TÜBİTAK

Turkish Journal of Veterinary and Animal Sciences

http://journals.tubitak.gov.tr/veterinary/

Review Article

Turk J Vet Anim Sci
(2014) 38: 606-611

doi:10.3906/vet-1402-46

Usefulness of short sequence repeat markers in goat genetic diversity studies on the Asian and African continents

Faiz M. M. T. MARIKAR[1,2,*], Muneeb M. MUSTHAFA[3]

[1]Department of Biochemistry, Faculty of Medicine and Allied Sciences, University of Rajarata, Saliyapura, Anuradhapura, Sri Lanka
[2]Staff Development Centre, General Sir John Kotelawela Defence University, Rathmalana, Sri Lanka
[3]Department of Zootechnics, Faculty of Agriculture, Ege University, İzmir, Turkey

Received: 12.02.2014 • **Accepted:** 26.05.2014 • **Published Online:** 24.10.2014 • **Printed:** 21.11.2014

Abstract: Goat genetic diversity studies are very important since extinction of germ plasma is increasing very rapidly. The African and Asian continents are the hotspots for indigenous animals with fewer genetic manipulations. Conservation studies using molecular markers have the capability to validate the real status of the animals. The use of molecular markers has revolutionized studies of genetic diversity. Even though a number of markers are used for these types of studies, short sequence repeats are in the forefront due to their superior features such as high variability, high mutation rate, large number, distribution throughout the genome, codominant inheritance, and neutrality with respect to selection. The aim of this review is to emphasize the importance of microsatellite markers for studies of genetic diversity in the goat and their use in conservation strategies in Asia and Africa.

Key words: Molecular markers, conservation, breeding, dominant, variability

1. Introduction

Domestication of animal species probably occurred during the Mesolithic period around 8000–7000 BC (1,2). Later, evolutionary forces of migration, mutation, selection, genetic drift, and creative human activity jointly contributed to the origin of numerous identifiable morphological characteristics and a colossal amount of variability in production performance. Hence, a vast array of landraces, populations, and breeds constitute domestic animal diversity. Interestingly, it was only in the 17th century that Robert Bakewell from Dishley, England, categorized animals with similar morphological characteristics into a population and developed the foundation of pedigree breeding based on the concept of "like begets like" and "breed the best to the best" (3).

In the 18th and 19th centuries, raising sheep was more or less traditional and under conditions of sedentary, nomadic, and seminomadic management. A number of sheep breeds evolved in the desert, tropical, temperate, and mountainous regions of the world where rainfall, wind, temperature, solar radiation, and vegetation varied. During this period, increased emphasis was placed on conformation, hardiness, and productivity, and this emphasis invigorated interest in the development of new sheep breeds derived from a combination of 2 or more breeds (4).

2. Historical background

History sometimes takes ironic twists, and the history of science is no exception. Microsatellites have been detected in eukaryote genomes for over 30 years, though they were regarded as sequences of no particular interest. With the rise of polymerase chain reaction (PCR), it was realized in the late 1980s that microsatellites may be the most powerful Mendelian markers ever found (see Table 1). They have since been widely studied in conjunction with some genetic diseases. They also have been used in mapping programs and by population biologists for kinship investigations and for more classical studies of population genetic structure (5–9).

Worldwide, recognition exists for the need for conservation of livestock diversity (10) and for characterization of breeds and populations including their genetic differentiation and relationships. These unique characteristics are the result of evolutionary forces and their interactions over long periods of time. However, the adaptations and unique characteristics might have been diluted due to intermixing, substructuring, and/or consequent genetic drift in the population over time. Moreover, the small population of microsatellites, approximately less than 5000 (11,12), makes them further vulnerable to the various forces of genetic change, thus

* Correspondence: faiz.marikar@fulbrightmail.org

modifying the foundation genetic structure of the breed (13). Therefore, an investigation of genetic variation within the breed and its body structure may help to evaluate these factors and provide genetic information to be used for conservation and improvement of goats of Asia and Africa (14,15).

The International Goat Genome Consortium (IGCC) is a very good initiative to increase the genomic tools and knowledge dissemination in the public sphere on goat species. The current projects of the IGCC are to produce a goat whole-genome reference sequence that will be initiated via de novo assembly from an expressed sequence tag-based virtual goat genome and bacterial artificial chromosome clones. Discovery of single nucleotide polymorphism (SNP) chips using next-generation sequencing techniques and mapping of markers for RH map and Hap Map developments are some of the other projects of the IGCC (16).

