Small Ruminant Research 136 (2016) 145–150

Contents lists available at ScienceDirect

Small Ruminant Research

journal homepage: www.elsevier.com/locate/smallrumres

Analysis of genetic structure of West African Dwarf goats by allozyme markers

Olukoya Kolawole Awobajo[a,*], Adebowale Emmanuel Salako[b], Mabel Omolara Akinyemi[b], Osamede Henry Osaiyuwu[b]

[a] Department of Agricultural Science Education, Tai Solarin University of Education, P. M. B. 2118 Ijebu-Ode, Ogun State, Nigeria
[b] Animal Breeding and Genetics Laboratory, Department of Animal Science, University of Ibadan, Ibadan, Nigeria

ARTICLE INFO

Article history:
Received 14 July 2015
Received in revised form 6 January 2016
Accepted 8 January 2016
Available online 13 January 2016

Keywords:
Genetic variation
Allozyme loci
Population structure
Diversity
Molecular markers
Native goats

ABSTRACT

Genetic variation at three allozyme (Haemoglobin, Carbonic Anhydrase and Transferrin) loci and population structure hypothesis were examined for West African Dwarf goat populations in four Southwestern state of Nigeria. One hundred and forty animals, twenty from each sampling area comprising Ijebu-Ode and Ado-Odo, (Ogun state), Ondo, (Ondo state), Ile–Ife, Osogbo and Iwo, (Osun state), and Ibadan, (Oyo state), were randomly selected. Estimates of genetic variability such as effective number of alleles and gene diversities revealed substantial genetic variation frequently displayed by allozyme markers. Numbers of alleles observed across the allozyme loci varied from 246 to 250 with an overall mean of 247.33 ± 2.31. Average polymorphism across the studied loci and expected gene diversity in the population were 0.63 ± 0.09 and 0.44 ± 0.09, respectively. Population was observed to be significantly differentiated into different groups, and showed fairly high level of outbreeding ($f = -0.16 \pm 0.44$) and excess heterozygosity.

1. Introduction

In humid and hot climate of West and Central Africa, the present day goats of this type tend to be dwarf, which is believed to be due to natural selection on thermoregulation under the unfavourable humid and hot climate. It is possible that this was deliberately selected for by owners just for its oddness. The distribution of this goat type extends southwards through Central Africa as far as Democratic Republic of Congo, Angola and the north of Namibia (Mason, 1984). The true type of this goat is considered to be confined to fifteen countries in West and Central Africa, all of which except the Central African Republic have an Atlantic coastline (Guinea Bissau, Guinea, Liberia, Sierra Leone, Cote d'Ivoire, Ghana, Togo, Benin, Nigeria, Cameroon, Congo, Equatorial Guinea, Gabon, Democratic Republic of Congo, and Central African Republic). It is also found in Senegal (Wilson, 1991). Goats constitute the largest group of small ruminant livestock in Nigeria totaling about 53.8 million and also constituting 6.2% of the World's goat population (FAOSTAT, 2011). Surveys have shown that up to 85% of rural households, poor farmers and small-time business people of all age groups and sexes keep them (FDLPCS, 2007). There are three main breeds of goat in Nigeria, the West African Dwarf, the Sokoto Red and the Sahel. Goats are renowned for their hardiness and can survive in most environments: West African Dwarf (WAD) goats are kept in the forest zones and in the Middle belt; Sokoto Red are kept throughout the north; and Sahel goats are restricted to a strip along the frontier with the Republic of Niger, (Bourn et al., 1994). Goats located in northern part of the country were found to be markedly more productive than WAD goats, with lower ages at first kidding and shorter kidding intervals, though they produced fewer kids per kidding (Bourn et al., 1994). In addition the WAD goat often has short bowed legs attributed to achondroplasia (Wilson, 1991). They are essentially confined to the humid forest zones with more than 240 growing days and in excess of 1500 mm rainfall/annum; most of this zone are infected with tsetse fly making trypanosome infections prevalent, the production system are agricultural, peri-urban and to a lesser extent agro-pastoral with ethnic group (Wilson, 1991). Livestock plays a significant role in the livelihood of rural populations and the agricultural development of Sub-Saharan Africa. In this region, livestock production is characterized by diverse and complex production systems (Udo and Cornelissen, 1998). Livestock production contributes significantly to improved family nutrition and health, and the sale of animals and their products helps to improve and stabilize household income.

