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Estimation of Genetic Correlation and Heritability for body conformations of three Rabbit Breeds from a 3 x 3 diallel crossing

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ABSTRACT

The genetic improvement of animals is fundamentally dependent on a thorough understanding of genetic parameters associated with economically important traits, among which heritability and genetic correlations are particularly critical. This study was conducted using New Zealand White (NZW), Chinchilla (CHC) and California White (CAW) breeds of rabbits and their progenies to estimate genetic correlations and heritability within the breeding groups. Thirty-six (36) rabbits, comprising nine (9) bucks (3 per breed) and twenty-seven (27) does (9 per breed) were mated at ratio1:3. Different parameters measured on both the parents and their progenies according to the different breeding groups includes Weaning weight (WW), Body Weight (BW), Body Length (BL), Body Width (BW), Shoulder to Tail length (ST), Ear Length (EL), Tail Length (TL), Length of Fore Limb (LFL) and Length of Hind Limb (LHL) from 4th week of age until 16th week of age. The results revealed that genetic correlation (rg) between birth weight and weaning weight was found to be negative in all the crosses except in male CAW x female NZW that yielded 0.05. Correlation between 12th week body weight and body length were positive for all the crosses except male NZW x female CHC, male CHC x NZW female and male CAW x female CAW that had -0.45,-0.06 and -0.56 respectively. Heritability (h^2) estimates from the linear body measurement were generally low to high ranging from 0.20 to 0.86 in all the weeks. However, male CAW x female CHC had the better h^2 compared to other pure and crossbred rabbits at all age considered. It could be concluded from this study that these correlated response and heritability could be exploited on genetic improvement for economic traits in rabbits while using crossbreeding.

Keywords: Breed of rabbit, Diallel crossing, genetic correlation, heritability, body measurements

INTRODUCTION

Genetic improvement of rabbits is important in order to increase their contribution to the much needed animal protein in Nigeria. A prerequisite for this improvement is the knowledge of their breeds and parity, litter growth and weaning characteristics in many generations (Amao, 2025; Niranjan *et al.,* 2010). Improvement of rabbit genetically, is a vital scope on the way to increasing their contribution to the much needed animal protein in developing countries (Ghosh *et al.,* 2008). However, the importance and efficacy of rabbit production in Nigeria has not been fully harnessed with respect to the profitability and their impact in meeting the much needed animal protein in Nigeria. In other to reduce the production cost and increase the profitability of rabbit production, genetic improvement of the adapted breed has to be undertaken. One of the pre-requisites for genetic improvement is the knowledge of genetic parameters for important economic traits (Akanno and Ibe, 2005).

In rabbits worldwide, in several productive reproductive variables, parent and offspring measurements, genetic and environmental parameters have been determined that influence the animal's productivity (Gambo *et al.,* 2021; Nagar *et al.,* 2020; Khan *et al.*, 2020). Rabbit has been used as an experimental animal in genetics and reproductive physiology since the beginning of the century. It was not until 1950 that first findings on quantitative genetics were published, about the maternal influence on birth weight in rabbits, and research on the genetic improvement of the rabbit for meat production (FAO, 1997). Rabbit is in the class of micro livestock that provides alternative to meat production instead of the traditional use of cattle, sheep and goat. It has gained much prominence in recent times due to its prolificacy, comparatively low production cost, and no religious restrictions (Ansah *et al.*, 2014). The rabbit has potentials to provide sustainable dietary animal proteins and incomes to poor households in developing countries like

Nigeria with a rapidly growing population. Attributes such as its miniature size, low space requirements, short gestation and generation intervals, high fecundity etc gives the rabbit leverage for increased exploitation (Chia and Machebe, 2025). Rabbit farming in Nigeria is gaining significant recognition as a promising and sustainable agricultural practice in recent years. This effort holds the potential to address pressing issues of food security, economic diversification, and environmental sustainability among others (Para *et al.,* 2015).