2.1. Comparison of goat genetic diversity

Methodology for research in population genetic diversity has improved tremendously over the past 2 decades since the application of advanced molecular techniques (17). Genetic characterization studies also showed a steep increase. Genetic characterization is carried out in livestock using various molecular biology techniques such as allozymes, restriction fragment length polymorphism (RFLP), protein polymorphism, randomly amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), mitochondrial DNA (mtDNA), short tandem repeat (STR or microsatellites), and SNPs (18–23). Comparisons of the attributes of some of these important molecular markers are listed in Table 1. Attempts have been made by using microsatellite (24,25) and mitochondrial (26) markers to establish breed characteristics and to determine relationships among indigenous goat breeds. Out of many genetic markers now available, microsatellite loci are best suited for answering some of these questions (27) because of their high variability, high mutation rate, large number, distribution throughout the genome, codominant inheritance, and neutrality with respect to selection (28). They are very useful to analyze the degree and pattern of genetic variability within and differences between populations.

Once extracted from the chosen matrix (animal tissue, blood, muscle, hair, sperm, feces, or even processed food such as cheese or canned meat), the DNA is analyzed by molecular markers to obtain a fingerprint or specific allelic frequencies allowing for individual, breed, or species identification. Since the introduction of PCR in 1989, many different markers have been studied. Presently the most widely used are microsatellites, which are also known as STRs and SNPs (29). Although DNA analysis furnishes different levels of identification, the individual one is of great interest for the verification of a meat cut for food safety purposes, while breed and species discrimination are of interest to detect fraud and to protect and validate typical productions. The use of these technologies in animals and their products is just an extension of techniques already in use for human testing and routinely applied in forensic casework (30).The most widely used markers are microsatellites (31–37) and, most recently, SNPs (35,38,39). The results from this research in goats, the type of markers utilized, and the breeds studied are shown in Table 1.

It is worth mentioning an important aspect when choosing the markers and the breeds to be analyzed (37): in a study on 4 cattle breeds, the informative content of each microsatellite varied among breeds depending on the breeds' allelic frequencies (alleles always present in one breed and always absent in the others), especially in genetic characterization studies. When implementing a genetic trace-back system it would be interesting to choose different panels for each breed to achieve good efficacy in all breeds. In both cases, preliminary analyses of all breeds are needed to determine the genetic structure of each population.

Another interesting trait of microsatellites is that we can relatively easily gain information on their molecular structure and mutation rate as well. This has not escaped the attention of population geneticists. Recent work at the population level may also shed light on the molecular forces acting on microsatellites. Microsatellites have

Table 1. Comparison of some of the important DNA markers.

Characters	RFLP	RAPD	SSR
Genomic abundance	High	Very high	Medium
Level of polymorphism	Medium	Medium	High
Dominance	Codominance	Dominance	Codominance
Quantity of DNA needed	2–10 µg	10–20 µg	50–100 µg
Sequence information requires	None	None	Yes
Null alleles	Rare	Not applicable	Occasional
Automation or multiplexing	Difficult	Possible	Possible
Radioactive probes	Yes/no	No	No

become widely applied for several types of studies, due to their advantages over other markers, such as the relative ease in obtaining markers, high polymorphism rates, neutrality, and easy automation of analytical procedure (40,41). Additionally, variation in simple nucleotide repeats, random and abundant distribution across the genome, and codominance can be determined (42).

Due to their close chromosomal resemblance, microsatellites developed for cattle and sheep normally work well in goats (43). The International Society of Animal Genetics described more than 1400 microsatellite markers that have been listed in cattle and around 40% of those markers can be amplified efficiently in goat (44).

Microsatellites are the marker of choice in animal genetic studies due to the above mentioned advantages, and these markers have been used in numerous studies all over the world. The use in goats is listed for the Asian and African continents in Table 2. At the turn of the century,

Table 2. Overview of goat genetic diversity studies in Asia and Africa, microsatellites used, observed sizes of their alleles, number of alleles (n_a), observed heterozygosity (Ho), and expected heterozygosity (He).

