The mean number of observed (Obs_ Hom) and expected (Exp_ Hom) homozygosity values for the 6 SSR markers was 0.77± 0.18 and 0.56 ±0.25 respectively. The highest and lowest observed (Obs_ Hom) homozygosity for a single locus were 0.80 for OarAE129, ILSTS011, and TGLA137 and 0.48 at MCMC527, respectively. The lowest (0.28) and the highest (0.90) expected (Exp_ Hom) homozygosity values were detected in RM32 and ILSTS011, respectively. The observed heterozygosity (Ho) ranged between 0.10 ((OarAE129, ILSTS01, and TGLA137) to 0.51 (MCMC527), while expected heterozygosity (He) ranged between 0.09 (ILSTS011) to 0.71 (RM32). The mean values of the observed and expected heterozygosity were 0.23 ± 0.18 and 0.44 ±0.25 in local Awassi sheep, respectively (Table 4). The Nei's unbiased gene diversity (HS) in local Awassi sheep varied between 0.09 in ILSTS011 and 0.70 in RM32 and the mean values were 0.43± 0.24 (Table 4). Inbreeding coefficients (F_{IS}) for all markers are also given in table (4). The mean value for overall SSR markers of local Awassi sheep was 0.41± 0.12 (ranging from -0.06 at MCMC527 to 0.80 in TGLA137).

The results showed that the (Exp_Hom) is less than the observed (Obs_Hom) homozygosity, and this indicates that the animals are improving and the genetic variation is increasing, but the observed (Obs_Het) and expected (Exp_Het) heterozygotes are also improving, and the reason is probably due to the use of males in different areas and low inbreeding. These results are in agreement with (Ebrahimi *et al.,* 2016; Mahmoud *et al*., 2020), but the results are lower than those (Pichler *et al.,* 2017; Jawasreh *et al.,* 2018; Sharma *et al.,* 2020). The Nei's measure of the average gene variation per locus, HS (Nei, 1973); the measure of average differences within and between populations. The results Nei's unbiased gene diversity of this research was low because the number of animals is small

and inbreeding is high. These results lower than (Mukhongo *et al*., 2014; Xia *et al*., 2021). The coefficient of inbreeding (F_{IS}) was positive in four SSR markers, but the others were negative, which indicates a low risk of inbreeding. This result is lower than (Zeng *et al.,* 2010) but higher than (Hristova *et al.,* 2017; Karsli *et al.,* 2020).

Table (4): Genetic variation at 6 SSR loci characterized in the indigenous Awassi sheep.

Locus	Obs_ Hom	Exp_ Hom	Obs_ Het	Exp_ Het	HS	F_{IS}
OarfCB20	0.86	0.36	0.14	0.63	0.62	0.77
OarAE129	0.90	0.83	0.10	0.16	0.16	0.38
ILSTS011	0.90	0.90	0.10	0.09	0.09	-0.05
TGLA137	0.90	0.48	0.10	0.51	0.51	0.80
RM32	0.60	0.28	0.40	0.71	0.70	0.43
MCMC527	0.48	0.51	0.51	0.48	0.47	-0.06
Mean	0.77	0.56	0.23	0.44	0.43	0.41
St. Dev	0.18	0.25	0.18	0.25	0.24	0.12

St. Dev.: Standard deviation; Obs_ Hom: Observed homozygosity; Exp_ Hom: Expected homozygosity; Ho: observed heterozygosity; He: expected heterozygosity; HS: Nei's unbiased gene diversity, and F_{IS}: coefficient of inbreeding.

According to the results in table (5), the within-population inbreeding coefficient Fis varied from -0.074 to 0.745 per marker with a positive overall mean (0.383), as presented in table (5). Four markers had positive Fis estimates (OarfCB20, OarAE129, TGLA137, and RM32). The total population Fit and subpopulation Fst values displayed positive values with mean values of 0.459 and 0.122. The average inbreeding coefficient of an individual related to the whole population (Fit varied between -0.071 for MCMC527 and 0.786 for TGLA137, and the measurement of population differentiation (Fst) ranged from 0.003 (MCMC527) to 0.216, obtained for OarfCB20. The mean gene flow (Nm = 1.506), and the range of 0.734 (ILSTS011) to 2.092 (OarAE129) for different SSR markers (Table 5). The values of the inbreeding within each population (Fis), the inbreeding coefficient for all populations (Fit), and the coefficient of genetic differentiation between populations (Fst). The Fst showed that only 12.2% of the total genetic variation in Awassi sheep breeds in the three regions is due to population differences, while the remaining 98.8% corresponds to differences among individuals. The low value of Fst shows that the studied sheep samples of the regions are not differentiated enough, because there is reasonable gene flow between different geographical populations. The low differentiation between Awassi sheep in Babylon City could be due to geographical proximity, similarity in the environment, breeding practices, and a common origin, but it is most likely due to past and present gene flow among them. These genetic differentiation estimates were higher than those reported in other genetic variation studies (Ibrahim *et al.,* 2010; Ocampo *et al.,* 2016; Markovic *et al.,* 2022), but lower than those (Kusza *et al.,* 2008; Musthafa *et al.,* 2012). The highest gene flow helps in decreasing the level of interbreeding. These results (mean = Nm) are lower than (Ibrahim *et al.,* 2010; Hristova *et al.,* 2017), but higher than (Jehan *et al.,* 2022).