Rabbits are characterized by high reproductive ability with a short generation interval and so can produce a high quantity of meat in a short period (Khan *et al.*, 2020). Samkol and Lukefahr, (2008) opined that rabbits are highly prolific and are 2.5 and 4 times more efficient in extracting protein from forages than sheep and beef cattle respectively. Crossbreeding is one of the tools with which the breeder improves his animals. Apori *et al.* (2014) observed that one major challenge in crossbreeding exercise is the choice of the breed to serve as sire or dam line, therefore, relying on reciprocal crossing brings out the hybrid vigoures.

In animal genetic improvement programs, quantitative tools are applied that facilitate the selection of the best animals based on their breeding values to increase their productive and reproductive efficiency genetically (El-Deghadi, 2019). Estimation of heritability (h_2), repeatability (R), and correlations (r_{xy}) among the traits of economic importance at the zootechnical level define the appropriate selection method; they also constitute determining factors in the selection response (Gambo et al., 2021; El-Deghadi, 2019). For this reason, their estimation must be as precise as possible (Ossa, 2017). Hagan and Opoku-Mensa, (2019) reported that heterosis were positive among rabbit crosses with combining ability for growth and reproductive traits. Rabbit production is a lucrative business such that a person with one pair of rabbits can produce 60 to 80 rabbits each year to eat or sell (Elmer, 1990). One of the pre-requisites for genetic improvement is knowledge of genetic parameters for important economic traits (Akano and Ibe, 2005) and genetic correlation and heritability are some of those genetic parameters. Correlation is about the relationship of two or more characters on an individual farm animal (Ibe, 1998). Genetic correlation (rg) is the correlation of the breeding or additive gene effects of the two traits, x, y in question.

Where:

COV (AxAy) = additive genetic covariance of traits x and y

VAx = additive genetic variances of traits x

VAy = additive genetic variances of traits y.

Heritability (h^2) estimates indicates the proportion of total phenotypic variation that is attributable to hereditary or a measure of the progress that can be made from generation to generation in a given trait (Campbell *et al.,*2003). It is not a biological constant and so can be affected by management procedure and the method of estimation (Khalil *et al.,*1986). Several reports on rabbit breeds had been documented in relation to heritability such Dige *et al.* (2012) who reported that the heritability estimate for BW ranged from low to moderate in new Zealand White rabbits, Chineke and Adeyemi (2001) and Argente *et al.* (2017) found heritability to be low to moderate and positive correlation for rabbits in their different studies. Ajayi *et al.* (2014) also signified the low to moderate heritability for heterogeneous rabbit stocks that were products of non-specific crosses of New Zealand White, California, Chinchilla and Flemish Giant breeds with the indication that this trait is lowly heritable therefore, within family selection and some out-breeding will be effective in the improvement of this trait in the population. Abe *et al.* (2018) found that the heritability estimates obtained for New Zealand White rabbits ranged from moderate to low with higher estimates from the sire model and the genetic, phenotypic and environmental correlations for weekly body weights were positive and high respectively.

Heritability (h^2) (narrow sense) is the measure of additive genetical variation in proportion to the phenotypical variation for a trait expressed in a rabbit population (Hashash, 2017). The analysis of variance (ANOVA) procedures are used to estimate variance components (Sire, dam, sire + dam) for heritability estimates. Therefore, from the unbiased estimates of ANOVA, heritability is calculated thus:

Materials and Methods

Experimental site

The study was carried out at the Rabbitary Unit of the Teaching and Research Farm of Agricultural Education Department of Emmanuel Alayande University of Education, Oyo, Oyo State. Oyo lies on the longitude 3° 7’ East of Greenwich meridian and Latitude 7° 5’ North of the equator. It is about 5 kilometers north-eastward from Ibadan, the capital of Oyo state. The altitude is between 300 and 600 meters above sea level. The mean annual temperature is about 27°C (GoogleMap, 2025) while that of rainfall is 1165mm.

