Global Veterinaria 15 (3): 304-308, 2015
ISSN 1992-6197

DOI: 10.5829/idosi.gv.2015.15.03.96249

Genetic Diversity among Three Goat Breeds in Saudi Arabia Using DNA Markers

[1]Ahmed Abdel Gadir Adam, [2]Nada Babiker Hamza,
[3]Manal Abdel Wahid Salim and [4]Khaleil Salah Khaleil

[1]University of Taif, Faculty of Art and Science Raniah Branch, Raniah, Kingdom of Saudi Arabia
[2]Comission for Biotechnology and Genetic Engineering,
National Centre for Research, P.O. Box 2404, Khartoum, Sudan
[3]Animal Production Research Center, Kuku, Khartoum North, Sudan
[4]Ministry of Agriculture, Raniah Province, Kingdom of Saudi Arabia

Abstract: The genetic variation in Ardi, Jabali and Shami Saudi goat breeds, prevailing in Raniah province of Makka district, was assessed and compared to Sudanese Nubian goat using RAPD technique. Five primers successfully amplified distinguishable 48 bands with 95% polymorphism. The result indicated that the Nubian goats are genetically distant and appeared as out-group to the Saudi breeds. The constructed UPGMA dendrogram showed that there are two main separate clades. The first main clade contained most of the Ardi goats breed. However, the second main clade was divided into three clusters. The first cluster contained the rest of the Ardi and one sample from Jabali goats, the second cluster included all Jabali goats, while the third cluster grouped the Shami goat together. Results also revealed that Ardi goat breed has high genetic variability in comparison with the other two Saudi goat breeds. The present study will help to clarify the image of the genetic diversity of these local Saudi goat breeds in Raniah province. Further studies are needed using large number of animals from different geographical regions in the kingdom.

Key words: Dendrogram · Genetic variability · RAPD-PCR · Saudi Goats

INTRODUCTION

Goat (*Capra hircus*) is one of domesticated small ruminants which are either managed for production of milk, meat, wool or leather. However, goats like other livestock species are facing a decline in genetic biodiversity and are at risk of extinction [1, 2]. The genetic biodiversity of livestock species, including goats, are threatened by indiscriminate crossbreeding with cosmopolitan breeds and uncontrolled intermixing [3]. This loss of genetic biodiversity has been leading into a loss of invaluable opportunities for both science and agriculture [4]. Comprehensive knowledge of the existing genetic variability is the first step for conservation and exploitations of domestic animal biodiversity.

In the Kingdom of Saudi Arabia (KSA), goat population is estimated to be 1.06 million [5]. In Raniah province, of Makka district alone, number of goats is estimated to be around 200,000 [6]. Widely spread goat breeds in KSA are mainly Ardi, Jabali and Shami goats. Ardi goats are medium-sized, black colored, well-adapted to arid conditions and produce less (3 litre/day for 120-150 days) but persistent milk production. The Shami goat is a native breed of Syria and other Near East countries. It has a reddish brown coat, white spots on the body, legs and face. The ears are long and pendulous and the head is long with a Roman nose. The JabaliI goats are black, with dropping ears and a curved head. Both sexes have horns with the majority of goats having no tassels [7]. Both Shami and Jabali goats are considered to be best dual-purpose breeds.

There is scarce information on the phylogeny and genetic variability of different Saudi goat breeds. Moreover, few steps have been undertaken for genetic improvement of these local adaptive genetic resources. This necessitates characterization of different Saudi goat breeds to determine their genetic variability. However, breed characterization requires the knowledge of genetic variation that can be effectively measured within and between populations. The traditional phenotypic

Corresponding Author: Ahmed Abdel Gadir Adam, University of Taif, Faculty of Art and Science Raniah Branch, Raniah, Kingdom of Saudi Arabia. Tel: +966550983644, E-mail: gadour_63@yahoo.com.

characterization can now be complemented by molecular markers and sophisticated statistical techniques for data analysis. Random amplified polymorphic DNA (RAPD) is a polymerase chain reaction (PCR) based fingerprinting technique that amplifies random DNA fragments with single short primers of arbitrary nucleotide sequence under low annealing stringency [8, 9]. It is a simple and easy method to use for estimation of genetic variability among breeds or species [10, 11]. This technique has an extra advantage that it does not require any sequence information on the target genome. The present study was conducted to assess the genetic diversity of three Saudi goat breeds (Ardi, Jabali and Shami) and Nubian goat as exotic breed using RAPD technique. It was hypothesized that Saudi goat breeds do not genetically differ among themselves or with other exotic breeds.

