GENETIC VARIATION IN A NON-DESCRIPT POPULATION OF GOATS IN KADUNA STATE, NIGERIA

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Abstract
A preliminary study involving 20 goats was conducted to assess the genetic variability of a non-descript goat population in Kaduna State, Nigeria. Tissue samples were collected from twenty (20) non-descript goats. Amplification of 25 microsatellite markers was by means of Polymerase Chain Reaction (PCR) technique. The PCR products were multiplexed and genotyped using an Applied Biosystems 3700 sequencer and bands were scored using Peakscanner(R) software. Allele number, observed and expected heterozygosities, as well as Shanon and Inbreeding index were computed using GenAlEX 6.5. Most of the markers were highly polymorphic with allele numbers ranging from 2 (ILSTS005) to 14 (ILST087), and above 4 in most cases. Genetic variability was high as observed by the values of the mean observed and expected heterozygosites (0.678 and 0.721 respectively). The Microsatellite markers used in this study showed their suitability for analysis of genetic variability in this population as demonstrated by the high mean Shannon index (1.607). However, further research using a larger sample size, together with the three indigenous goat breeds of the country should be considered to assist the conservation decision and management of indigenous breeds.

Introduction

Goats (*Capra hircus*) possesses certain unique characteristics such as a short reproductive cycle, high kidding rate as compared to large ruminants, they are hardy in nature surviving harsh climatic and feeding conditions and tolerant to infectious diseases and parasites. They are important reserviours of valuable genetic traits and contribute significantly to the livelihoods of farmers in Nigeria. (Odoi *et al.*, 2000; Ajala, 2008)
Despite these unique characteristics/significance of goats to the Nigerian farmers, indigenous goats are faced with a major challenge (lack of genetic purity) which has affected their genetic merit resulting in genetic erosion, loss of genetic diversity and opportunities for efficient utilization of the existing goat genetic resources.
According to FAO report (FAO 1999), animal genetic resources in developing countries are gradually eroding which may lead to loss of breed specificity. This loss may have resulted from indiscriminate introduction of exotic genetic resources prior to proper characterization, utilization and conservation of our indigenous breeds.
The first step for the conservation and exploitation of domestic animal resources is having a good/comprehensive knowledge of the existing genetic variability within animal populations (Li *et al.*, 2002). This knowledge is essential for designing appropriate breeding plans as well as policy formulation and implementation.
Microsatellite markers have been effectively used to carry out genetic diversity studies in Nigerian goats (Adebambo *et al.*, 2011, Okpeku *et al.*, 2011, Yakubu *et al.*, 2014, Ojo *et al.*, 2015).
Microsatellite markers are short tandem repeats and are more advantageous among other methods in genetic assessment because of their high polymorphism, low mutation rate, small product size, abundance in nature and ease of amplification through PCR (Adebambo *et al.*, 2011, Okpeku *et al.*, 2011). This study is therefore aimed at evaluating the genetic characteristics of a non-descript population of goats using microsatellite markers. This is a preliminary study that will guide future researchers in carrying out further studies towards achieving genetic improvement, conservation and utilization of our indigenous goat populations in Nigeria.

Materials and Methods

Tissue samples from the ears of 20 non-descript goats of both sexes in Zaria, Kaduna state were used for this study. DNA was extracted from the tissue cells using commercial Kits (Pure Link™ Genomic DNA Mini Kits for purification of genomic DNA with Catalog numbers K1820-01, K1820-02) according to the manufacturer's specifications and protocol.

A master mix was prepared containing water, buffer, dNTP's, primers and TaqDNA polymerase in a single tube and later aliquoted into individual tubes. Magnesium Chloride ($MgCl_2$) and template DNA solutions were then added. The sample was gently vortexed and briefly centrifuged to collect all drops from the walls of the tube. The samples were placed in a thermo cycler using the following settings: an initial denaturation at 95°C (4 minutes), annealing at 50°C (45 seconds) and extension at 72°C (15 minutes) for 35 cycles.