Experimental Animals and Management

A total of thirty-six (36) rabbits, comprising nine (9) bucks (3 per breed i.e. 3 New Zealand White bucks -NZW, 3 Chinchilla bucks – CHC and 3 California White bucks -CAW) and twenty-seven (27) does (9 per breed i.e. 9 New Zealand White does -NZW, 9 Chinchilla does - CHC and 9 California White does -CAW) were used and assigned into the experimental hutch cages at a mating ratio of 1:3. The 27 does were in the age group of 7-8 months and weighed 2.20 to 2.50 kg, while the 9 bucks belong to the age category of 8-9 months and weighed 2.30 to 2.60 kg. The mating plan adopted was as described by Khan *et al.* (2020). The mating design in a 3 x 3 diallel crossing is as follows:

	NZW	CHC	CAW
NZW	NZW x NZW	NZW x CHC	NZW X CAW
CHC	CHC x NZW	CHC x CHC	CHC x CAW
CAW	CAW x NZW	CAW x CHC	CAW x CAW

NZW = New Zealand White, CHC = Chinchilla, CAW = California White

Feeds and Feeding of the rabbits

Mashed concentrate diet was given at 100 g in the morning and green roughages (such as Centrosema pubescens, Tridax procumbens, Aspillia africana or Aspilia Americana) were supplied *ad libitum* in the afternoon. Composition of feed was similar for all experimental rabbits and in accordance with specifications of Khan *et al.* (2020): Maize - 40%, maize offal - 22%, Groundnut cake - 12%, soya Bean meal – 18%, Trace ingredients - 5%, vitamin and mineral mixture - 2.5%, common salt - 0.5%. The proximate composition of the diet was Dry Matter - 93.14, Crude Protein - 14.48, Ash - 7.15, Ether Extract - 10.25, Crude Fibre - 10.64, Non Fibre Extract -57.83 and Moisture context - 92.88%, respectively. Other routine management was the same.

Data Collection

The parameters from the offering includes Weaning weight (WW), Body Weight (BW), Body Length (BL), Body Width (BWT), Shoulder to Tail length (ST), Ear Length (EL), Tail Length (TL), Length of Fore Limb (LFL) and Length of Hind Limb (LHL) from 4th week of age until 16th week of age. The weight measurements were obtained using a sensitive digital scale with two decimal place calibration in grams (g). These growth traits were obtained by the procedure described by Food and Agricultural Organization -FAO, (2012).

Statistical analysis

The statistical package used was Statistical Product and Service Solutions (SPSS, Version, 25) in which variance components from the procedures of analysis of variance (ANOVA) were used to estimate heritability. The model adopted was as shown below:

$Z_{ij} - \alpha_i = \mu + \beta (X_{ij} - x) + e_{ij}$ (Becker, 1992)

Where:

Z_{ij} = is the mean of the records of the offspring from a mating of i^{th} sire to the j^{th} dam
μ = common mean
α_i = the effect of the i^{th} sire
β = the regression co-efficient of Z on X
X_{ij} = the record on the j^{th} dam mated to the i^{th} sire
x = the phenotypic mean of the dams
e_{ij} = the deviation of the means of the progeny.

The regressions from the sire families are pooled to obtain the common regression co-efficient, β. Sire effect was removed by obtaining the regression of offspring on dam within the sire.

RESULTS

The estimates of genetic correlation of some growth traits of the breeding groups are as shown in Table 1. The results revealed that birth weight and weaning weight in all the groups were negative except CHC x NZW and CAW x NZW which yielded low but positive correlation of 0.06 and 0.05 respectively. Likewise, weaning weight at 6 week and week 12 weight were negative except NZW x NZW, CHC x CHC, CAW x CAW and CAW x CHC that yielded low but positive correlations of 0.01, 0.02, 0.03 and 0.03 respectively. However, week 12 body weight and week 12 body length yielded moderate to high and positive correlations in all the groups except NZW x CHC, CHC x NZW and CAW x CAW that were negatives.