MATERIALS AND METHODS

Study Area: The study was conducted in Raniah Province of Makkah district (12° 30 N, 42° E) in the western part of Saudi Arabia extending over 62,000 km^2. The study area is characterized by hot arid desert type climate, with average annual rainfalls and a relative humidity of 90 mm and 22%, respectively. Temperature ranges between 34 - 45°C and zero - 20°C during summer and winter, respectively [6].

Animals and Collection of Blood Samples: Blood samples were collected from twenty eight adult (Full-mouthed) unrelated females, which were randomly selected from three Saudi goat breeds (Ardi, Jabali and Shami) and Sudanese Nubian goat breed. Sixteen, seven, two and three individual goats were randomly sampled from Ardi, Jabali, Shami and Sudanese Nubian breed, respectively. Blood samples were collected from sampled individual goat breed into EDTA coated vacutainers and were kept at -20°C before being used for extraction of genomic DNA.

Genomic DNA Extraction and PCR Amplification: Genomic DNA was extracted from peripheral blood leukocytes according to instructions of blood DNA preparation kit (Jena Bioscience, Germany). The PCR amplification was performed in a 25µl reaction volume, using Promega PCR Master Mix according to the instructions by the manufacturer with 30 Pmol from each of the 18 primers tested. Amplification was done through initial denaturation at 94°C for 2 min, followed by 35 cycles consisting of denaturation at 94°C for 30 s, annealing at 55°C for 30 s, extension at 72°C for 2 min and a final extension at 72°C for 2 min. Thereafter, amplified products were electrophoresed on 1.5% agarose gel at constant voltage and 1X TBE for approximately 1.5 h. Thereafter, products were visualized by staining with ethidium bromide, photographed under ultraviolet light and their molecular weights were estimated using 1Kbp DNA ladder.

Scoring and Statistical Analysis: Amplification profiles of four breeds of goat were compared with each other. The presence of a band of amplified DNA was scored as (1) and absence as (0). The genetic dissimilarity matrix among genotypes was estimated according to Nei and Lei [12]. Pairwise genetic distances between individuals were calculated by the percentage disagreement method. These data were used in cluster analysis with the unweighted pair-group method using arithmetic averages (UPGMA), in which samples were grouped based on their similarity with the aid of statistical software package [13].

RESULTS AND DISCUSSION

Recently, attention has been paid to the use of DNA marker in studying genetic characterization of Saudi goat [14]. However, genetic characterization should be a continuous process of surveying and monitoring of the different breeds [15]. Therefore, this study also investigated the genetic diversity of Saudi goat breeds prevailing in Raniah province. Five primers, out of 18 tested, successfully amplified polymorphic identical band patterns with similar intensity (Figure 1). Out of the total distinguished 48 amplified fragments, 46 were polymorphic bands with an average of 9.2 bands per primer. The maximum number of fragment (13 bands) was produced by primers OPE-18 with 100 % polymorphism, while the minimum numbers of fragments were produced by primer OPB-3 with 83.33% polymorphic rate (Table 1). The high proportion of polymorphic bands (95.8%) noted in the present study was an indication of high genetic diversity among the studied Saudi goat breeds. The results show that DNA markers may be used to resolve genetic difference of even closely related goats. Moreover, the existence of a large gene pool in goat breeds could be important for future breed conservation and development of sustainable goat production systems. Therefore this result suggests that Saudi goat breeds possess substantial genetic pool which could be required for further genetic improvement.