Table (5): Summary of F-statistics and gene flow for all SSR loci in the local Awassi sheep breeds.

Locus	Fis	Fit	Fst	Nm
OarfCB20	0.674	0.744	0.216	0.907
OarAE129	0.306	0.380	0.106	2.092
ILSTS011	-0.070	-0.049	0.025	0.734
TGLA137	0.745	0.786	0.163	1.284
RM32	0.345	0.416	0.108	2.057
MCMC527	-0.074	-0.071	0.003	1.963
Mean	0.383	0.459	0.122	1.506

Fis: within-population inbreeding coefficient; Fit: total population inbreeding coefficient, Fst: genetic differentiation coefficient between subpopulations (North, Middle, South), and Nm: gene flow.

The Nei (1978) standard genetic distance (D_A) matrix showed that the Middle and North Awassi sheep were the closest apart (0.797), whereas the South and North native Awassi sheep were the furthest (0.965) (Table 6). Also, the highest genetic identity was observed between the North and Middle local Awassi sheep (0.225). The lowest genetic identity (0.034) was between the North sheep and the South sheep Awassi breed.

In this result, the genetic distances within the examined sheep populations were relatively low, because some indicate certain differences in their genetic structure. The standard genetic distance matrix showed that the North and South local Awassi sheep were the furthest whereas the Middle and South were the closet. The closest genetic relatedness was found between North and South local Awassi sheep in accordance with their similar phenotypic traits. The reason is that all sheep live in the same geographical area, with similar phenotypic traits and there are common genes among them. These results are similar to (El Nahas *et al.,* 2008; Ibrahim *et al.,* 2010; Xia *et al*., 2021).

Table (6): Matrix of Nei's standard genetic distances among Awassi sheep in the studied Babylon regions.

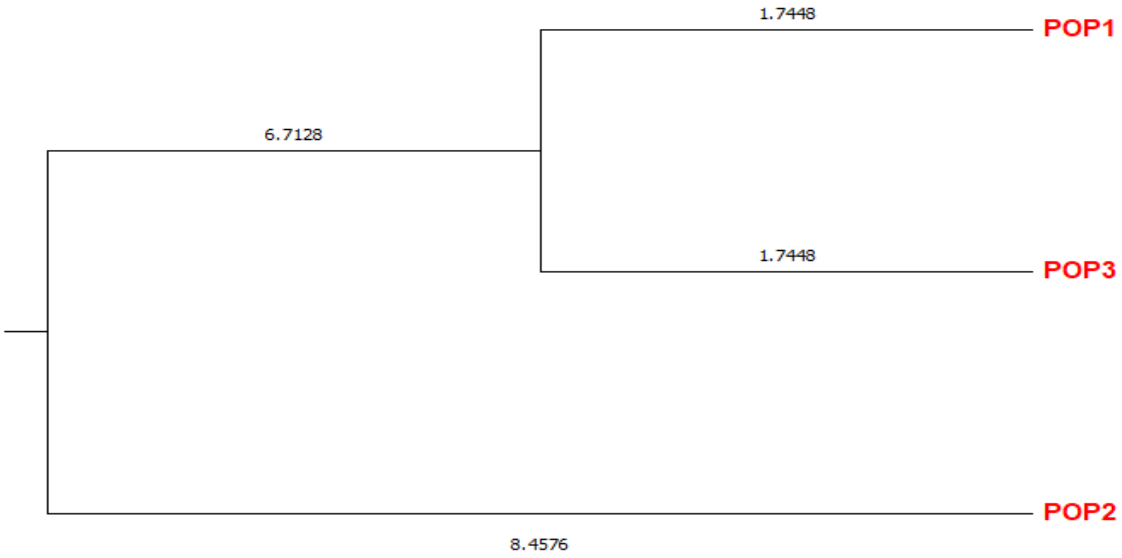
Local sheep regions	South	Middle	North
South	0.000	0.893	0.965
Middle	0.112	0.000	0.797
North	0.034	0.225	0.000

Genetic distance (above diagonal) and genetic identity (below diagonal).