Table 1: Estimates of genetic correlation of some growth traits of the breeding groups

Breeding groups	BW and WW	WW6 and W 12	W12 and BL 12
NZW_m x NZW_f	-0.78	0.01	0.55
NZW_m x CHC_f	-0.45	-0.05	-0.45
NZW_m x CAW_f	-0.61	-0.04	0.67
CHC_m x CHC_f	-0.76	0.02	0.78
CHC_m x NZW_f	0.06	-0.28	-0.06
CHC_m x CAW_f	-0.45	-0.36	0.64
CAW_m x CAW_f	-0.32	0.03	-0.15
CAW_m x NZW_f	0.05	-0.32	0.71
CAW_m x CHC_f	-0.67	0.03	0.65

NZW_m x NZW_f = pure New Zealand White, NZW_m x CHC_f = New Zealand White Chinchilla crossbred, NZW_m x CAW_f = New Zealand White California White crossbred, CHC_m x CHC_f = pure Chinchilla, CHC_m x NZW_f = Chinchilla New Zealand White crossbred, CHC_m x CAW_f = Chinchilla California White crossbred, CAW_m x CAW_f = pure California White, CAW_m x NZW_f = California White New Zealand White crossbred, CAW_m x CHC_m = California White Chinchilla crossbred. BW = Body weight, WW = Weaning weight at 6 week, W 12 = Weight at 12 week, BL 12 = Body length at 12 week.

Table 2 shows the heritability estimates of linear body measurements of the nine breeding groups and their h^2± S.E (h^2) at 4 weeks of age. The results indicated that the body length is low to moderate heritability for all the crosses with the range of 0.44 to 0.48. The body width recorded for all crosses for heritability is also low to moderate heritability with values of 0.41 to 0.46. The shoulder to tail heritability observed for all crosses indicated low heritability while tail length heritability obtained shows low (0.25) to high (0.50) heritability. The ear length heritability recorded for all the crosses was also low (0.30-0.34) while length of forelimb heritability obtained for the crosses was low (0.20) to high (0.56). The length of hind limb heritability values observed was low (0.32) to high (0.55).

Table 2 shows the heritability estimates of linear body measurements of the nine breeding

Breeding group	BW(cm)	BL(cm)	ST(cm)	TL(cm)	EL(cm)	LFL(cm)	LHL(cm)
NZW_m x NZW_f	0.45±0.01	0.44±0.02	0.30±0.01	0.25±0.01	0.30±0.01	0.20±0.01	0.32±0.01
NZW_m x CHC_f	0.46±0.01	0.45±0.02	0.32±0.01	0.26±0.01	0.30±0.01	0.52±0.02	0.35±0.02
NZW_m x CAW_f	0.47±0.01	0.43±0.02	0.31±0.01	0.27±0.01	0.32±0.01	0.30±0.01	0.32±0.02
CHC_m x CHC_f	0.44±0.01	0.43±0.01	0.32±0.01	0.28±0.01	0.32±0.01	0.45±0.02	0.35±0.01
CHC_m x NZW_f	0.47±0.01	0.42±0.01	0.35±0.02	0.45±0.02	0.31±0.01	0.55±0.03	0.45±0.01
CHC_m x CAW_f	0.48±0.02	0.43±0.01	0.36±0.02	0.43±0.02	0.33±0.02	0.47±0.01	0.50±0.02
CAW_m x CAW_f	0.46±0.02	0.41±0.01	0.36±0.01	0.45±0.02	0.30±0.02	0.48±0.01	0.48±0.01
CAW_m x NZW_f	0.46±0.03	0.43±0.02	0.33±0.02	0.47±0.03	0.32±0.02	0.53±0.01	0.49±0.02
CAW_m x CHC_f	0.47±0.02	0.46±0.02	0.38±0.02	0.50±0.03	0.34±0.01	0.56±0.01	0.55±0.03

