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Genetic analysis of growth trait of West African Dwarf Goat reared in the humid tropical rainforests of Southeastern Nigeria

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Abstract

The study was conducted to evaluate the heritability and genetic relation between growth traits of West African Dwarf (WAD) goats. Fifty mature intensively managed goats were used for the experiment comprising 40 does (dams) and 10 bucks (sires). The goats were classified into 10 breeding groups of 4 Does (dams) and one buck (sire). Fresh water and forage were provided *ad libitum* in addition to 1kg concentrates *Cajanus cajan* to each animal per day. Data were collected on body weights and linear body measurements. Paternal Half-sib Analysis model was used to estimate heritability of the traits studied. Phenotypic and genotypic correlations between growth traits were also calculated. The heritability estimates for birth weight was low (0.15), while height at withers and body length at 6 months recorded high heritability. Moderate (Medium) heritability were recorded for weaning weight (0.50), Body weight at 6 months (0.55), Arm length at 6 months (0.34), Body length at birth (0.33), Height at Withers at birth (0.31) and arms length at birth (0.30). Phenotypic and genotypic correlation between pairs of the growth traits ranged from 0.18 to 0.85. Based on the finds of this study it was concluded that WAD goats could be used for selective breeding at weaning and 6months of age, to enhance the overall genetic improvement of growth traits. Thus, appreciable genetic progress for growth traits can be achieved in the WAD goats in the humid tropics.

Keywords: Local Goats, Heritability, Selection, Genetic Gain

Introduction

The 2019 national census gave the current population of Nigeria as 201 million people (worldpopulationreview.com/countries/Nigeria-population, 2019). With the rate of population growth and rapid loss of indigenous livestock species, the present gap in the supply of animal protein is bound to widen. To bridge the animal protein demand and supply gap, the Nigeria government has been

importing temperate breeds of livestock, but unfortunately these efforts have not been quite successful, principally because the exotic breeds cannot adapt to the tropical Nigerian environment as the challenges of tropical pests and diseases are unbearable to them. Locally adapted breeds (indigenous breeds) are better able to survive and produce valuable products in low input, pests and variable environments (AGRI, 2002).

The genetic improvement of indigenous breeds of goats is currently very important because they have valuable resources for economic development and poverty alleviation (Okafor et al., 2016). They can adapt to extreme harsh environmental conditions, pests and diseases; and as such be more productive in their own environment than exotic breeds (Fajemilehin and Salako, 2008). The indigenous breeds of goats are valuable experimental animals because of their potential store of unique genes (Salako and Ngere, 2002). Of the several indigenous breed in Nigeria, the WAD goat is predominant in the humid rainforest agro-ecology of southern Nigeria. They are highly prolific, hardy and have a short generation interval (Ngongeh and Onyeabor, 2015). Morphological characterization of the WAD goat has been undertaken in a number of studies (Situma et al., 2014; Shoyombo et al., 2015; Birteeb et al., 2015). These studies have shown the interrelationships between various linear body measurements and body weight at different ages. Early evaluation of growth parameters also minimizes the effect of environmental variation (Ogbu et al., 2015) and by so doing improves genetic evaluation of the WAD goats (Akpa et al., 2013).

It is a laudable proposition that more attention be given to the genetic importance and development of the WAD goats, since its productivity can offer a quicker means of bridging the gap currently existing in animal protein consumption in the country (Muyideen *et al.*, 2018). Improvement in WAD goats will increase meat and milk production, which will provide animal protein that are indispensable to a balanced human diet, as such go a long way to solve the present acute animal protein shortage in Nigeria.

It is, therefore, imperative that efforts be channeled towards the improvement and breeding progress of WAD goat which is indigenous to the tropics. Breeding programs depend on the identification of various useful traits of high heritability (Mohammed et al., 2018) and ease to measure for breeding improvement. To optimize gains, growth traits which are important objectives in selection, knowledge of heritability, phenotypic and genetic correlation between growth traits is of utmost importance. A genetic correlation is favorable when selection on one trait produces a desirable outcome in another trait. As a result, a trait can have a positive favorable correlation, or a negative favorable correlation. Traits that are cheap or easy to measure but that have favorable genetic correlations with economically important traits that are more difficult or expensive to

measure can be utilized as indicator traits (Bullock *et al.*, 2016).

It is therefore of utmost importance to estimate the genetic and phenotypic parameter of growth traits which are scarce in goats reared under humid tropical conditions and where such information is available, analytical methods may be different. The aim of this study was therefore to provide information on the heritability estimates and genetic correlation of these traits and their application to selection for genetic improvement of these traits of WAD goat population reared in the humid tropics.