* Corresponding author.
E-mail address: koyakola@gmail.com (O.K. Awobajo).

http://dx.doi.org/10.1016/j.smallrumres.2016.01.013
0921-4488/

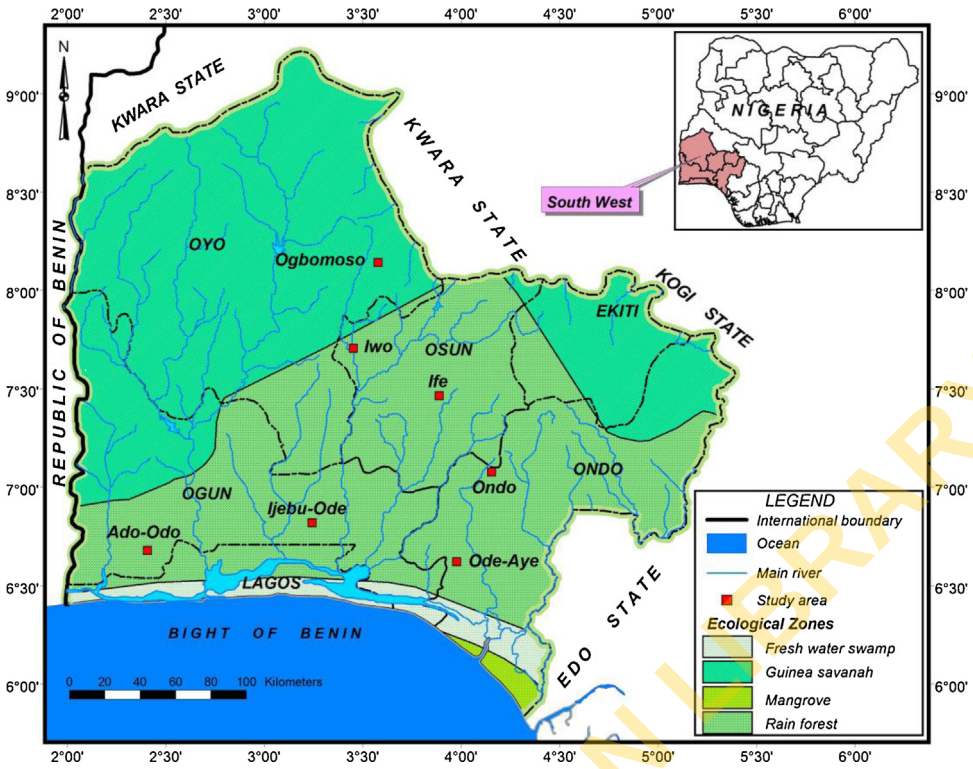

Fig. 1. Map of Southwestern Nigeria indicating sample area.

The intangible products obtained from animals are important in areas lacking formal insurance and developed financial markets (Udo and Cornelissen, 1998). Goat, sheep and poultry are considered as forms of security and sources of independent income especially for poor women (Paris, 2002). Furthermore, animals are used in social cultural functions e.g., in religious ceremonies (Jahnke et al., 1988; Jabbar et al., 1995). The ability of goats to tolerate harsh climates, the presence of trypanotolerance in some breeds (Salako, 2004), suitability to traditional systems on account of small size, short generation interval (Abdul-Aziz, 2010) and ability to thrive on poor quality diets provided by scarce grazing on marginal lands (Adedeji et al., 2011) all combine to make small ruminants strategic to increasing livestock productivity in rural agricultural systems (Adebambo et al., 2004; Adedeji et al., 2011). Despite these advantages, little attention had been paid to the genetic characterization and possible improvement of small ruminants in Nigeria.

The future development of livestock production in Sub-Saharan Africa is hindered by limited knowledge of the genetic potential of the local genetic resources and ways to best utilize these resources in a sustainable manner. The genetic makeup of the indigenous animal is often associated with low production potential in indigenous animals (Bosso, 2006). However, according to him, indigenous animals have not been adequately characterized for their production potential and this have led to the growing recognition of the need to characterize, utilize and conserve indigenous Animal Genetic Resources (AnGR). Because of this lack of information, decisions on genetic improvement of indigenous animals are often made which have negative consequences on indigenous AnGR (Rege et al., 2002). It is important to know the diversity and relationship between the African breeds and strains of livestock. Moreover, it is important because, quite often, the same breed may be known by different names or two breeds may be known by the same name, based on geographical locations of such populations (Gwakisa et al., 1994). The need to curb the threats of dilution and extinction of the African animal genetic resources, by strategic development and conservation has never been more justifiable and is now, with the available technology, timely. Efficient strategies for conservation require sets of genetic markers, which characterize distinct populations (Kemp and Teale, 1994). Genetic improvement of indigenous breeds of livestock is very valuable because of high adaptability to harsh environmental conditions of nutrition, climate and disease compared with exotic breeds (Fitzhugh et al., 1992). According to Groeneveld et al. (2010) many breeds of livestock may become lost germplasm in many third world countries due to crossing with exotics, which in addition to uncontrolled breeding in extensive management systems pose a great risk for the loss of valuable genes. To understand natural genetic variation in native goats as well as formulate conservation policies, better genetic characterization is required to balance the competing needs of genetic improvement and conservation of native germplasm to preserve the age-long relationship between native livestock and dwellers in rural agricultural systems (Groeneveld et al., 2010). The primary aim of studying genetic diversity is to understand the extent of differentiation of populations within species. According to Hanotte and Jianlin (2005) population genetics is about microevolution and it is the study of genetic variation in populations. This variation involves the change of allele frequencies, genotype frequencies and phenotype frequencies. Population genetics predicts diversity that is determined by a number of factors including selection, mutation rate, recombination, genetic drift and effective population size. The amount and nature of genetic variation in a population allows estimates of effective population size, population history (migration, bottleneck, recent expansion), population structure, how selection acts on genes and location of diseases genes (Qualitative Trace Loci (QTL) mapping). Primary indicators of animal genetic diversity should address both between-breed and within-breed components. Priority breeds for conservation should be the ones with the largest within breed diversity and should maximize the conservation of between breed diversity. Both within and between breed diversity parameters are classically measured using molecular

