



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



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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.

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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.

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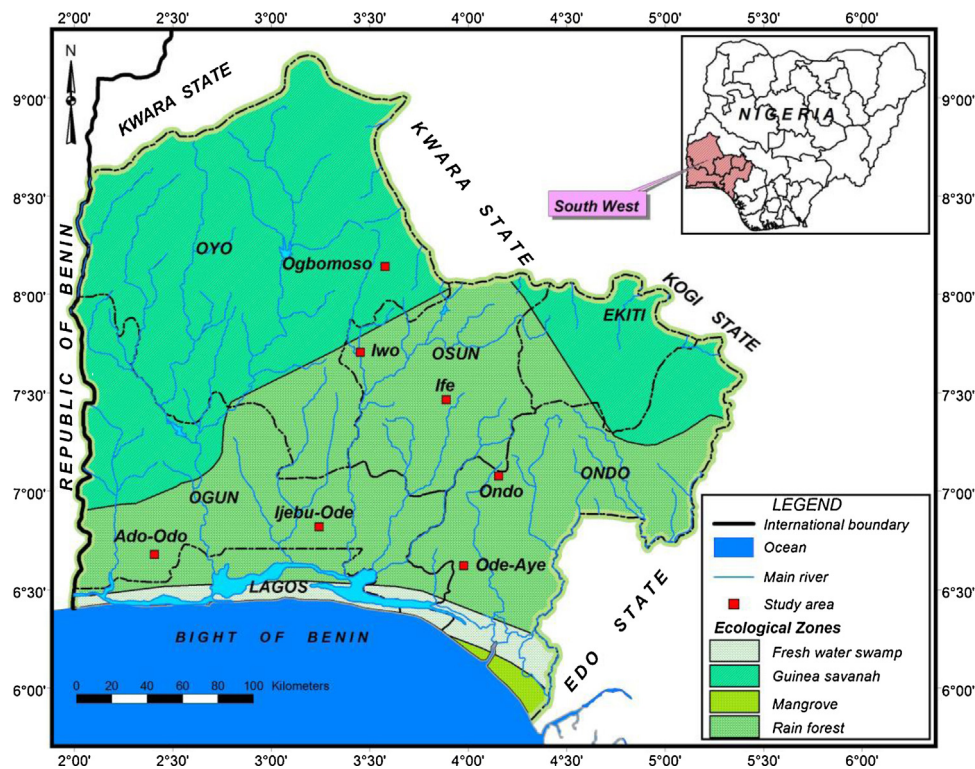


Fig. 1. Map of Southwestern Nigeria indicating sample area.

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

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