EVALUATION OF SERUM PROTEIN POLYMORPHISMS IN WEST AFRICAN DWARF AND RED SOKOTO GOATS IN SOUTH-WEST NIGERIA

B. A. Ogunfuye, C. O. N. Ikeobi, O. F. Smith, M. A. Adeleke, A. O. Adebambo, M. Wheto, D. O. Ogunlakin, A. A. Mohammed, J. S. Decampos and A. S. Adenaike.

College of Animal Science and Livestock Production, Federal University of Agriculture, Abeokuta

Corresponding author: todufuye@yahoo.com 08032567047

Abstract

Genetic similarities and variations in West African Dwarf and Red Sokoto goats in the South-West Nigeria were investigated on the basis of serum protein polymorphisms using sodium dodecyl sulphate poly-acrylamide gel electrophoresis (SDS-PAGE). Sera extracted from 200 West African Dwarf (WAD) and Red Sokoto (RS) goats were subjected to discontinuous system of SDS-PAGE to separate the proteins into five different zones; two globulin types (AA and BB) and three albumin types (AA, AB and BB). The formation of protein bands observed in variable loci within each zone (globulin and albumin zones) was an indication of diversification of goats in South-West Nigeria, while observation of bands in corresponding loci was an indication of relatedness in goat protein polymorphisms. Closer genetic attributes were exhibited in WAD goats than in Red Sokoto goats, that is, globulin and albumin banding pattern in the same breed are more similar when compared to the other breed. High polymorphisms existed among WAD goats, while low polymorphisms existed among the Red Sokoto goats (in terms of faint and thick bands). Similar banding pattern observed in few of the Red Sokoto and WAD goats indicated genetic similarity. There is a need for further study on effects of serum protein polymorphisms on morphometric traits using highly polymorphic protein or DNA markers for better understanding of breed characterization, conservation and genetic improvement of WAD and Red Sokoto goats in South-West Nigeria.

Key words; Goats, serum protein, polymorphisms, South-West.

Introduction

Goats are mostly domesticated in the world for their meat (chevon), milk, manure (faeces) and other beneficial products (Banerjee, 2011). West African Dwarf (WAD) goats are mostly raised under extensive management system in Southern part of Nigeria, while Red Sokoto goats are majorly found in the Northern part of Nigeria (Adu *et al.*,1988; Adebambo *et al.*, 2011). The production of small ruminant is beset by many problems which include poor management, exposure to harsh weather (disease) and malnutrition (**Ngere *et al.*, 1984;** Perez *et al.*, 2003; Muema *et al.*, 2009). As a result of this there is need for proper selective measure with reference to combined effects of blood proteins at specific regions which will serve as a guide towards selection and disease diagnosis. This will also serve as a means of providing fundamental information for effective treatment, disease control or prevention strategies (FAO, 2007; Yakubu *et al.*, 2011). Although attempts have been made on fundamental morphological characterization of goats in certain parts of Nigeria, but there is little information on preliminary study of blood serum-protein polymorphisms and their genetic characterization in South-West region of Nigeria. Therefore, this study was aimed at the assessment of blood serum-proteins as means of assessing genetic diversity and relatedness in Nigerian indigenous goats.

Materials and methods

A total of 200 West African Dwarf and Red Sokoto goats were sampled in some villages and Institutions of Lagos, Ogun and Osun States of Nigeria. The breed, sex, age and location of the goats were noted. Sera collected were subjected to Laemmli SDS-PAGE discontinuous method of protein analysis (Laemmli, 1970). Sodium dodecyl sulphate-poly-acrylamide gel electrophoresis (SDS-PAGE) used for collected samples consisted of acrylamide/ bisacrylamide (30%T, 2.67%); 87.6g acrylamide (29.2g/100ml); 2.4g of N'N'-bis-methylene acrylamide (0.8g/100ml). These were made to 300ml with deionized water and later filtered and store at 4°C in the dark. Ten percent was extracted by dissolving 10g of this SDS in 90 ml of distilled water with gentle stirring. Buffer for separating gel consisted of 1.5M Tris-HCl at pH of 8.8, 27.32g Tris base (18.15g/100ml), 80 ml of deionized water, adjust to pH with 6µHCl. These were made to 150ml with deionized water and store at 4° C. While buffer for stacking gel consisted of 0.5M Tris-HCl at pH of 6.8, 6g Tris base, 60 ml of deionized water (stored at 4°C).

Sample buffer-SDS reducing buffer consisted of 3.8ml, 0.5M Tris-HCl at pH of 6.8 (1.0ml), 0.8ml of glycerol, 10% of SDS, 1% of bromopherol blue (0.4ml), 2 mercaptoethanol (0.4ml). Electrode running buffer consisted of 9 g Tris base (at 15g/litre), 43.2g of glycine (72g/litre) and 3g of acrylamide/bisacrylamide (5g /litre). Each serum sample was diluted with sample buffer at ratio 1:6 (10µl:60µl), the mixture was heated at 95°C for 4 minutes in water bath and allowed to cool at room temperature. Stacking gel used for this experiment contained the distilled water (6.1 ml), 0.5 M Tris-HCl at pH of 6.8 (2.5 ml), 10 percent SDS (100µl), acrylamide bisacrylamide solution (1.3µl), 10 percent ammonium tetraoxosulphate IV (50µl) and initiator or N'N'N'N' Tetramethylene Diamine (TEMED)/ ($C_6H_{16}N_2$) (10µl).