NZW_m x NZW_f = pure New Zealand White, NZW_m x CHC_f = New Zealand White Chinchilla crossbred, NZW_m x CAW_f = New Zealand White California White crossbred, CHC_m x CHC_f = pure Chinchilla, CHC_m x NZW_f = Chinchilla New Zealand White crossbred, CHC_m x CAW_f = Chinchilla California White crossbred, CAW_m x CAW_f = pure California White, CAW_m x NZW_f = California White New Zealand White crossbred, CAW_m x CHC_m = California White Chinchilla crossbred, BL (cm) = Body length in centimeter, BW (cm) = Body width, ST = shoulder to tail, TL = Tail length, EL = Ear length, LFL = Length of forelimb, LHL = Length of hind limb, h^2 = Heritability, S.E (h^2) = Standard error of h^2

The heritability estimates of linear body measurements of the nine breeding groups and their h^2± S.E (h^2) at 8 weeks of age are presented in Table 3. The results indicated that the body length is moderate to high heritability for all the crosses with the range of 0.53 to 0.64. The body width recorded for all crosses for heritability is also low to moderate heritability with values of 0.26 to 0.37. The shoulder to tail heritability observed for all crosses indicated moderate heritability while tail length heritability obtained shows low (0.35) to high (0.53) heritability. The ear length heritability recorded for all the crosses was also low to moderate (0.21-0.42) while length of forelimb heritability obtained for the crosses was low (0.28) to high (0.56). The length of hind limb heritability values observed was low (0.12) to high (0.51).

Table 3: Heritability estimates of linear body measurements of the nine breeding groups and their h^2± S.E (h^2) at 8 weeks of age

Breeding group	BW(cm)	BL(cm)	ST(cm)	TL(cm)	EL(cm)	LFL(cm)	LHL(cm)
NZW_m x NZW_f	0.26±0.02	0.64±0.02	0.40±0.01	0.35±0.04	0.20±0.03	0.28±0.01	0.12±0.01
NZW_m x CHC_f	0.28±0.03	0.56±0.02	0.42±0.01	0.36±0.05	0.31±0.05	0.42±0.02	0.33±0.02
NZW_m x CAW_f	0.27±0.01	0.53±0.02	0.41±0.01	0.37±0.03	0.38±0.03	0.30±0.01	0.34±0.02
CHC_m x CHC_f	0.34±0.01	0.63±0.01	0.42±0.01	0.38±0.01	0.32±0.04	0.42±0.02	0.38±0.01
CHC_m x NZW_f	0.37±0.01	0.52±0.01	0.45±0.02	0.48±0.02	0.21±0.01	0.52±0.03	0.35±0.11
CHC_m x CAW_f	0.34±0.02	0.53±0.01	0.46±0.02	0.49±0.02	0.23±0.02	0.48±0.02	0.20±0.02
CAW_m x CAW_f	0.36±0.02	0.61±0.01	0.46±0.01	0.48±0.02	0.34±0.02	0.28±0.03	0.38±0.01
CAW_m x NZW_f	0.37±0.03	0.53±0.02	0.40±0.02	0.48±0.03	0.40±0.02	0.46±0.05	0.42±0.02
CAW_m x CHC_f	0.36±0.02	0.53±0.02	0.48±0.02	0.53±0.03	0.42±0.01	0.56±0.11	0.51±0.03