Materials and Methods

Location of the Study

This study was carried out at a goat farm in Trans-Ekulu, Enugu East Local Government Area of Enugu State located at latitude 6° 30 N and longitude 7° 30 E (Federal Republic of Nigeria Official Gazette 15 May, 2007). Enugu falls within semi-tropical rainfall forest belt of the south with an average annual rainfall of 2,000 millimeter, and the main daily temperature of 26.7° C or 80.1° F (Sanni, 2007).

Management of Experimental Animals

Fifty mature intensively managed WAD goats were used for the study. Ten matured bucks (males) and forty sexually mature does aged 7-8 months were used for the study. Body weight ranged between 9.0 and The animals were kept for two weeks to acclimatize before introducing them in to 10 experimental pens prepared. The pens were dry, free of dampness and pests and rodents and were adequate ventilated for optimum health. Pens were kept clean with fresh hay or straw for bedding. They were fenced adequately to avoid indiscriminate mating and also for protection. All routine health management was carried out by a veterinarian. The animals were vaccinated against enterotoxaemia, tetanus, contagious caprine pleuro-pneomonia and paste-petit-ruminants (PPR). Fresh drinking water was provided in clean containers at all times. Fresh forage was provided ad libitum in addition to 1kg concentrates-pigeon pea (Cajanus cajan) which was mixed with little salt and water to each animal per day.

Management of Pregnant Does

Natural mating was used during breeding. Breeding females were vaccinated 4 to 6 weeks before kidding and de-wormed 2 to 3 weeks prior to kidding. Following birth, kids were vaccinated against enterotoxaemia and tetanus at 8 weeks of age, followed by a booster at 12 weeks of age. After birth, iodine was used to disinfect the navel.

Data Collection

The kids born were ear-tagged for identification purposes and weighed. Each of the animals selected for measurements was restrained before measurements were taken to ensure that they are not unnecessarily stressed. The traits measured were thus:

Growth Performance: Birth weight (BW₀), weaning weight (WWT) (at four months), and body weight at 6 (BW₆) months of age.

Linear Body Measurements: Body length at birth (BL_0) , Body length at birth (BL_6) , Height at withers at weaning (HW_0) Height at withers at 6 months (HW_6) Arm length at birth (AL_0) , Arm length at 6 months (AL_6) .

Genetic Analysis

Analysis of variance using yielded estimate of sire component of variance from which the genetic heritability of the individual traits were calculated using the method of Becker (1992).

$$h^2 = \underbrace{\frac{4^2 s}{2}}_{2s+w}$$

Where

h²=heritability

²_s=variance sire

²_w=residual variance

The paternal half-sib analysis assumes all effect are random, normal and independent with expectation zero. The statistical model was given as:

$$Y_{ij} = u + A_i + e_{ij}$$

Where Y_{ij} = an observation of a trait on the i^{th} sire U=Overall mean A_i =Random effects of the i^{th} sire E_{ij} =Random error

Genetic, phenotypic and environmental correlations

The genetic correlation (r_g) between any two of the traits being considered was obtained using the following relationship by Becker (1992).

$$r_g = CoV_{S_{x,y}} / s_{(x)x} s_{(y)}$$

where,

 r_g = genetic correlation between traits x and y $CoVs_{x,y}$ = additive genetic (sire component) covariance between traits x and y

s(x, y) = additive genetic standard deviation for traits x and y respectively.

Phenotypic Correlation (r_p)

The phenotypic correlation (r_p) between any two of the traits was obtained The computation formula is however given by Becker (1992) as:

$$cov_{w(x, y)} + Cov_{s(x, y)} / (w_{x(x)} + w_{s(x)}) (w_{y(y)} + w_{s(y)})$$

Where, $cov_{w(x, y)} + Cov_{s(x, y)} = Cov_{P(x,y)} =$ phenotypic covariance between traits x and y.

 $\mathbf{w}(\mathbf{x})$ + $\mathbf{s}(\mathbf{x})$ = phenotypic standard deviation of trait \mathbf{x} $\mathbf{w}(\mathbf{y})$ + $\mathbf{s}(\mathbf{y})$ = phenotypic standard deviation of trait \mathbf{y}