The separation of proteins were carried out with the aid of Bio-Rad Electrophoresis system using the Bio-Rad Mini Protein II Cell. Gels were carefully removed and gently placed in water before being placed in a staining solution of 0.1% coomassie blue in 1:4 glacial ethanoic acids (CH_3OH) and later destained with destaining solution that contained 40% distilled water in 1:4 glacial ethanoic and methanol. The destained gels were scanned and bands were observed. Thick fractions of each band region were designated with '1', faint region were designated with '2' while absence of fractions at each region were designated with '0'. Dendrogram was constructed from the Nei's standard genetic distance (D_{ST}) using the unweighed pair group method with arithmetic mean (UPGMA) implemented in POPTREE 2 software package (Nei *et al.*, 1983; Ota, 1993; Yeh, 1999;Thairu-Muigai, 2002). The genetic relationship was measured by determining genetic distance between populations.

Results and discussion

The polypeptide chains of the goats assessed exhibited thick fraction, faint fraction, large fraction and small fraction at five loci examined (main-albumin type, AA; pre-albumin type, AB; post-albumin type, BB; main-globulins type, AA; and post-globulins type, BB). Very large bands that are distinctly formed suggested the presence of predominant polypeptides, most especially in main-albumin type, AA, regions, while moderate size bands were attributed to main-globulin type, AA, regions. These findings correspond to the findings of Bindu and Raghavan (2010) who reported the predominance of bands at HbA than HbB frequencies when blood samples were exposed to electrophoresis. These observations could also be related to the studies of protein polymorphisms in goats where higher genotype frequencies of HbAA were reported in Tunisian goats (Nafti *et al.*, 2013). The dendrogram constructed revealed the genetic structure on the basis of detected albumin and globulin bands on WAD and Red Sokoto goats. Albumin structure of Red Sokoto goats in Lagos State was close to WAD goats in Ogun State. This could be as the results of closeness of the two States, similarities in availability of non-genetic factors influencing protein polymorphisms. WAD goats in Ogun State were close to WAD goats in Osun State. This could be as a result of similar banding pattern of albumin type which emanated from the same breed or similarities in the mode of response to environmental factor. WAD goats in Osun State were close to Red Sokoto goats of Osun State. This could be as a result of availability of similar environmental factors which led to similarities in banding pattern of albumin type. The far apart distant range of Red Sokoto goats in Osun and Lagos State could be as a result of dissimilarities in non-genetic factors affecting growth and development of the goats or far apart ecological zone that would have led to irregular mode of response towards environmental factors (Figure 1).

Globulin structure of Red Sokoto goats in Lagos State was close to WAD goats in Osun State, unlike the case of albumin bands. This may be due to availability of similar banding pattern of globulin polypeptide chains that are present in close amount in both breeds or due to the fact that globulin banding pattern could have been influenced by a combination of unconsidered or hidden factors (Storz, 2010; Cheviron and Brumfield, 2011).

Conclusion

Serum protein polymorphisms on SDS-PAGE revealed that globulin and albumin banding patterns are more similar in WAD goats than in Red Sokoto goats. This was due to the observed closer genetic relationship and high polymorphisms in WAD goats than in Red Sokoto goats in South-West of Nigeria.

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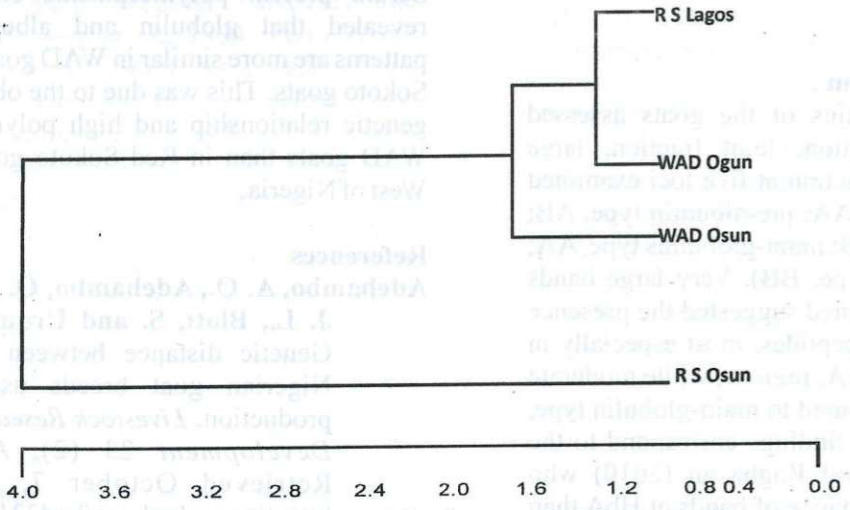

Figure 1. Dendrogram of diversity of albumin type and morphometric traits