Breed/origin	n_a	H_o	H_e	Reference
South Asian breeds (n)				
Jamunapari	4.91	0.42	0.54	(45)
Kutchi	12	0.59	0.80	(46)
Gohilwari	10.12	0.51	0.69	(47)
Marwari	5.8	0.45	0.63	(48)
Barbari	6.33	0.85–1.0	0.62–0.85	(49)
Zalawadi	7	0.6	0.58	(50)
Gohilwadi	7.82	0.63	0.67	(50)
Surti	7.06	0.58	0.64	(50)
Mehsana	12.28	0.65	0.77	(51)
Indian domestic goats (7)	8.1–9.7	0.37–0.43	0.74–0.78	(52)
Kanniadu	5-14	0.71–0.98	0.64–0.87	(53)
Sirohi	5-25	0.5	0.79	(54)
Chegu	6-11	0.66	0.81	(25)
South Indian goats (5)	7-31	0.11–0.81	0.51–0.92	(55)
Bangladesh goats (5)	5.23–6.08	0.51–0.56	0.53–0.59	(56)
East Asian breeds				
East Asian goats (18)	5.8	0.31–0.71	0.30–0.72	(57)
Chinese goats (12)	5.24–7.77	0.60–0.78	0.61–0.78	(18)
Korean goats	3.4	0.36	0.38	(58)
Western Asian breeds				
Markhoz	8.1	-	0.80	(59)
Tali	7.4	-	0.74	(60)
Lori	7	-	0.78	(43)
Raeini	7.8	-	0.81	(60)
Taleshi	6.7	0.42	0.74	(61)
Native breeds (3)	7.3–11	-	0.74–0.8	(43)
African goats				
Namibia (4)	4.67–6	-	0.6–0.71	(62)
Burkina Faso (3)	4–33	0.02–0.86	0.02–0.93	(63)
Kalahari Red	7.77	-	0.63	(64)
South Africa (3)	9–10	0.49–0.69	0.46–0.67	(65)
Sub-Saharan Africa (19)	3.82–5.91	0.44–0.56	0.45–0.54	(66)
Egyptian goats (3)	5.3–7.6	0.61–0.66	0.67–0.79	(67)
West African local (9)	11.7	0.60–0.73	-	(66)

African and Asian researchers have concentrated on genetic diversity studies using microsatellites. From these studies, we can conclude that goat genetic diversity studies using microsatellites markers have been extensively conducted on the African and Asian continents. These studies have paved the way for future genetic and conservation studies. As an overall observation, the admixtures of local and foreign breeds have shown greater genetic diversity than single breed structures (16).

3. Conclusion

At present, DNA-based techniques seem to be the appropriate tool for the verification of the origin of animal breeds. In conclusion, microsatellite markers are a useful and trusted tool for identification of goat breeds and their usage could be the solution to conservation with high confidence. However, to be really applicable, more cooperation among researchers and people involved in conservation is necessary.