The following 25 Microsatellite Markers were studied: SRCRSP03, ILSTS005, SPS113, CSRD247, MAF209, McM527, SRCRSP5, ILSTS087, SRCRSP9, OarFCB304, ILSTS11, ETH10, MAF065, OarCP34, ILSTS029, INRA023, MAF70, INRA063, BM6444, OarFCB48, INRABERN172, INRABERN185, TCRVB6, SRYM18 and OarFCB20. These Microsatellite Markers were proposed by FAO and ISAG for biodiversity studies in goats. Amplification of markers was by means of Polymerase Chain Reaction (PCR) technique and PCR products were separated by electrophoresis in an automated sequencer according to Martinez *et al* (2006). The PCR products were multiplexed and genotyped using an Applied Biosystems 3700 sequencer and bands were scored using Peakscanner(R) software (Applied Biosystems Foster City, CA, USA). Allele number, observed and expected heterozygosities, as well as Shanon and Inbreeding index were computed using GenAlEX 6.5 genetic analysis statistical package of Peakall and Smouse (2012). DNA extraction, amplification and sequencing were carried out at the International Livestock Research Institute (ILRI) Nairobi, Kenya

Results and Discussion

Allelic Frequencies, observed and expected heterozygosity and fixation-index (F_{is}) for a non-descript goat population in Kaduna State.

The number of effective alleles (Ne), observed (Ho) and expected heterozygosity (He) as well as fixation index (F_{is}) for this population are revealed in Table 1. The number of available alleles per locus ranged from 2-14 (ILSTS 005 to ILSTS 087). Most of the primer/markers used for this population were informative and displayed sufficient polymorphism with the exception of ILSTS 005 and INRABERN 185 which had allele numbers of 2 and 3 respectively.

The standard practice is that microsatellite markers should have at least 4 alleles for it to be effective for genetic diversity studies, although Wang *et al.* (2011); Yakubu *et al.* (2014) and Ojo *et al.* (2015) have been able to evaluate diversity studies using 2-3 alleles per locus. The number of alleles per locus indicates the measure of genetic variability as well as genetic differentiation within a population. The Shannon index (I) for this population ranged from 0.234 to 2.395, with a mean of 1.607, in most cases they were above 1. This further reveals high level of polymorphism in the microsatellite markers used which is an indication of their application in parentage analysis and biodiversity studies of other goat breeds in Nigeria.

The highest value obtained for the effective allele was 8.989 (ILSTS 087) while the least was 1.133 (ILSTS 005).

The observed heterozygosity (Ho) ranged from 0.125 (ILST 005) to 1.000 (SPS 113 and SRYM 18), the expected heterozygosity (He) ranged from 0.117 (ILSTS 005) to 0.889 (ILST 087 and MAF 65), while the mean observed and expected heterozygosities were 0.678 and 0.721 respectively. The mean heterozygosities is a reflection of the degree of genetic diversity within the population. The mean observed and expected heterozygosities obtained by Okpeku *et al.* (2011) was higher than what was obtained in this study for the Nigerian goats (0.720 and 0.747) respectively. However, the mean heterozygosities were higher than 0.54 reported by Muema *et al.* 2009, 0.51 by Adebambo *et al.* (2011) in Nigerian goats. Earlier researchers obtained estimates for mean heterozygosity as 0.70 in Portuguese goat (Bruno-de-Sousa *et al.*, 2011), 0.72 for Egyptian goats (Agha *et al.*, 2008), 0.63-0.69 in South African goats (Visser *et al.*, 2004), 0.68 in the Brown Short haired goat in the Czech Republic (Jandurova *et al.*, 2004), 0.611-0.84 for Chinese goats (Qi *et al.*, 2009) and 0.61-0.77 in Spanish Guadarrama goats (Serrrano *et al.*, 2009).These variations may have resulted from population and breed differences.

Some loci had their observed heterozygosities lower than the expected values [OarFCB 20 (0.429), CSRD 247 (0.789), ETH 10 (0.650), INRA023 (0.750), INRABERN 172 (0.471), MAF 65 (0.750), MAF 70 (0.611), MCM 527 (0.500), OarFCB 48 (0.650), SRCRSP 3 (0.647), OarPC 34 (0.643), SRCSP 5 (0.737), MAF 209 (0.600) and INRA 063 (0.588)]. These values indicates departure from random mating which implies homozygosis in this population and suggests on-going selection, which may be linked to other loci affecting morphological, productive or adaptive traits (Dixit *et al.*, 2008; Bruno-de-Sousa *et al.*, 2011) or may have resulted from mating closely related individuals (Inbreeding).