Table 1
Measures of genetic variation at studied blood protein loci in West African Dwarf goat.

SN	Loci	Sample size	Observed no of alleles	Effective number of alleles	Shannon's information index	Heterozygosity			Heterozygote deficiency
						Observed	Expected	Nei's	
1	Hb	123	246	1.52	0.53	0.34	0.34	0.34	0.28
2	CA	123	246	1.94	0.68	0.46	0.49	0.48	−0.70
3	Tf	125	250	2.00	0.69	0.84	0.50	0.50	−0.13
Mean		123.67	247.33	1.82	0.63	0.55	0.44	0.44	−0.18
St. dev			2.31	0.26	0.09	0.26	0.09	0.09	0.50

Hb— Haemoglobin, CA—Carbonic anhydrase, Tf—Transferrin.

genetic markers. In both cases soundly-based priority decisions for conservation at the global level will require the availability of large datasets. The mean number of alleles (MNA) observed (H_O) and expected (H_E) heterozygosity are the most commonly calculated population genetic parameters for assessing within breed diversity (Hanotte and Jianlin, 2005).

Traditional methods used to study genetic variability of animals and populations employed polymorphism in protein markers and genetic variation of haemoglobin (Hb) (Buvanendra et al., 1981; Imumori et al., 1999) and transferrin (Tf) types in goats (Moruppa, 1985; Kitalyi, 1998; Yakubu et al., 2010a,b; Mourad et al., 2001). Although DNA-based technologies are now the methods of choice for genetic characterization of livestock (Arora et al., 2011), several alternative assays, such as protein/allozyme polymorphisms, remain tremendously useful, especially in developing countries, because of their utility, ease, cost and amount of genetic information accessed or simplicity of data interpretation (Rege and Okeyo, 2006). Mwacharo et al. (2002) reported that for populations whose genetic status is unknown, protein polymorphism may be used first to verify the degree of genetic relationship. Various electrophoresis techniques have made rapid progress since Smithies successful segregation in 1955 of serum protein using starch gel electrophoresis. Protein polymorphism indicates that the analogous protein has two or more genetic variations. It is caused by nucleotide alternation in the DNA chain that results in the substitution of amino acid of polypeptide chain (Lu et al., 2006). Analysis of genetic markers based on protein variants detected by electrophoretic method has been a tool for studying genetic differentiation among breeds and in phylogenetic studies (Imumorin et al., 1999; Menrad et al., 2002; Nyamsamba et al., 2003; Ibeagha-Awemu and Erhardt, 2004a; Camoglu and Elmaci, 2005). However, biochemical variants of different proteins may present higher accuracy procedures for a better measurement of genetic variation in WAD goat breeds because of their polymorphism and simple mode of inheritance.

However, there is very little baseline information on the extent of natural genetic variation in WAD goats in Nigeria. Therefore, the present study aimed at using the allozyme analysis in investigating and estimating genetic diversity among different populations of WAD goat breeds in Southwestern Nigeria. The results of this study will provide useful genetic information essential for developing more effective extensive molecular characterization of WAD goat in Nigeria and understand the genetic diversity of WAD goat to implement steps so as to ensure their conservation and rational utilization for improvement of these genetic resources and productivity for the benefit of the farmers. The main objective of the study is to investigate and estimate the genetic diversity among WAD goat population within Southwestern state in Nigeria.