References

1. Zeuner FE. A History of Domesticated Animals. London, UK: Hutchinson; 1963.
2. Ryder ML. Sheep and Man. London, UK: Duckworth; 1983.
3. Lush JL. Animal Breeding Plans. Ames, IA, USA: Iowa State University Press; 1945.
4. Shrestha JNB. Conserving domestic animal diversity among composite populations. Small Ruminant Res 2005; 56: 3–20.
5. Queller DC, Strassmann LE, Hughes CR. Microsatellites and kinship. Trends Ecol Evolut 1993; 8: 285–288.
6. Charlesworth B, Sniegowski P, Stephan W. The evolutionary dynamics of repetitive DNA in eukaryotes. Nature 1994; 371: 215–220.
7. Di Rienzo A, Peterson AC, Garza JC, Valdes AM, Slatkin M, Freimer NB. Mutational processes of simple-sequence repeat loci in human populations. Proc Natl Acad Sci U S A 1994; 91: 3166–3170.
8. Estoup A, Garney L, Solignac M, Cornuet JM. Microsatellite variation in honey bee (*Apis mellifera* L.) populations: hierarchical genetic structure and test of the infinite allele and stepwise mutation models. Genetics 1995; 140: 679–695.
9. Philippe L, Pierre JLL. Microsatellites, from molecules to populations and back. Tree 1996; 2: 5–10.
10. FAO. Global Project for the Maintenance of Domestic Animal Genetic Diversity (MoDAD)-Draft Project Formulation Report. Rome, Italy: FAO; 1995.
11. Acharya RM. Sheep and Goat Breeds of India. FAO Animal Production and Health Paper 30. Rome, Italy: FAO; 1982.
12. Nivsarkar AE, Gupta SC, Vij PK. Stemming the threat to Indian livestock. Diversity. 1996; 12: 31–33.
13. Digpal SG, Geetu M, Ahlawat SPS, Pandey AK, Sharma R, Gupta N, Gupta SC, Bisen PS, Kumara D. Analysis of genetic structure of Jamunapari goats by microsatellite markers. Small Ruminant Res 2006; 66: 140–149.
14. Tosser KG, Bardou P, Bouchez O, Cabau C, Crooijmans R. Design and characterization of a 52K SNP chip for goats. PLoS ONE 2014; 9: e86227.
15. Bang ZL, Taiki K, Makoto K, Hirokazu M, Shinji S, Hideyuki M. Genetic diversity and structure in Asian native goat analyzed by newly developed SNP markers. Anim Sci 2013; 84: 579–584.
16. International Goat Genome Consortium. Goat Genome. 2014 [cited 2014; available from http://www. goatgenome.org/].
17. Excoffier L, Smouse PE, Quattro JM. Analysis of molecular variance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA restriction data. Genetics 1992; 131: 479–491.
18. Li M, Zhao S, Bian C, Wang H, Wei H, Liu B, Yu M, Fan B, Chen S, Zhu M et al. Genetic relationships among twelve Chinese indigenous goat populations based on microsatellite analysis. Genet Select Evol 2002; 34: 729–744.
19. Vignal A, Milan D, Sancristobal M, Eggen A. A review on SNP and other types of molecular markers and their use in animal genetics. Genet Select Evol 2002; 34: 275–305.
20. David L, Rosenberg NA, Lavi U, Feldman MW, Hillel J. Genetic diversity and population structure inferred from the partially duplicated genome of domesticated carp, *Cyprinus carpio* L. Genet Select Evol 2007; 39: 319–340.
21. Ajmone-Marsan P, GLOBALDIV Consortium. A global view of livestock biodiversity and conservation –GLOBALDIV. Anim Genet 2010; 41: 1–5.
22. Güneren G, Akyüz B, Ertugrul O. Use of RAPD-PCR for genetic analyses on the native cattle breeds in Turkey. Ankara Üniv Vet Fak Derg 2010; 57: 167–172.
23. Khaldi Z, Rekik B, Haddad B, Zourgui L, Souid S. Genetic characterization of three ovine breeds in Tunisia using randomly amplified polymorphic DNA markers. Lives Res Rural Deve 2010; 22: 47.
24. Ganai NA, Yadav BR. Genetic variation within and among three Indian breeds of goat using heterologous microsatellite markers. Anim Biotech 2001; 12: 121–136.
25. Behl R, Sheoran N, Behl J, Vijh RK, Tantia MS. Analysis of 22 heterologous microsatellite markers for genetic variability in Indian goats. Anim Biotech 2003; 14: 167–175.
26. Joshi MB, Rout PK, Mandal AK, Tyler-Smith C, Singh L, Thangaraj K. Phylogeography and origin of Indian domestic goats. Mol Biol Evol 2004; 21: 454–462.
27. Goldstein DB, Pollock DD. Launching microsatellites: a review of mutation processes and methods of phylogenetic inference. J Hered 1997; 88: 335–342.

28. Boyce WM, Hedrick PW, Muggli-Cockett NE, Kalinowski S, Penedo MC, Ramey RR. Genetic variation of major histocompatibilty complex and microsatellite loci: a comparison in Bighorn sheep. Genetics, 1996; 145: 421–433.

29. Mariani P, Panzitta F, Nardelli Costa J, Lazzari B, Crepaldi P, Marilli M, Fornarelli F, Fusi M, Milanesi E, Negrini R et al. Metodi molecolari per la tracciabilita dei prodotti di origine animale. In: Proceedings of the 4th World Italian Beef Cattle Congress; 2005 (in Italian).

30. Cunningham EP, Meghen CM. Biological identification systems: genetic markers. Rev Sci Tech 2001; 20: 491–499.

31. Peelman LJ, Mortiaux F, Van Zeveren A, Dansercoer A, Mommens G, Coopman F. Evaluation of the genetic variability of 23 bovine microsatellite markers in four Belgian cattle breeds. Anim Genet 1998; 29: 161–167.