Results and Discussion

Heritability estimates from sire variance component of Growth traits

Heritability estimates provide an insight on the genetic influence of a trait. The result of the study revealed that, heritability estimates of HW₆ (0.77), BL₆ (0.75), were high; WWT (0.50), (BW_6) (0.55), AL_6 (0.34), BL_0 (0.33), HW_0 (0.31), AL_0 (0.30), were medium (Table 1). High values indicate that such traits are highly heritable and can be transfer from parents to offsprings. The highly heritable values could give a guide on the appropriate selection method that breeders could use when planning an effective breeding programme. The estimates in this study were higher than those reported in literature for the same age which ranged from 0.06 to 0.17 in different goat breeds (Ekambaram et al., 2010; Roy et al., 2011https://www.ncbi.nlm.nih.gov/pmc/articles/PMC 6054051/ - bib0060). The differences in these could be ascribed to different population parameter such as number of records, the methods of estimation of heritability, levels of inbreeding, breed of the goat, and location of the study. The high heritability recorded in factors had more influence on early kid gains than on gains later in the kid's life (Mohammed *et al.*, 2018). These estimates suggest that with mass selection at an early age, much improvement can be achieved in the

population. With this high heritability of the traits, progeny improvement and progress in improving future generations will be rapid.

Table 1: Heritability estimates for performance traits at various age periods for the West African Dwarf goats.

Traits	Heritability
Birth weight (BW ₀)	0.15±0.35
Weaning weight (WWT)	0.50±0.44
Body weight at 6 months (BW ₆)	0.55±0.44
Body length at birth (BL ₀)	0.33±0.38
Body length at 6 months (BL ₆)	0.75±0.46
Height at withers at birth (HW ₀)	0.31±0.44
Height at withers at 6 months (HW ₆)	0.77±0.44
Arm length at birth (AL ₀)	0.30±0.45
Arm length at 6 months (AL ₆)	0.34±0.45

On the other hand, low heritability estimates were obtained in BL_0 (0.33) and BW_0 (0.15). The low values obtained in this study were in agreement with Das (2008) who recorded 0.15±0.04 for blended goats at Malya, Tanzania but different from 0.39±0.09 obtained by Alade (2010) in his own study. The low estimates of heritability for these traits may suggest that genetic variation is unobservable due to environmental factors. This may also be attributed to the high maternal influence associated with kid growth performance which has the tendency to increase the component of environmental variance thereby lowering heritability estimates (Das et al., 2018). The difference in heritability values reported by different authors could be as a result of sampling problems, high managerial and non-genetic factors (Das, 2008) and due to differential gene control at different stages

of growth or it may be a sampling bias due to unavailability of same record due to pre-weaning mortality.

Genetic and phenotypic correlation of growth triats of the WAD goats

The genetic and phenotypic correlation estimates between growth triats of the WAD goats are presented in Table 2. The phenotypic correlations (rP) between BW $_0$ and HW $_4$ (0.21); BW $_0$ -WWT (0.23), HW $_0$ BW $_6$ (0.10) were positive, low and insignificant (p>0.05). The estimates of phenotypic correlation in this study were generally higher than that of genetic correlations. On the other hand, BL $_0$ -BW $_6$ (0.65), BL $_4$ -WWT (0.35) had significant (p<0.05) and positive phenotypic correlations (rP).

Table 2: Phenotypic, Genotypic between body weight and body measurements at various ages.

Traits	$r_{ m P}$	$r_{ m G}$
BW_0 - HW_4	0.21	0.18
BW ₀ - WWT	0.23	0.09
HW_0 - BW_6	0.10	0.06
BL_0 - BW_6	0.65*	0.22
BL ₄ - WWT	0.35*	0.08
BL_6 - BW_6	0.23	0.23
Bw0-WWT	0.34	0.22

Key: = Hw= height at withers; BW=body weight; BL=body length, r_p , r_G ,=Phenotypic and Genotypic respectively; *=significant (P<0.05).

In all, genetic correlation estimates (table 2) between growth traits studied were positive, low and not significant (p >0.05). However, genetic correlation between BW_0 -WWT (0.20) was positive significant (p < 0.05). Genetic correlation, measures the degree of association between two traits. A highly positive genetic correlation as noted on growth traits would mean that selection for one trait will result in the improvement of the other (Sodini et al., 2018). A genetic correlation is favorable when selection on one trait produces a desirable outcome in another trait. Genetic correlations are also believed to be strongly influenced by gene frequencies (Barton, 2017), so they may differ markedly in different populations, and just as heritabilities are expected to change after selection has been applied. Information on the magnitude and direction of genetic correlations among traits is very important in planning improvement program for the traits of interest.

Conclusion

Heritability estimates for growth traits at various age periods were low and moderate. This study indicated that a high genetic progress in growth trait can be achieved through direct selection in WAD goats. The positive correlations between the traits studied reveals that they are all being controlled by similar genes. This implies that selection for one will lead to increase performance of the other trait. It could be concluded that any improvement in body weight will bring about good improvement on the morphometric traits. Improvement in performance of growth traits of WAD goat and probably in other farm animal species will help in no small measure in enhancing the protein production, supply and consumption by the populace.

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