2. Material and methods

2.1. Experimental procedure

One hundred and forty animals, twenty from each sampling area comprising Ijebu-Ode and Ado-Odo, (Ogun state), Ondo, (Ondo state), Ile–Ife, Osogbo and Iwo, (Osun state), and Ibadan, (Oyo state) as shown in Fig. 1, were randomly selected. 5 mL of blood was collected from each animal by jugular venipuncture and placed in heparinized tubes to prevent coagulation. Procedure describe by RIKEN (2006) was followed in rest of the processes carried out. Red blood cell was prepared from the erythrocyte fraction of heparinised blood by centrifuging at 2500–3000 rpm for 10 min at 4 °C. The Red Blood Cell (RBC) was washed in saline (0.155 M NaCl) three times and centrifuged at 2500–3000 rpm for 5 min at 4 °C. The RBCs were lysed with a fourthfold volume of distilled H_2O to release Hb. The plasma fraction is separated from the erythrocyte fraction of haparinized blood by centrifuging at 2500–3000 rpm and the supernatant was used. Cellulose acetate plates were soaked in the same buffer as the electrode buffer. Samples were applied on to the plate using the applicator and once loaded; plates are rested on the wicks in the tank. The loaded zone on the plate was positioned at the cathodal end of the tank for the majority of the enzyme systems which migrate anodally. For those systems which migrate cathodally e.g carbonic anhydrase (CA), the loading zone was placed on the anodal end. The plates were removed from the tank and placed in an empty Petri dish after the completion of the gel run. They were stained with Ponceau stain before they dry out. After 20 min the plate was sufficiently stained, it was destained several times until clear and sharp bands appear, the bands were scored visually based on their migratory pattern as described by RIKEN (2006) and direct counting was used for calculating gene frequencies.

Table 2
Wright's *F*-statistics analyses for 3 protein loci in WAD goats.

Locus	$f(F_{IS})$	$\theta(F_{ST})$	$F(F_{IT})$	Nm[a]
Hb	0.13	0.06	0.18	3.68
CA	0.05	0.03	0.08	8.15
Tf	−0.67	0.01	−0.66	32.40
Mean	−0.16	0.03	−0.17	13.51
S.E.[a]	0.44	0.03	0.46	16.85

[a] Nm—Gene flow estimated from $F_{ST} = 0.25(1 - F_{ST})/F_{ST}$; Hb—Haemoglobin; CA—Carbonic anhydrase; Tf—Transferrin.

2.2. Statistical analysis

Tools for Population Genetic Analyses (TFPGA) (Miller, 1997) software was used to generate the genetic distance according to Nei's (1972), the allele frequency, observed and expected heterozygosity, Hardy-Weinberg Equilibrium, the inbreeding coefficients i.e. Wright's Fis and Fit, Fst estimates, and drawing UnPaired Group Method of Algorithm (UPGMA) dendrograms.

3. Results and discussion

Various measures of genetic variation are presented in Table 1. The *F*-statistics estimates of population structure are presented in Table 2. The number of alleles observed across the allozyme loci varied from 246 (Hb and CA) and 250 (Tf) with the mean of 247.33 ± 2.31 (Table 1). The observed number of alleles across the loci was more than the effective number of alleles (1.52–2.00) as expected. The Shannon information index showed that most of the

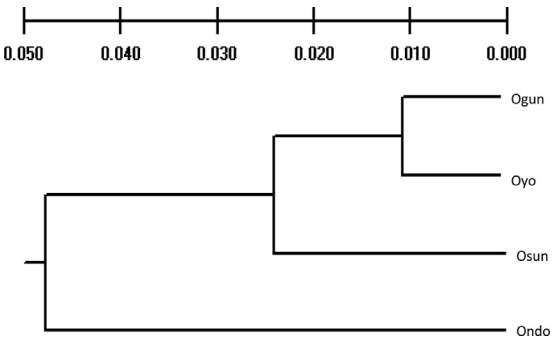

Fig. 2. Dendrogram showing similarity among four populations of WAD goat in Southwestern Nigeria based on blood protein analysis.

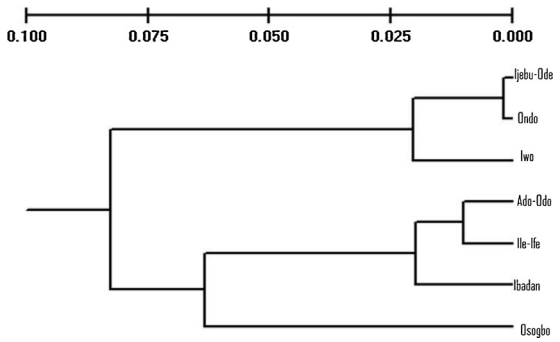

Fig. 3. Dendrogram of WAD goat populations showing similarity among seven sampled areas in Southwestern Nigeria based on blood protein analysis.