32. Sancristobal-Gaudy M, Renand G, Amigues Y, Boscher MY, Leveziel H, Bibe B. Traçabilité individuelle des viandes bovines à l'aide de marqueurs génétiques. INRA Prod Anim 2000; 13: 269–276 (in French).

33. Arana A, Soret B, Lasa I, Alfonso L. Meat traceability using DNA markers: application to the beef industry. Meat Sci 2002; 61: 367–373.

34. Vázquez JF, Pérez T, Ureña F, Gudín E, Albornoz J, Domínguez A. Practical application of DNA fingerprinting to trace beef. J Food Prot 2004; 67: 972–979.

35. Herraeza DL, Schafer H, Mosner J, Fries HR, Wink M. Comparison of microsatellite and single nucleotide polymorphism markers for the genetic analysis of a Galloway cattle population. Zeitschrift Naturforschung 2005; 60: 637–643.

36. Dalvit C, Targhetta C, Gervaso M, De Marchi M, Mantovani R, Cassandro M. Application of a panel of microsatellite markers for the genetic traceability of bovine origin products. In: Proceedings of 57th Annual Meeting of the European Association for Animal Production; 2006. p. 26.

37. Orrú L, Napolitano F, Catillo G, Moioli B. Meat molecular traceability: How to choose the best set of microsatellites? Meat Sci 2006; 72: 312–317.

38. Heaton MP, Harhay GP, Bennett GL, Stone RT, Grosse WM, Casas E. Selection and use of SNP markers for animal identification and paternity analysis in U.S. beef cattle. Mamm Genome 2002; 13: 272–281.

39. Heaton MP, Keen JE, Clawson ML, Harhay GP, Bauer N, Schultz C. Use of bovine single nucleotide polymorphism markers to verify sample tracking in beef processing. J Am Vet Med Asso 2005; 226: 1311–1314.

40. Cannon J, Alexandrino P, Bessa I, Carleos C, Carretero Y, Dunner S, Ferran N, Garcia D, Jordana J, Laloe D et al., Genetic diversity of local European beef cattle breeds for conservation purposes. Genet Select Evol 2001; 33: 311–332.

41. Erhardt E, Weimann C. Use of molecular markers for evaluation of genetic diversity and in animal production. Archivos Latinoamericanos de Produccion Animal 2007; 15: 63–66.

42. Bruford M, Cheesman DJ, Coote T, Green HAA, Haines SA, O'Ryan C, Williams TR. Microsatellites and their application to conservation genetics. In: Smith TB, Wayne RK, editors. Molecular Genetic Approaches in Conservation. New York, NY, USA: Oxford University Press; 1996. pp. 278–297.

43. Mahmoudi B, Bayat M, Sadeghi R, Babayev M, Abdollahi H. Genetic diversity among three goat populations assessed by microsatellite DNA markers in Iran. Global Vet 2012; 4: 118–124.

44. Vaiman D, Schibler L, Bourgeois F, Oustry F, Amigues Y, Cribiu EP. A genetic linkage map of the male goat genome. Genetics 1996; 144: 279–305.

45. Gour D, Malik G, Ahlawat SPS, Pandey AK, Sharma R, Gupta N, Gupta SC, Bisen PS, Kumar D. Analysis of genetic structure of Jamunapari goats by microsatellite markers. Small Ruminant Res 2006; 66: 140–149.

46. Dixit SP, Verma NK, Ahlawat SPS, Aggarwal RAK, Kumar S, Chander R, Singh KP. Molecular genetic characterization of Kutchi breed of goat. Curr Sci 2008; 95: 946–952.

47. Kumar S, Dixit SP, Verma NK, Singh DK, Pande A, Kumar S, Chander R, Singh LB. Genetic diversity analysis of the Gohilwari breed of Indian goat (*Capra hircus*) using microsatellite markers. Am J Animal Vet Sci 2009; 4: 49–57.

48. Kumar S, Dixit SP, Sharma R, Pande AK, Sirohi G, Patel AK, Aggarwal NK, Gour DS, Ahlawat SPS. Population structure, genetic variation and management of Marwari goats. Small Ruminant Res 2005; 59: 41–48.

49. Ramamoorthi J, Thilagam K, Sivaselvam SN, Karthickeyan SMK. Genetic characterization of Barbari goats using microsatellite markers. J Vet Sci 2009; 10: 73–76.