Based on Nei's genetic distance, the UPMGA method was used for cluster analysis of three Awassi sheep populations, the phylogenetic and phylogeographic analysis revealed that the relationships among Awassi sheep breeds showed some degree of consistency with their geographical distribution, origin, and production. These results indicated that POP2 (Middle) was the more distanced local Awassi sheep, while POP1 (South) was more closely related to the POP3 (North) Awassi sheep breeds (Fig. 3).

The phylogenetic tree showed that POP1 (North) was grouped together with POP3 (South), but the POP2 (Middle) Awassi sheep furthest. This can again be explained in terms of the history and geographic location of these local sheep. The genetic distances between these populations are consistent with the expected relationships between ecotypes, given that the study areas are located in the same city and also due to the common rams used. These results are similar to (Elfawal *et*

al., 2008; Agaviezor *et al*., 2012; Karsli *et al*., 2020).



(**POP1**: South, **POP2**: Middle, and **POP3**: North)

Fig. (3): UPGMA tree constructed from D_A distances, showing the relationships among Awassi sheep populations in the three Babylon regions.

Based on the level of admixture in each sheep, the genetic population was determined. Each individual analyzed was shown by a single vertical line divided into colored parts (Fig. 4). Bayesian clustering analysis recovered three genetic clusters, and the K = 4 (Fig. 4A) based on the structure Harvester (Earl & VonHoldt, 2012). The value suggests that the studied Awassi sheep were superior defined by three genetic clusters. As it was found that the best genetic variation is found in the animals located in the south of Babylon, and the lowest in the middle (Fig.4. B). Fig. (4C) showed cluster analysis of 50 animals of three Awassi sheep populations, and the colors showed the extent of the similarity between individuals.

The distribution of genetic admixture alleles and classification was obtained based on the model. In fig. (4B), which is related to the sheep population of the South region, the size (range) of the colors assigned to that population is more than the other two populations, and these colors indicate the number of alleles in that population, and fig. (4C), which is related to the Awassi sheep population of three regions, shows that the individuals of these regions are very similar in the city of Babylon. This result is expected because the sheep live in the same area, there is an overlap between genes, and their migration between the areas is very easy. These results agree with some researchers (Harkat *et al*., 2017; Schönherz *et al*., 2020; Ben Sassi-Zaidy *et al*., 2022).