loci were highly informative indicating the polymorphism across the loci with an overall mean of 0.63 ± 0.09. The average H_O was more than the H_E (Table 1). The average expected gene diversity (Nei, 1973) within the population ranged from 0.34 (Hb) to 0.50 (Tf) with an overall mean of 0.44 ± 0.09. Only Tf showed significant deviations from Hardy–Weinberg equilibrium out of the three loci. All the loci except Tf showed significant heterozygote deficiency in the WAD goat population. The overall means for the Wright's *F*-statistics for population subdivision were significantly different from zero (Table 2). The average genetic variation (0.55) observed in this study was lower than the values reported for Indian breeds of goat, Black Bengal (0.69), Chegu (0.66), (Behl et al., 2003; Ganai and Yadav, 2001; Kumar et al., 2005) and West African Dwarf goat (0.75) (Okpeku et al., 2011), though they were all microsatellite based which are highly polymorphic than allozymes. However, it was higher than what was reported for Marwari (0.45), Barbari (0.50), Asian goat breeds of Sri Lanka South (0.48), Sri Lanka N-Central (0.49), Hat Yai (0.43); Australia (0.45) (Barker et al., 2001) and Swiss goats 0.51–0.58 (Saitbekova et al., 1999). Despite the fact that they were microsatellite based, it was higher than magnitude of genetic variation reported among populations of Asian breeds of goat, Chiang Mai (0.39), Sabah (0.31), Sarawak (0.33), Ujung-Pandang (0.38), (Barker et al., 2001) and Korean goats (0.36) (Kim et al., 2002) and Sub-Saharan African goat breeds of Kigezi (0.38), Mubende (0.36), Ndebele (0.34), West African Dwarf (0.37), Northwest Highland (0.41) and Pafuri (0.38) (Chenyambuga et al., 2004). All f (F_{IS}) estimates (Table 2) across the loci except Tf were significantly positive (significant heterozygote deficit) based on table wide randomizations ($P < 0.05$). The f estimates ranged from 0.05 to 0.13 with an average of −0.16 ± 0.44 indicating an outbred population or excess heterozygosity. The lower genetic variations observed in this study as compared to what was reported by Okpeku et al. (2011) for WAD goat may be due to a higher rate of inbreeding in this goat population and also due to high level of polymorphism in the microsatellites marker compare to allozymes. The F_{ST} values ranged from 0.01 for Tf to 0.06 for Hb. Low F_{ST} indicates some measure of gene flow between the sampled populations, with Hb locus recording the highest gene flow of 0.06. Mujibi (2005) reported a low F_{ST} of 5.8% for WAD goats in Kenya; therefore, gene flow estimates in this study suggest mobility and considerable exchange of genetic material among these WAD goat populations (Figs. 2 and 3).

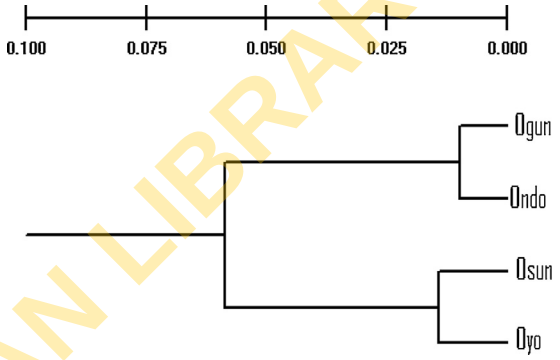

Fig. 4. Dendrogram showing similarity among four populations of WAD goat in Southwestern Nigeria at the haemoglobin locus.

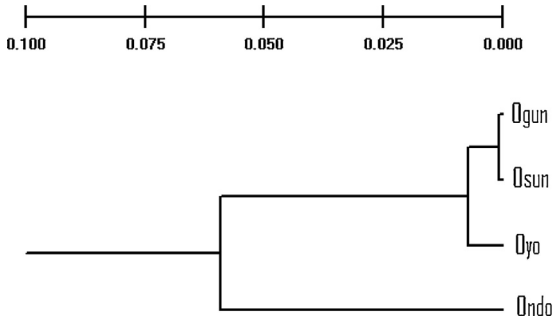

Fig. 5. Dendrogram showing similarity among four populations of WAD goat in Southwestern Nigeria at the Carbonic anahydrase.

4. The dendrogram

The dendrogram showed a measure of close relationship among the WAD goat populations until it branched into two main groups with populations from Ogun, Oyo and Osun state clustering together and population from Ondo state forming another branch then later the second branch that late emerged in which population from Osun branched away leaving population from Ogun and Oyo to clustered together (Figs. 4), Toro and Maki-Tanila (2007) suggested that the high genetic diversity observed within population groups could arise from overlapping generations and population mixtures from different geographical locations, with natural selection favouring heterozygosity or subdivision accompanied by genetic drift. The effect of these factors according to Agha et al., (2008) is more pronounced when the effective population size is very large, which is supported by the poor infrastructure on ground presently for livestock improvement and lack of proper breeding policy in Nigeria (Figs. 5 and 6).