Table 1: The sequences of primers used and their polymorphic bands among three Saudi goat breeds

Primer	Sequence of primer (5' -3')	Total No. of bands	No. of polymorphic bands	No. of monomorphic bands	% of polymorphic bands
OPL-11	ACGATGAGCC	8	8	0	100
OPAL-20	AGGAGTCGGA	12	11	1	91.67
OPAL-15	AGGGGACACC	9	9	0	100
OPE-18	GGACTGCAGA	13	13	0	100
OPB-3	CATCCCCCTG	6	5	1	83.33
Total		48	46	2	
Average		9.6	9.2	0.4	95.8

RAPD primers from Operon Technologies Inc. (Alameda Calif., USA)

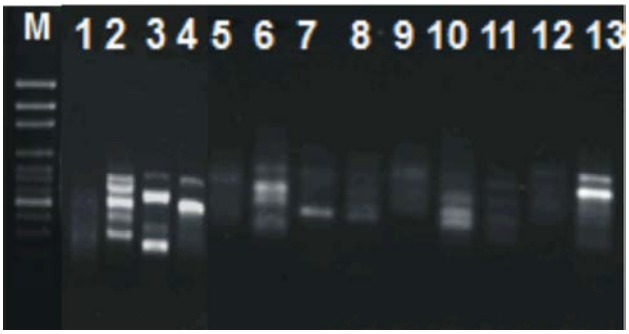

Fig. 1: RAPD fingerprint generated from Ardi goats using OPE18 primer

Table 2: Matrix of RAPD dissimilarity among three Saudi goat and Nubian breeds based on Nei & Lei coefficients

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	0.00																											
2	0.15	0.00																										
3	0.13	0.10	0.00																									
4	0.23	0.17	0.15	0.00																								
5	0.25	0.27	0.25	0.23	0.00																							
6	0.19	0.17	0.19	0.25	0.19	0.00																						
7	0.29	0.19	0.25	0.19	0.29	0.23	0.00																					
8	0.25	0.19	0.21	0.19	0.25	0.10	0.13	0.00																				
9	0.27	0.25	0.31	0.33	0.31	0.21	0.19	0.19	0.00																			
10	0.27	0.21	0.27	0.29	0.27	0.13	0.10	0.15	0.13	0.00																		
11	0.23	0.21	0.27	0.33	0.27	0.17	0.23	0.19	0.25	0.17	0.00																	
12	0.27	0.25	0.27	0.25	0.40	0.25	0.23	0.15	0.33	0.29	0.25	0.00																
13	0.27	0.25	0.27	0.29	0.31	0.29	0.27	0.23	0.42	0.33	0.25	0.08	0.00															
14	0.25	0.27	0.29	0.31	0.33	0.19	0.25	0.21	0.31	0.19	0.15	0.15	0.19	0.00														
15	0.38	0.40	0.33	0.35	0.38	0.35	0.29	0.25	0.40	0.31	0.27	0.27	0.27	0.25	0.00													
16	0.25	0.31	0.25	0.27	0.33	0.27	0.25	0.21	0.35	0.27	0.19	0.19	0.19	0.13	0.17	0.00												
17	0.29	0.35	0.25	0.31	0.29	0.31	0.29	0.25	0.40	0.31	0.19	0.23	0.23	0.17	0.17	0.08	0.00											
18	0.33	0.40	0.29	0.40	0.38	0.35	0.33	0.33	0.44	0.35	0.27	0.27	0.23	0.21	0.17	0.17	0.17	0.00										
19	0.29	0.40	0.33	0.40	0.50	0.35	0.38	0.29	0.44	0.40	0.31	0.19	0.27	0.21	0.29	0.21	0.25	0.21	0.00									
20	0.29	0.40	0.33	0.40	0.42	0.35	0.33	0.29	0.44	0.35	0.27	0.23	0.23	0.21	0.21	0.13	0.17	0.17	0.13	0.00								
21	0.25	0.35	0.29	0.35	0.42	0.31	0.33	0.25	0.40	0.35	0.27	0.23	0.27	0.25	0.25	0.17	0.21	0.21	0.08	0.08	0.00							
22	0.27	0.38	0.31	0.42	0.40	0.38	0.40	0.35	0.50	0.42	0.29	0.29	0.21	0.27	0.27	0.19	0.23	0.27	0.27	0.23	0.23	0.00						
23	0.27	0.33	0.35	0.42	0.40	0.29	0.35	0.31	0.46	0.33	0.29	0.33	0.29	0.27	0.31	0.27	0.31	0.31	0.31	0.23	0.23	0.21	0.00					
24	0.29	0.35	0.25	0.35	0.25	0.27	0.33	0.25	0.40	0.31	0.23	0.40	0.31	0.33	0.25	0.25	0.21	0.25	0.33	0.29	0.25	0.23	0.27	0.00				
25	0.31	0.38	0.35	0.46	0.35	0.33	0.27	0.31	0.25	0.29	0.25	0.42	0.38	0.35	0.31	0.27	0.27	0.27	0.40	0.31	0.31	0.33	0.29	0.19	0.00			
26	0.33	0.44	0.38	0.44	0.46	0.35	0.42	0.38	0.44	0.40	0.35	0.40	0.40	0.29	0.46	0.29	0.38	0.33	0.38	0.42	0.42	0.44	0.40	0.42	0.40	0.00		
27	0.33	0.44	0.42	0.48	0.46	0.35	0.42	0.42	0.40	0.35	0.35	0.44	0.44	0.29	0.46	0.33	0.42	0.33	0.42	0.46	0.46	0.48	0.40	0.46	0.40	0.04	0.00	
28	0.44	0.54	0.44	0.46	0.48	0.46	0.48	0.48	0.50	0.46	0.46	0.50	0.50	0.40	0.44	0.40	0.44	0.31	0.44	0.48	0.48	0.54	0.46	0.44	0.42	0.10	0.10	0.00

