ABG -36

Genetic Structure of West African Dwarf Goats in South East Nigeria Using Inter-Simple Sequence Repeat Markers (ISSR)

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Abstract
In this study, the genetic structure of 50 goats of West African Dwarf (WAD) origin was evaluated. Five (5) inter-simple sequence repeat (ISSR) markers were used. The markers include – ISSR HB- 8, ISSR HB-10, ISSR HB-13, ISSR UBC-816 and ISSR UBC- 826. The ISSR markers were found to be polymorphic, informative and revealing. DNA was extracted from whole blood using CTAB extraction method according to manufacturers' protocol. The samples were randomly collected from markets, farms and households. A total of eleven (11) samples were collected in Imo State, twelve (12) in Anambra State, ten (10) in Abia State, seven (7) in Ebonyi State and ten (10) in Enugu State. . A dendrogram of the 50 WAD goat UPGMA procedure clustered the goats into ten major groups. The edge length sum of 7.167 was detected; the dissimilarity maximum value was 1, while that of the minimum was 4.7619 x 10^{-2} at 95% percentile. The principal component analysis of the fifty WAD goat resulted in five clusters while the dimensional scatter plot of the principal component analysis showed that there were no distinct clusters for each state. The genetic variability within the limits of observed small genetic distance in WAD goat could be harnessed considering the colour variates for genetic characterization purpose. The ISSR marker could be included in the formulation of effective conservation strategies and identification of the quantitative trait loci for marker-assisted selection in goat genetic improvement.

Keywords: Genetic structure, WAD goat, ISSR markers, principal component analysis

Introduction

Genetic variation is the basis of animal breeding and selection. The genetic characterization of domestic animal is the first step in considering the sustainable management or conservation of a particular population (William and Micheal, 2002). Genetic variation between and within a breed is described as diversity and it is a valuable asset as the adaptability of a population, depends on it (Woolliams *et al.*, 2005).Genetic structure of goat breeds can provide reliable information for the selection of parental material and assist in breeding programs. Goat (*Capra hircus*) is one of the smallest domesticated ruminants which are managed for the production of milk, meat, wool and leather particularly in arid, semitropical or mountainous countries (Morand-Frhed, 2004). In Africa, indigenous goats are important resource for farmers, providing meat, milk, manure, fibres and hides, and satisfying various cultural and religious functions (TECA, 2006). Survival of indigenous goat population in Africa is threatened by diseases, adverse climatic conditions, civil strife, the pressure of economic development, abandonment of traditional farming practices, and more importantly crossbreeding or replacement with animals from the developed world (Tesfaye, 2014). Eighty-eight percent (88%) of the world goat populations are located in Asia and Africa, mostly in the tropics and sub-tropics (Mohammed and Sayed, 2012). Genetic markers play an important part in the revealing of diversities at DNA level which can be detected and monitored in subsequent generations (Spooner *et al.*, 2015).

WAD goats are believed to have come from the Coastal West and Central Africa, it is also believed to be a result of natural selection in response to the conditions in the humid forest of West and Central Africa. WAD goat is multi-coloured, and anindication that it has not been deeply subjected to the forces of artificial selection. There is a characteristics feature of meatiness owing to their having a broad chest, straight back, and relatively long neck. WAD goat is mostly raised for meat and milk production. It is adaptable to all climatic conditions, a rare feature that makes it stronger than other breeds (Wikipedia, 2017).

In line with above, this study attempted to check the genetic structure of WAD goats using inter-simple sequence repeat (ISSR) markers in South East Nigeria.