NZW_m x NZW_f = pure New Zealand White, NZW_m x CHC_f = New Zealand White Chinchilla crossbred, NZW_m x CAW_f = New Zealand White California White crossbred, CHC_m x CHC_f = pure Chinchilla, CHC_m x NZW_f = Chinchilla New Zealand White crossbred, CHC_m x CAW_f = Chinchilla California White crossbred, CAW_mx CAW_f = pure California White, CAW_mx NZW_f = California White New Zealand White crossbred, CAW_m x CHC_m = California White Chinchilla crossbred, BL (cm) = Body length in centimeter, BW (cm) = Body width, ST = shoulder to tail, TL = Tail length, EL = Ear length, LFL = Length of forelimb, LHL = Length of hind limb, h^2 = Heritability, S.E (h^2) = Standard error of h^2

Table 4 revealed the heritability estimates of linear body measurements of the nine breeding groups and their h^2± S.E (h^2) at 12 weeks of age. The result shows that the body length is moderate to high heritability for all the crosses with the range of 0.41 to 0.53. The body width recorded for all crosses for heritability is also moderate to high heritability with values of 0.54 to 0.75. The shoulder to tail heritability observed for all crosses indicated moderate to high heritability while tail length heritability obtained shows low (0.26) to high (0.55) heritability. The ear length heritability recorded for all the crosses was also low to high (0.36-0.64) while length of forelimb heritability obtained for the crosses was low (0.22) to high (0.58). The length of hind limb heritability values observed was low (0.12) to moderate (0.40).

Table 4: Heritability estimates of linear body measurements of the nine breeding groups and their h^2± S.E (h^2) at 12 weeks of age

Breeding group	BW(cm)	BL(cm)	ST(cm)	TL(cm)	EL(cm)	LFL(cm)	LHL(cm)
NZW_m x NZW_f	0.55±0.03	0.41±0.01	0.60±0.03	0.35±0.02	0.36±0.02	0.28±0.01	0.28±0.01
NZW_m x CHC_f	0.66±0.02	0.42±0.01	0.62±0.02	0.26±0.02	0.33±0.03	0.32±0.03	0.27±0.02
NZW_m x CAW_f	0.67±0.03	0.41±0.02	0.61±0.02	0.37±0.03	0.39±0.01	0.22±0.02	0.26±0.02
CHC_m x CHC_f	0.54±0.02	0.40±0.01	0.62±0.02	0.29±0.02	0.35±0.03	0.42±0.03	0.31±0.01
CHC_m x NZW_f	0.67±0.02	0.40±0.02	0.65±0.01	0.45±0.02	0.37±0.02	0.58±0.01	0.41±0.01
CHC_m x CAW_f	0.68±0.01	0.48±0.03	0.38±0.01	0.55±0.02	0.53±0.01	0.45±0.02	0.25±0.02
CAW_m x CAW_f	0.76±0.01	0.49±0.03	0.39±0.04	0.35±0.02	0.64±0.01	0.44±0.03	0.40±0.01
CAW_m x NZW_f	0.67±0.02	0.49±0.02	0.67±0.04	0.47±0.03	0.62±0.01	0.46±0.03	0.39±0.02
CAW_m x CHC_f	0.86±0.03	0.53±0.01	0.68±0.03	0.50±0.03	0.60±0.03	0.43±0.02	0.30±0.03

NZW$_m$ x NZW$_f$ = pure New Zealand White, NZW$_m$ x CHC$_f$ = New Zealand White Chinchilla crossbred, NZW$_m$ x CAW$_f$ = New Zealand White California White crossbred, CHC$_m$ x CHC$_f$ = pure Chinchilla, CHC$_m$ x NZW$_f$ = Chinchilla New Zealand White crossbred, CHC$_m$ x CAW$_f$ = Chinchilla California White crossbred, CAW$_m$x CAW$_f$ = pure California White, CAW$_m$x NZW$_f$ = California White New Zealand White crossbred, CAW$_m$ x CHC$_m$ = California White Chinchilla crossbred, BL (cm) = Body length in centimeter, BW (cm) = Body width, ST = shoulder to tail, TL = Tail length, EL = Ear length, LFL = Length of forelimb, LHL = Length of hind limb, h^2 = Heritability, S.E (h^2) = Standard error of h^2