Matrix of RAPD dissimilarity among three Saudi goat and Nubian breeds based on Nei & Lei coefficients is shown in Table 2. Individuals designated 1 to 16, 17 to 23, 24 to 25 and 26 to 28 belonged to Ardi, Jabali, Shami and Nubian goats, respectively. The highest genetic distance (0.54) was found between Ardi individual (N2) and Jabali individual (N22) in one site and Nubian individuals (N28) on the other site. These results showed that Nubian goat is genetically distant from these Saudi breeds. On the other hand, the least genetic distance (0.08) was found between Jabali individuals (N19) and (N21) and also between Jabali Individuals (N20) and (N21). Very low genetic distance (0.10) was also recorded between Nubain gaots (N26), (N27) and (N28). Genetic distance value of

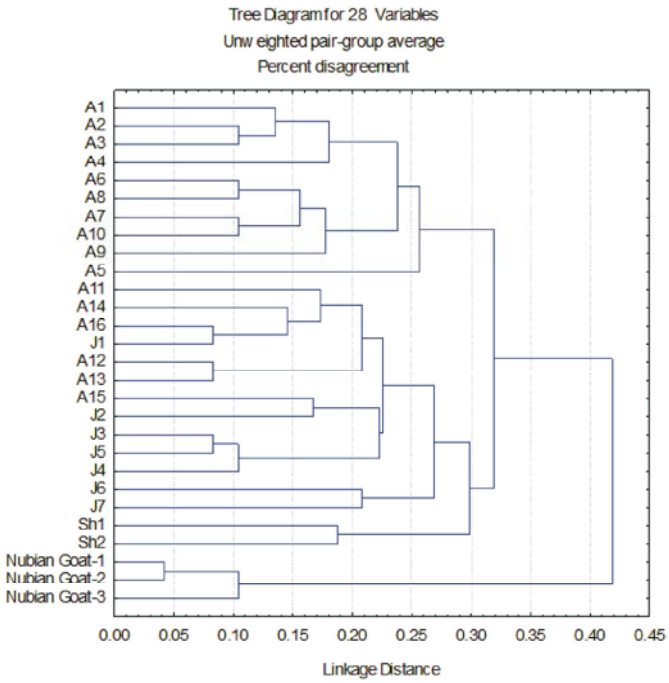

Fig. 2: Dendrogram showing relationships between goat breeds obtained by RAPD technique using five primers. Individuals designated with A are Ardi, with J are Jabali and with Sh are Shami goat breed.

0.0 reflects very high similarity between any two individuals. The distance measure between two clusters is calculated from the formula: *D=1-C* Where, D is the Distance and C the correlation between object clusters. If objects are highly correlated, they will have a correlation value close to 1 and genetic distance value close to zero. Therefore, highly correlated clusters are nearer to the bottom of the dendrogram. Object clusters that are not correlated have a correlation value of zero and a corresponding genetic distance value of 1. Objects that are negatively correlated, will have a correlation value of minus 1 and genetic distance of 2.

