Analysis of genetic structure of Nigerian West African Dwarf goats by microsatellite markers

Olukoya Kolawole Awobajo [a,*], Adebowale Emmanuel Salako [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

ABSTRACT

Genetic variation at 12 microsatellite loci and population structure hypothesis was examined for West African Dwarf (WAD) goat populations found in four Southwestern states in Nigeria. Estimates of genetic variability such as effective number of alleles and gene diversities revealed substantial genetic variation frequently displayed by microsatellite markers. Number of alleles observed across the microsatellite loci varied from 6 to 17 with an overall mean of 10.75 ± 3.22. Average polymorphism across the studied loci and expected gene diversity in the population were 1.66 ± 0.49 and 0.72 ± 0.17, respectively. Population was observed to be significantly differentiated into different groups, and showed fairly high level of inbreeding ($f = 0.95 \pm 0.15$) and global heterozygote deficit.

© 2015 Elsevier B.V. All rights reserved.

1. Introduction

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 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 (Ho) and expected (He) heterozygosity are the most commonly calculated population genetic parameters for assessing within breed diversity. (Hanotte and Jianlin, 2005). According to (Mason, 1984), the short-eared and short-horned goat maintained their presence in the equatorial West, Central and East Africa. 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 unfavorable humid and hot climate. In addition, the West African Dwarf (WAD) goat often has

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

short bowed legs attributed to achondroplasia (Wilson, 1991). 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 Zaire, Angola and the north of Namibia (Mason, 1984). WAD goat probably evolved specially in response to the conditions of the humid forest zone by selection of recessive genes for dwarfism (Wilson, 1991). 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, Zaire, and Central African Republic). It is also found in Senegal (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. 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. Several reports on performance characteristics have been published by Odubote and Akinokun (1992), Odubote (1994a,b), Ebozoje and Ngere (1995), Ozoje (1998) and Imumorin et al. (1999). Goats constitute the largest group of small ruminant livestock in Nigeria totaling about 53.8 million and also constituting 6.2 percent of the World's goat population (FAOSTAT, 2011). Surveys have shown that up to 85 percent 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 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). According to them, 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. 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). 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 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. He continued

that there is growing recognition of the need to characterize, utilize and conserve indigenous Animal Genetic Resources (AnGR). He further stated that lack of knowledge is a major limitation to effective genetic improvement of local indigenous breeds and it also limits the decision-making capability of national, regional and international agencies implementing programmes. 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). Traditional methods used to study genetic variability of animals and populations employed polymorphism in protein markers and genetic variation of haemoglobin (Buvanendra et al., 1981; Imumorin et al., 1999) and transferrin types in goats (Moruppa, 1985; Kitalyi, 1998; Yakubu et al., 2010a,b; Mourad et al., 2001). 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, 2004; Camoglu and Elmaci, 2005). However, these techniques lack the power to resolve differences between closely related breeds, since a great deal of genetic variation remains undetectable by using protein markers (Gwakisa, 2002). Moreover, according to him, the genotype frequencies estimated from protein markers may be influenced by natural selection among alleles, making it difficult to interpret inter-population comparisons. He continued that with recent developments in molecular genetics, it has been established that a measure of relative genetic diversity in animal populations can be attained through description of nucleotide sequence differences and similarities in the deoxyribonucleic acid (DNA) of animals in such populations. He continued that more recently, molecular data from DNA markers have received particular attention in the study of population variability because of their possible use in determining the chronology of evolutionary events and this is because DNA markers are much less subject to natural selection than are phenotypic traits. However, there is very little baseline information on the extent of natural genetic variation in WAD goats in Nigeria. Therefore, the present study aims at applying microsatellite 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. Molecular techniques

Eighty blood samples were collected from genetically unrelated animals of Southwestern Nigeria, representing the breeding region of WAD goat. The sampling was done from each of the four subpopulations of the breeding region in four Southwestern state of Nigeria. Before collecting blood sample from animals owners were asked of their relatedness. A random stratified technique was used to select the sampling area in the breeding region. Genomic DNA was isolated by the method described by the MagneSil® KF, Genomic System (Promega, 2003). As microsatellite markers are co-dominant, the 80 samples represent 160 alleles for a single locus. A battery of 12 microsatellite markers prepared in two multiplexes