Result s and Discussion

Dendrogram of Fifty West African Dwarf goats using ISSR Markers: A dendrogram based on unweighted pair group method with arithmetic mean and accompanied by bootstrapping with 1000 permutation was carried out. This clustered the goats into ten major groups. Group I consisted of BMEEB-40, BRBLFAB-32, WFIMAN-10, BRBLFEE-34 and WFIA-14 with 69% bootstrap value. They contained goats from places such as Ebonyi, Abia, Imo and Anambra States. The goat WFIA-14 is the most genetically isolated one in the group with bootstrap value of 69%. Group II included BMIA-18, WBLFIA-12, WBLFIA-17, WBLMEE-42, and WBLFIA-11 with 67% bootstrap value and they were collected from Anambra (WBLFIA-12, WBLFIA-17, BMIA-18), Imo (WBLFIA-11) and Enugu (WBLMEE-42) States. In this group, the goat WBLFIA-17 is highly isolated compared to other four goats that got similarly clustered to each. Group III cluster had only BMIMA-8 with 76% bootstrap value and was

collected from Imo State. Group IV contained WFIMA-15, WBrFIA-1 and WBLFIMA-3 with a bootstrap value of 79% and they were sampled from Imo (WBrFIA-1 and WBLFIMA-3) and Anambra (WFIMA-15) States. Group V had 82% of bootstrap value and was subdivided into subgroup I (SGI) and subgroup II (SGII). The SGI had WBLMEE-41, BMAB-25, BRFAB-26, WBRMEE-46, WFENEB-35 and BLFAB-27 with value of 78%, while group SGII had BFIMAN-22, WBLFIA-19, WBLMIA-2, WFIMAN-4 and WBLMEE-37 with a value of 65%. Group VI had WFAB-33 with a value of 89%. Group VII clustered together WBLMIA-13 and WBLFIA-5 with a value of 88%. Group VIII had a bootstrap value of 94% and was subdivided into subgroups I (SGI) and II (SGII). The SGI contained WFIMA-23, WBLMIA-21, WBLFIA-6, BLBRMAB-28, WBLFEE-38, WBLMAB-31, WBLMEE-39, BFENEB-44, WBRBLMA-24 and WBLFIA-7 with the value of 85%, while SGII contained only WBLFEE-36 with a value of 90% and it is estimated to be the most genetically isolated one among the members of the group. Group IX had a bootstrap value of 95% and was subdivided into two subgroups, subgroup I (SGI) and subgroup II (SGII). The SGI clustered together BRFEEB-47, WBLFIA-16, WBLMIA-9, BLBRFAB-29, WFENEB-48, BFENEB-45, and BRFEEB-43 with a value of 92% while SGII had WFAB-30 and WBRBLFIA-20 with a value of 93%. Group X consisted of two, namely, WBLFEEB-50 and WBLFEEB-49 with a value of 96%. The edge length sum of 7.167 was detected. The dissimilarity maximum value was 1, while that of the minimum was 4.7619 x 10^{-2} at 95% percentile.

Principal component analysis of the fifty WAD goat: Principal component analysis of the fifty WAD goat resulted in five clusters. Cluster I comprises of animal from Anambra State(,WBRBLFIA-20), Abia State(BLBRFAB-29), and Ebonyi State(WBLFEEB-49, WBLFEEB-50); Cluster II consist of animal from Imo State(WBrFIA-1, WFIMAN-4, WBLFIA-6) Anambra State(WFIMA-15), Abia State(BLFAB-27), and Ebonyi State(WBLMEE-37); Cluster III consist of animal from Imo State(BMIMA-8), Anambra State(WBLMIA-13, WBLFIA-16), Abia State(WFAB-30) and Enugu State(BRFEEB-47, WFENEB-48); Cluster IV consist of animal from the five states studied Imo State(WBLFIA-7); Anambra State(WFIA-14), Abia State(WBRBLMA-24, BRFAB-26, WBLMAB-31) and Cluster V consist of animal from Enugu State only(BRFEEB-43, BFENEB).The dimensional scatter plot of the principal component analysis showed that there were no distinct clusters for each state for the West African Dwarf goat population studied.

Dendrogram of fifty West African Dwarf goats using ISSR marker: A dendrogram of 50 WAD goat UPGMA procedure clustered the goats into ten major groups, with high bootstrap value of above 70% observed in almost all the ten groups and this indicates reliable clustering (Hills and Bulls, 1992). Each group has a colour peculiar to it with some exception in some groups. Group I was predominantly black goats and with two(2) white goats. Group II had mostly a white and black combination with a pure black goat. Group III had only one animal with a pure black colour. Group IV majorly had a white colour. There was a mix of white and black colour in Group V and predominant white colour in Group VI and Group VII. Group VIII and IX had a colour mix with black and brown majorly. Group X had two animals with white and black colouration. The mix in colour could be as a result of random mating, trading system and movement of animals as determined by man.