5. Conclusion

The present study reveals that the WAD goat has substantial genetic variation but there is fairly high degree of outbreeding as indicated by f value (−0.16) indicating excess heterozygosity. The influx of other germplasm is affecting the founder alleles in the gene pool of WAD and breed purity is at stake. It becomes more pertinent especially in a country where breed wise census is not

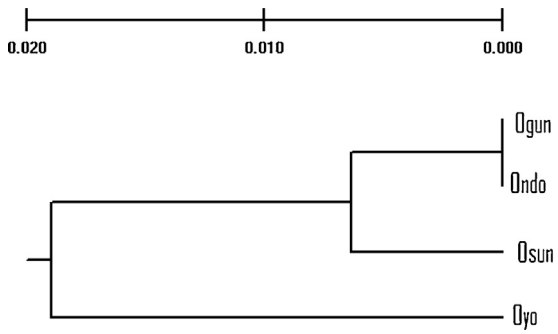

Fig. 6. Dendrogram showing similarity among four populations of WAD goat in Southwestern Nigeria at the Transfferin locus.

available. This is the high time but still safe enough to strengthen the conservation programme. For conservation, efforts should be made to provide elite breeding bucks to the farmer as male: female sex ratio is drastically low. Breeding strategies should therefore be designed under field conditions for conservation and improvement of this breed of Southwestern Nigeria having unique attributes like body size, trypanosotolerant adaptability to the rain forest zone of Nigeria with high fecundity and productivity under harsh conditions and minimal/zero input system.

Conflict of interest

The authors declare no conflict of interest regarding this article.

Acknowledgment

The authors would like to thank Dr. A.E. Salako, of Animal Breeding and Genetics Laboratory, Department of Animal Science, University of Ibadan Ibadan, Nigeria for collaboration in the laboratory work and for providing laboratory facility.