The UPGMA dendrogram of genetic variation among studied four goat breeds is shown in Figure 2. The result again showed that the Nubian goats are genetically distant and appeared as out-group to the Saudi breeds. The constructed UPGMA dendrogram showed that there are two main separate clades. The first main clade contained most of Ardi goats. The second main clade was divided into three clusters. The first cluster contained the rest of the Ardi goats and one sample from Jabali goat. All Jabali goats were grouped in the second cluster of the second main clade close to each other, with only one sample from Ardi. The Shami goat grouped together in the third cluster of the second main clade and appeared as genetically very close to each other. This result reflects the diversity of the Ardi goats as individuals from this breed appeared scattered in the two main clades. This finding is consistent with Aljumaah *et al*. [14] who studied Ardi goat population in Saudi Arabia using microsatellites markers, reporting that Ardi goat breed has high genetic variability in comparison with other goat breeds of the world.

CONCLUSION

The high polymorphism among the studied Saudi goat breeds (95.8%) indicates that these goat breeds possess the needed amount of genetic variation required for further genetic improvement. The present study help to clarify the image of the genetic diversity of the local Saudi goat breeds, in Raniah province. However, to get the precise estimation of the phylogeny of these local genetic resources, further studies using large number of animals from different geographical regions in the kingdom are needed.

ACKNOWLEDGMENT

This research was funded by a grant-in-aid from Taif University vice Presidency of Graduate Studies and Academic Research (Grant 1- 435-3225).

REFERENCES

1. FAO, 2000. Domestic Animal Diversity Information System (DAD-IS 2.0): http://dad.fao.org/dad-is/home.htm.
2. Kunene, W., C. Bezuidenhoutb and V. Nsahlaic, 2009. Genetic and phenotypic diversity in Zulu sheep populations: Implications for exploitation and conservation. Small Ruminant Research, 84: 100-107.
3. Hanotte, O. and T.K.S. Dessie, 2010. Time to tap Africa's livestock genomes. Science, 328: 1640-1641.
4. Ajmone-Marsan, P.L., J.L. Colli, A. Han, H. Achilli, S. Lancioni, P. Joost, F. Crepaldi, A. Pilla, P. Stella, P. Taberlet, R. Boettcherl, J.A. Negrini and Lenstra, 2014. Italian Goat Consortium, Econogene Consortium, Econo. Gene Consortium, Globaldiv Consortium. The characterization of goat genetic diversity: Towards agenomic approach. Small Ruminant Research, 121: 58-72.
5. Ministry of Agriculture, 2011. Agricultural statistics year book. Kingdom of Saudi Arabia.
6. Al Faraj, S.A., 2003. Basic Agriculture information in Raniah Province and its villages (No.274), Ministry of Agriculture, Raniah branch, KSA. (in Arabic).
7. Wurzinger, M., L. Iñiguez, M. Zaklouta, M. Hilali and J. Solkner, 2008. The Syrian Jabali goat and its production system. Journal of Arid Environments, 72: 384-391.
8. Williams, G., R. Kubelik, J. Livak, A. Rafalski and V. Tingey, 1999. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. Nucleic Acid Research, 18: 6531-6535.
9. Awad, N.M., A. Sally, H.M. Ayman and Z. Margueriet, 2010. Fingerprinting and assessment of genetic variability of Varroa destructor in Egypt. Journal of Agricultural Research, 49: 251-256.
10. Kumar, S., A.P. Kolte, B.R. Yadav, S. Kumar, A.L. Arora and V.K. Singh, 2008. Genetic variability among sheep breeds by random amplified polymorphic DNA-PCR. Indian Journal of Biotechnology, 7: 482-486.
11. Ruane, J., 2000. A framework for prioritizing domestic animal breeds for conservation purposes at the national level: a Norwegian case study. Conservation Biology, 14: 1385-1393.
12. Nei, M. and W. Lie, 1979. Mathematical model for studying genetic variation in term of restriction endonuclease. Proceeding of Natural Academic Science, USA, 76: 5369-5273.
13. StatSoft lnc., 2009. STATISTCA (data analysis software system), version 9.
14. Aljumaah, R.S., M.M. Musthafa, M.A. Al-Shaikh, O.A. Badri and M.F. Hussein, 2012. Genetic diversity of Ardi goat based on microsatellite analysis. African Journal of Biotehnology, 11: 6539-16545.
15. Sabir, J.S.M., A.M. Sabry, N.S. Awad, A.A. Mohamed and M.H.Z. Mutawakil, 2013. Najdi, Harri and Aradi Saudi goat breeds possess genetic variation required for genetic improvement. World Applied Science Journal, 26(7): 867-872.