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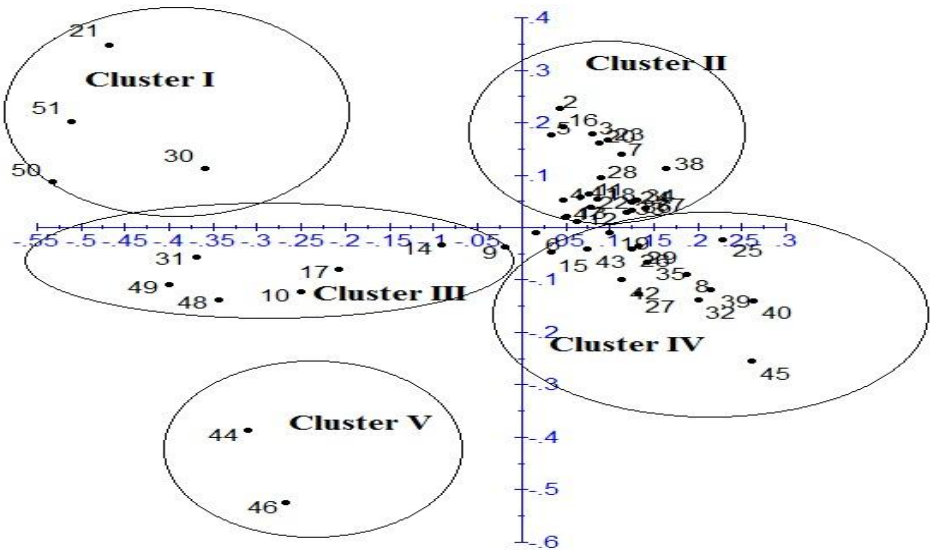

Fig.I: Principal component analysis of 50 WAD goat revealedbyISSR markers

Principal component analysis of the fifty WAD goat: The principal component analysis clustered the goats into five (5) clusters with peculiar colours particular to certain states. Cluster I had majorly white animals from Anambra, Ebonyi and Abia; Cluster III also had predominant white colour with brown colour from Enugu State. Cluster II had predominant white colour with a black goat from Abia State. Group IV again had a predominantly white colour with black and brown colour from Enugu and Abia. Cluster V had a black and a brown animal, both from Enugu State. It could be generally said that white and black colourationis predominant in Imo and Anambra State, while Ebonyi State, Enugu State and Abia State goats have alternate colours of black and brown. The resemblance in Ebonyi State, Enugu State and Abia State may arise from the fact that the three (3) states have a common transportation route. There exists a straight market road from Ebonyi State through Enugu State to Abia State. Exchange of animals in these three states is very easy. Though there is no clear demarcation between the five south-east states, Imo state and Anambra state have many entry routes to one another, and this may give rise to white and black goats predominantly found in this two states. The result of this work is similar to the findings of Meutchieye *et al.* (2008) who classified indigenous Cameroon breed into four (4) clusters. West African Dwarf goat having inter-related structures could be as a result of same breed factor, regardless of their location. The goat population studied by (Udeh, 2015) showed how breeds were clearly separated from each other, similar observation of population clustering has been reported in cattle (Machugh *et al.,* 1997) and Chicken (Wimmers *et al.,* 2000).

Conclusion

The genetic structure of West African Dwarf goat showed slight variability in the different states studied, with the genetic trees revealing common ancestral origin of WAD goat. The genetic variability in WAD goat could be harnessed for genetic characterization of Nigerian indigenous goat breeds. The inter-simple sequence repeat markers used in this study were very revealing and informative and could be included in the formulation of effective conservation strategies and identification of quantitative trait loci for marker-assisted selection in goat genetic improvement. Conservation sites should be established to preserve genetic traits of the West African Dwarf goat which could be lost through cross-breeding and urbanization.

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