The inbreeding index (F_{is}) ranged between (-0.012 to 0.444) with a mean of 0.041implying low

inbreeding and was negative at eleven loci for this population (BM6444, ILSTS005, ILSTS11, ILSTS029, ILSTS087, INRABERN185, OarFCB304, SPS113, SRYM18, SRCSP9, TCRVB6).

The negative F_{is} values located at eleven (11) loci indicates the presence of more homozygotes at those loci. These negative F_{is} may have arisen from population sub-division owing to genetic drift, null alleles and selection against heterozygotes or inbreeding. Earlier researchers have obtained negative values in other studies on goats (Agha *et al.*, 2008; Rout *et al.*, 2008; Dixit *et al.*, 2009, Rout *et al.*, 2012).

Conclusion/ Recommendations

The panel of microsatellite markers used in this study showed their suitability for analysis of genetic variability in non-descript population of goats in Kaduna state. High genetic diversity was observed for this population as seen in the values obtained for the mean observed and expected heterozygosites (0.678 and 0.721 respectively), however, due to the traditional system of rearing goats, some level of inbreeding was observed (0.041). These results could be used to establish a national conservation and breed improvement strategies for economic traits in goats however, further research using a larger sample size together with the three indigenous goat breeds in the country will be required.

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Table 1: Allelic Frequencies, Heterozygosity and F-statistics (F_{is}) in non-descript goats of Kaduna State, Nigeria.

Locus	N	Na	Ne	I	Ho	He	F_{is}
OarFCB20	14	5.000	4.170	1.509	0.429	**0.760**	0.436
BM6444h	20	8.000	2.676	1.331	0.750	**0.626**	-0.198
CSRD247	19	9.000	5.870	1.933	0.789	**0.830**	0.048
ETH10	20	13.000	7.143	2.235	0.650	**0.860**	0.244
ILSTS005	16	2.000	1.133	0.234	0.125	**0.117**	-0.067
ILSTS11	18	8.000	2.521	1.307	0.722	**0.603**	-0.197
ILSTS029	20	4.000	1.891	0.899	0.500	**0.471**	-0.061
ILSTS087	20	14.000	8.989	2.394	0.950	**0.889**	-0.069
INRA023	16	8.000	4.876	1.793	0.750	**0.795**	0.057
INRABERNI185	13	3.000	1.807	0.733	0.615	**0.447**	-0.377
INRABERN172	17	11.000	6.494	2.104	0.471	**0.846**	0.444
MAF65	8	9.000	8.000	2.133	0.750	**0.889**	0.143
MAF70	18	6.000	3.447	1.448	0.611	**0.710**	0.143
MCM527	20	4.000	2.432	1.074	0.500	**0.589**	0.151
OarFCB48	20	9.000	6.612	2.005	0.650	**0.849**	0.234
OarFCB304	20	10.000	6.250	2.048	0.850	**0.840**	-0.012
SPS113	20	8.000	3.774	1.586	1.000	**0.735**	-0.361
SRCRSP3	17	5.000	3.524	1.352	0.647	**0.716**	0.097
SRCSP9	20	7.000	4.348	1.622	0.800	**0.770**	-0.039
SRYM18	20	12.000	7.767	2.220	1.000	**0.871**	-0.148
TCRVB6	12	7.000	5.143	1.772	0.833	**0.806**	-0.039
OarPC34	14	7.000	4.840	1.729	0.643	**0.793**	0.190
SRCSP5	19	10.000	6.067	1.972	0.737	**0.835**	0.118
MAF209	20	6.000	3.941	1.530	0.600	**0.746**	0.196
INRA063	17	5.000	2.861	1.209	0.588	**0.651**	0.096
Mean	17.520	7.600	4.663	1.607	0.678	**0.721**	0.041

N=sample size, Na= no. of alleles, Ne = no. of effective alleles, I = Shannon index, Ho = observed heterozygosity, He = expected heterozygosity and F_{is} = fixation index/inbreeding coefficient.