50. Fatima S, Bhong CD, Rank DN, Joshi CG. Genetic variability and bottleneck studies in Zalawadi, Gohilwadi and Surti goat breeds of Gujarat (India) using microsatellites. Small Ruminant Res 2008; 77: 58–64.

51. Aggarwal RAK, Dixit SP, Verma NK, Ahlawat SPS, Kumar Y, Kumar S, Chander R, Singh KP. Population genetics analysis of Mehsana goat based on microsatellite markers. Curr Sci 2007; 92: 1133–1137.

52. Rout KP, Joshi MB, Mandal A, Laloe D, Singh L, Thangaraj K. Microsatellite-based phylogeny of Indian domestic goats. BMC Genetics 2008; 9: 1–11.

53. Thilagam K, Ramamoorthi J, Sivaselvam SN, Karthickeyan SMK, Thangaraju P. Kanniadu goats of Tamilnadu, India: genetic characterisation through microsatellite markers. Livestock Res Rural Develop 2006; 18: 149.

54. Verma NK, Dixit SP, Aggarwal RAK, Chander R, Kumar S, Ahlawat SPS. Genetic analysis of the Sirohi breed of Indian goat (*Capra hircus*). Korean J Genetics 2007; 29: 129–136.

55. Dixit SP, Verma NK, Aggarwal RAK, Vyas MK, Rana J, Sharma A, Tyagi P, Arya P, Ulmek BR. Genetic diversity and relationship among southern Indian goat breeds based on microsatellite markers. Small Ruminant Res 2010; 91: 153–159.

56. Afroz MF, Faruque MO, Husain SS, Han JL, Paul B. Genetic variation and relations in different goat population of Bangladesh. Bangaldesh J Animal Sci 2010; 39: 1–8.

57. Nomura K, Ishii K, Dadi H, Takahashi Y, Minezawa M, Cho CY, Sutopo Faruque MO, Nyamsamba D, Amano T. Microsatellite DNA markers indicate three genetic lineages in East Asian indigenous goat populations. Anim Genet 2012; 43: 760–767.

58. Kim KS, Yeo JS, Lee JW, Kim JW, Choi CB. Genetic diversity of goats from Korea and China using microsatellite analysis. Asian Austral J Anim 2002; 15: 461–465.

59. Mahmoudi B, Babayev M. The investigation of genetic variation in Taleshi goat using microsatellite markers. Res J Biol Sci 2009; 4: 644–646.

60. Sadegi R, Mahmoudi B, Babayev MS, Rameshknia Y, Daliri M. Genetic diversity of Tali goats based on 13 microsatellite markers. Res J Biol Sci 2009; 4: 734–737.

61. Mahmoudi B, Daliri M, Babayev M, Sadegi R. Genetic diversity of Markhoz goat breed based on microsatellite markers. J Anim Vet Adv 2009; 8: 1815–1818.

62. Els JF, Kotze A, Swart H. Genetic diversity of indigenous goats in Namibia using microsatellite markers: preliminary results. S Afr J Animal Sci 2004; 34: 65–67.

63. Traoré A, Álvarez I, Tamboura HH, Fernández I, Kaboré A, Royo LJ, Gutiérrez JP, Sangaré M, Ouédraogo-Sanou G, Toguyeni A et al. Genetic characterisation of Burkina Faso goats using microsatellite polymorphism. Livest Sci 2009; 123: 322–328.

64. Kotze A, Swart H, Grobler JP, Nemaangani A. A genetic profile of Kalahari goat breed from South Africa. S Afr J Animal Sci 2004; 34: 10–12.

65. Visser C, Crooijmans RPMA, Marle-Köster E. A Genetic linkage map for the South African Angora goat. Small Ruminant Res 2010; 93: 171–179.

66. Missohou A, Poutya MR, Nenonene A, Dayo GK, Ayssiwede SB, Talaki E, Issa Y, Fane A. Genetic diversity and differentiation in nine West African local goat breeds assessed via microsatellite polymorphism. Small Ruminant Res 2011; 99: 20–24.

67. Agha SH, Pilla F, Galal S, Shaat I, D'Andrea M, Reale S, Abdelsalam AZ, Li MH. Genetic diversity in Egyptian and Italian goat breeds measured with microsatellite polymorphism. J Anim Breed Genet 2008; 125: 194–200.