References

Abdul-Aziz, M., 2010. Present status of the world goat populations and their productivity. Lohman Inf. 45, 42–52.
Adebambo, O.A., Williams, J.L., Blott, S., Urquhart, B., 2004. Genetic relationship between native sheep breeds in Nigeria based on microsatellite DNA polymorphism. Anim. Genet. Resour. Inf. 34, 27–39.
Adedeji, T.A., Ozoje, M.O., Peters, S.O., Sanusi, A.O., Ojedapo, L.O., Ige, A.O., 2011. Coat pigmentation and Wattle genes effect on some haematological characteristics of heat stressed and extensively reared West African Dwarf goats. World J. Life Sci. Med. Res. 3, 48–55.
Agha, S.H., Pilla, F., Galal, S., Shaat, I., D'Andrea, M., Reale, S., Abdelsalam, A.Z., Li, M.H., 2008. Genetic diversity in Egyptian and Italian goat breeds measured with microsatellite polymorphism. J. Anim. Breed. Genet. 125 (3), 194–200.
Arora, R., Bhatia, S., Mishra, B.P., Joshi, B.K., 2011. Population structure in Indian sheep ascertained using microsatellite information. Anim. Genet. 42, 242–250.
Barker, J.S.F., Tan, S.G., Moore, S.S., Mukherjee, T.K., Matheson, J.L., Selvaraj, O.S., 2001. Genetic variation within and relationships among populations of Asian goats (*Capra hircus*). J. Anim. Breed. Genet. 118, 213–233.
Behl, R., Sheoran, N., Behl, J., Vijh, R.K., Tantia, M.S., 2003. Analysis of 22 heterologous microsatellite markers for genetic variability in Indian goats. Anim. Biotechnol. 14, 167–175.
Bosso, N.A., 2006. Genetic improvement of livestock in tsetse infested areas in West Africa. In: Doctoral Thesis. Animal Breeding and Genetics Group, Department of Animal Sciences, Wageningen University, P.O. Box 338, 6700 AH Wageningen, The Netherlands, pp. 13.
Bourn, D., Wint, W., Blench, R., Woolley, E., 1994. Nigerian livestock resources survey. World Anim. Rev. 78 (1), 49–58.
Buvanendra, V., Sooriyamoorthy, T., Ogunsusi, R.A., Adu, I.F., 1981. Haemoglobin polymorphism and resistance to helminths in Red Sokoto goats. Trop. Anim. Health Prod. 13, 217–221.
Camoglu, G., Elmaci, C., 2005. Carbonic anhydrase (Ca) and X-protein (X-p) types in Turkish sheep breeds. J. Appl. Anim. Res. 28, 125–128.
Chenyambuga, S.W., Hanotte, O., Hirbo, J., Watts, P.C., Kemp, S.J., Kifaro, G.C., Gwakisa, P.S., Petersen, P.H., Rege, J.E.O., 2004. Genetic characterization of indigenous goats of sub-saharan Africa using microsatellite DNA markers. Asian–Aust. J. Anim. Sci. 17, 445–452.
FAOSTAT. 2011. Food and Agricultural Organization of the United Nations FAOSTAT Database on Agriculture. Rome, Italy: 2011, http://faostat.fao.org/default.aspx (accessed 19.07.11.).
FDLPCS. Federal Department of Livestock and Pest Control Services FLDPCS Nigerian. Livestock Resources. National Synthesis, 2007, 440 pp.
Fitzhugh, H.A., Ehui, S.K., Lahlou-Kassi, A., 1992. Research strategies for development of animal agriculture. World Anim. Rev. 72, 9–19.
Ganai, N.A., Yadav, B.R., 2001. Genetic variation within and among three Indian breeds of goat using heterologous microsatellite markers. Anim. Biotechnol. 12, 121–136.
Groeneveld, L.F., Lenstra, J.A., Eding, H., Toro, M.A., Scherf, B., Pilling, D., Negrini, R., Finlay, E.K., Jianlin, H., Groeneveld, E., Weigend, S., GLOBALDIV Consortium, 2010. Genetic diversity in farm animals—a review. Anim. Genet. 41 (Suppl. 1), 6–31.
Gwakisa, P.S., Kemp, S.J., Teale, A.J., 1994. Characterization of zebu cattle breeds in Tanzania using random amplified polymorphic DNA markers. Anim. Genet. 25, 89–94.
Hanotte, O., Jianlin, H., 2005 Genetic characterization of livestock populations and Its use in conservation decision-making in the role of biotechnology Villa Gualino, Turin Italy –5-7 March 2005.
Ibeagha-Awemu, E.M., Erhardt, G., 2004a. An evaluation of genetic diversity indices of the Red Bororo and White Fulani cattle breeds with different molecular markers and their implications for current and future improvement options. Trop. Anim. Health Production 38, 431–441.
Imumorin, I.G., Ologun, A.G., Oyeyemi, M.O., 1999. Preliminary observations on effects of hemoglobin genotype and estimate of genetic distance at the Hb locus in West African Dwarf and Red Sokoto goats. Trop. J. Anim. Sci. 1, 1–9.
Jabbar, M.A., Ehui, S., Fitzhugh, H., 1995. The contribution of livestock to food security and sustainable development. Livestock development strategies for low income countries. In: Wilson, R.T., Ehui, S., Mack, S. (Eds.), Proceedings of the Joint FAO/ILRI Roundtable on Livestock Development Strategies for Low Income Countries. ILRI, Addis Ababa, Ethiopia, 27 February–02 March, 1995. Food and Agriculture Organization/International Livestock Research Institute, Nairobi, Kenya.
Jahnke, H.E., Tacher, G., Keil, P., Rojat, D., 1988. Livestock production in tropical Africa with special reference to the tsetse-afferent zone. In: Proceedings of a Meeting of the African Trypanotolerant Livestock Network, Nairobi 23–27 November 1987. International Livestock Centre for Africa and the International Laboratory for Research on Animal Diseases, Nairobi, pp. 3–21.
Kemp, S.J., Teale, A.J., 1994. Randomly primed PCR amplification of pooled DNA reveals polymorphism in a ruminant repetitive DNA sequence which differentiates Bos indicus and B. taurus. Anim. Genetics 25, 83–88.
Kim, K.S., Yeo, J.S., Lee, J.W., Kim, J.W., Choi, C.B., 2002. Genetic diversity of goats from Korea and China using microsatellite analysis. Asian–Aust. J. Anim. Sci. 15, 461–465.
Kitalyi, A.J., 1998. Village chicken production systems in rural Africa: household food security and gender issues. FAO Anim. Prod. Health Pap. 142, p81.
Kumar, D., Dixit, S.P., Sharma, R., Pandey, A.K., Sirohi, G., Patel, A.K., Aggarwal, R.A.K., Verma, N.K., Gour, D.S., Ahlawat, S.P.S., 2005. Population structure, genetic variation and management of Marwari goats. Small Rumin. Res. 59, 41–48.
Lu, S.X., Chang, H., Ji, D.J., Tsunoda, K., Ren, Z.J., Ren, X.L., Sun, W., Yang Ceriotti, G., Caroli, A., Rizzi, R., Crimella, C., Genetic, Z.P., Chang, G.B., 2006. The levels of genetic differentiation of small-tailed Han sheep and Tan sheep populations using structural loci. Agric. Sci. Chin. 5, 865–872.
Miller, Mark P. 1997 Tool for population genetic analyses (TFPGA) 1.3: A windos programme for the analysis of allozyme and molecular population genetic data. Computer software distributed by author.
Mason, I.L., 1984. Goat. In: Mason, L.L. (Ed.), Evolution of Domesticated Animals. Longman, London, pp. 85–99.
Menrad, M., Stier, C.H., Geldermann, H., Gall, C.F., 2002. A study on the Changthangi Pashmina and the Bakerwali goat breeds in Kashmir: I. Analysis of blood protein polymorphisms and genetic variability within and between the populations. Small Rumin. Res. 43 (1), 3–14.
Moruppa, S.M., 1985. A comparative study of Borno White and Red Sokoto (Maradi) goat breeds. In: M.Sc. Thesis. University of Ibadan, Ibadan, Nigeria.
Mourad, M., Gbanamou, G., Balde, I.B., 2001. Performance of Djallonke sheep under an extensive system of production in Faranah, Guinea. Trop. Anim. Health Production 33 (5), 413–422.
Mujibi, N.F., 2005. Genetic characterization of West African Dwarf (WAD) goats using microsatellite markers. In: M. Sc. Thesis. Department of Biochemistry and Biotechnology, Kenyatta University, Nairobi, Kenya.
Mwacharo, J.M., Otieno, C.J., Okeyo, A.M., Aman, R.A., 2002. Characterization of indigenous fat-tailed and fat-rumped hair sheep in Kenya: diversity in blood proteins. Trop. Anim. Health Production 34, 515–524.
Nei, M., 1972. Genetic distance between populations. Am. Natur. 106, 283–292.
Nei, M., 1973. Analysis of gene diversity in subdivided populations. Proc. Natl. Acad. Sci. U. S. A. 70, 3321–3323.
Nyamsamba, D., Nomura, K., Nozawa, M., Yokohama, K., YoZagdsuren, K., Amano, T., 2003. Genetic relationship among Mongolian native goat populations estimated by blood protein polymorphism. Small Rumin. Res. 47, 171–181.
Okpeku, M., Peters, S.O., Ozoje, M.O., Adebambo, O.A., Agaviezor, B.O., ONeill, M.J., Imumorin, I.G., 2011. Preliminary analysis of microsatellite-based genetic diversity of goats in southern Nigeria. Animal Genetic Resources, 49. Food and Agriculture Organization of the United Nations, pp. 33–41.