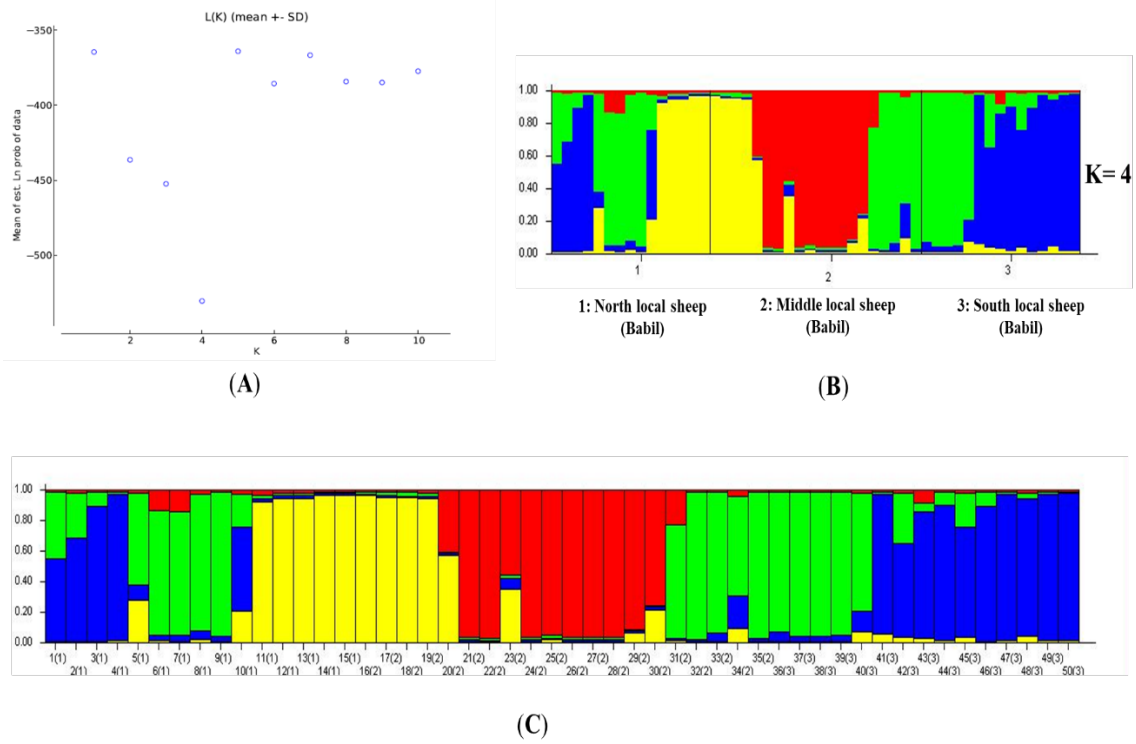


Fig. (4): A. The plot of delta "K" values from the structure analyses of indigenous sheep populations. B. Genetic structures of three regions. C. Cluster analysis of 50 animals of three Awassi sheep populations.

Conclusion

The findings of this study advance our understanding of the genetic diversity and morphology of the ancestral Awassi sheep breeds in the Babylonian province. In addition to ensuring sustainable management, conservation efforts, and maintenance of local genetic resources to preserve the sheep's genetic heritage, the resulting information can be a valuable resource for breeding management to decrease the lack of heterozygosity, improve the breed and increase production. Overall, the findings demonstrated that sheep had improved genetically through the application of precise sequences. Scientific management is needed to protect genetic diversity indicators, valuable genetic resources in danger of becoming extinct.

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Contributions of authors

H.R.A.: Research idea, collecting samples, lab work and writing.

A. J.: The statistical analysis the data.

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Conflicts of interest

We declare that there is no conflict of interest.

Ethical approval

The ethical approval was obtained from the Institutional Animal Care and Use Committee No. 2538 dated 2/9/2023 from Al-Furat Al-Awsat Technical University.

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بعض معايير التباين الوراثي في قطعان الأغنام العراقية باستخدام واسمات SSR في مدينة بابل

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المستخلص: تركز هذه الدراسة على تحليل التباين الوراثي باستخدام واسمات التتابعات الدقيقة. تم استخدام التوزيع التكراري لاليلات ستة تتابعات متكررة للتسلسل البسيط (SSR)موزعة على ثلاث كروموسومات مختلفة لتحديد التباين الوراثي بين 50 رأس من الاغنام المحلية (15 من الشمال، 20 من الوسط، و15 من جنوب مدينة بابل) التي كانت عينات من القطعان العامة. أظهرت نتائج هذا البحث أن الواسم RM32 يحتوي على ترددات عالية وأكثر التراكيب الوراثية مقارنة بالتتابعات الدقيقة الأخرى. كان متوسط عدد الأليلات المشاهد (NA)، العدد الفعال للأليلات المتوقع (NE)، مؤشر شانون (I)، ومحتوى معلومات تعدد الأشكال (PIC)لكل موقع 2.66 ± 0.81، 2.05 ± 0.87، 0.73 ± 0.42، و0.37 ± 0.26 على التوالي. كان متوسط تجانس الهيموزايكوت المشاهد (Obs_Hom)، الهيموزايكوت المتوقع (Exp_Hom)، الهيتيروزايكوت المشاهد (Obs_Het)، الهيتيروزايكوت المتوقع (Exp_Het)، تغاير الزايكوت المتوقع لـ Nei، ومعامل التربية الداخلية (F_{IS}) هو 0.77 ± 0.18، 0.56± 0.25، 0.44±0.18، 0.43±0.24، 0.41± 0.12على التوالي. كشفت نتائج تحليل بايزي أن جميع مجتمع الاغنام كانوا متجانسين وكان هناك تداخل واضح بين الأفراد وتم تشكيل ثلاث مجموعات متميزة. وعلى هذا الأساس نستنتج أن الأغنام المحلية في مدينة بابل المدروسة لديها تباين وراثي معقول.

الكلمات المفتاحية: التباين الوراثي، الأغنام العواسية المحلية، عدد الأليلات، مؤشر شانون، التتابعات الدقيقة SSR.