Paris, T.R., 2002. Crop animal systems in Asia: socio-economic benefits and impacts on rural livelihoods. Agric. Syst. 71, 147–168.
Rege, J.E.O., Baker, R.L., Hanotte, O., 2002. Improving our understanding and utilisation of indigenous African livestock breeds: key research challenges Commission on Animal Genetics. In: Proceedings of the 53rd EAAP Annual Meeting, 1–4 September 2002, Cairo, Egypt.C ommission on Animal Genetics (G) Session 2, Characterisation and Utilisation of Genetic Resources, p. 7.
Rege, J.E.O., Okeyo, A.M., 2006. Improving our knowledge of tropical indigenous animal genetic resource. In: Malmfors, B. (Ed.), Version II, Module 2. In: Animal Genetic Training Resource Version 2, 2006. International Livestock Research Institute Nairobi, Kenya and Swedish University of Agricultural Science, Uppsala, Sweden.
RIKEN, 2006. Genetic Quality Monitoring by Biochemical Isozymes RIKEN Bioresource Center. Experimental Animal Division RIKEN BioResource Center 6 September 2006. https://www.brc.riken.jp/lab/animal/pdf/biochemical_pro.pdf.
Saitbekova, N., Gaillard, C., Obexer-Ruff, G., Dolf, G., 1999. Genetic diversity in Swiss goat breeds based on microsatellite analysis. Anim. Genet. 30, 36–41.
Salako, A.E., 2004. Maturity rate of some morphometric traits in the West African Dwarf sheep of Nigeria. Trop. J. Anim. Sci. 7 (1), 51–55.
Toro, M., Maki-Tanila, A., 2007. Genomics reveals domestication history and facilitates breed development. In: Oldenbroek, K. (Ed.), Utilization and Conservation of Farm Animal Genetic Resources. Wageningen Academic Publishers, Wageningen, The Netherlands, pp. 75–102.
Udo, H., Cornelissen, T., 1998. Livestock in resource-poor farming systems. Outlook Agric. 27 (4), 237–242.
Wilson, R.T., 1991. Small ruminant production and the small ruminant genetic resource in tropical Africa. In: FAO Animal production and Health papers 88. FAO (Food and Agricultural Organization of the United Nations), Rome, Italy, pp. 231.
Yakubu, A., Raji, A.O., Omeje, J.N., 2010a. Genetic and phenotypic differentiation of qualitative traits in nigerian indigenous goat and sheep populations. Asian Research Publishing Network (ARPN). J. Agric. Biol. Sci. vol. 5 (2), 58–66.
Yakubu, A., Salako, A.E., Imumorin, I.G., Ige, A.O., Akinyemi, M.O., 2010b. Discriminant analysis of morphometric differentiation in the West African Dwarf and Red Sokoto goats, South African. J. Anim. Sci. 40 (4).