The heritability estimates of linear body measurements of the nine breeding groups and their h^2± S.E (h^2) at 16 weeks of age is as shown in Table 5. The results indicated that the body length is moderate to high heritability for all the crosses with the range of 0.36 to 0.68. The body width observed for all crosses for heritability is also low to high heritability with values of 0.25 to 0.60. The shoulder to tail heritability observed for all crosses indicated low to high heritability (0.22-0.57) while tail length heritability obtained shows low (0.28) to high (0.51) heritability. The ear length heritability recorded for all the crosses was also low to moderate (0.30-0.48) while length of forelimb heritability obtained for the crosses was low (0.29) to high (0.59). The length of hind limb heritability values observed was low (0.22) to moderate (0.55).

Table 5: Heritability estimates of linear body measurements of the nine breeding groups Breeding groups and their h^2± S.E (h^2) at 16 weeks of age

Breeding group	BW(cm)	BL(cm)	ST(cm)	TL(cm)	EL(cm)	LFL(cm)	LHL(cm)
NZW$_m$ x NZW$_f$	0.25±0.02	0.54±0.01	0.36±0.01	0.28±0.02	0.37±0.01	0.29±0.03	0.22±0.02
NZW$_m$ x CHC$_f$	0.40±0.02	0.36±0.03	0.22±0.01	0.36±0.02	0.33±0.02	0.52±0.03	0.25±0.01
NZW$_m$ x CAW$_f$	0.45±0.02	0.63±0.01	0.37±0.01	0.37±0.02	0.33±0.02	0.33±0.03	0.38±0.02
CHC$_m$ x CHC$_f$	0.48±0.04	0.53±0.02	0.36±0.01	0.38±0.01	0.36±0.01	0.49±0.01	0.37±0.02
CHC$_m$ x NZW$_f$	0.45±0.04	0.52±0.02	0.39±0.02	0.43±0.01	0.37±0.02	0.56±0.02	0.35±0.02
CHC$_m$ x CAW$_f$	0.43±0.03	0.53±0.02	0.38±0.02	0.45±0.01	0.30±0.01	0.45±0.01	0.55±0.03
CAW$_m$ x CAW$_f$	0.46±0.03	0.48±0.02	0.46±0.01	0.40±0.01	0.39±0.01	0.46±0.02	0.38±0.03
CAW$_m$ x NZW$_f$	0.42±0.03	0.63±0.01	0.48±0.02	0.48±0.02	0.48±0.01	0.57±0.01	0.29±0.02
CAW$_m$ x CHC$_f$	0.60±0.03	0.68±0.04	0.57±0.02	0.51±0.02	0.45±0.01	0.59±0.02	0.25±0.01

NZW$_m$ x NZW$_f$ = pure New Zealand White, NZW$_m$ x CHC$_f$ = New Zealand White Chinchilla crossbred, NZW$_m$ x CAW$_f$ = New Zealand White California White crossbred, CHC$_m$ x CHC$_f$ = pure Chinchilla, CHC$_m$ x NZW$_f$ = Chinchilla New Zealand White crossbred, CHC$_m$ x CAW$_f$ = Chinchilla California White crossbred, CAW$_m$x CAW$_f$ = pure California White, CAW$_m$x NZW$_f$ = California White New Zealand White crossbred, CAW$_m$ x CHC$_m$ = California White Chinchilla crossbred, BL (cm) = Body length in centimeter, BW (cm) = Body width, ST = shoulder to tail, TL = Tail length, EL = Ear length, LFL = Length of forelimb, LHL = Length of hind limb, h^2 = Heritability, S.E (h^2) = Standard error of h^2

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Discussion

The results of genetic correlation of some growth traits of pure and crossbred rabbits that revealed negatives correlation for most of the breeds with low positive correlation of some breeds was corroborated the earlier results of Montes-Vergara *et al*. (2020); Hagan and Opoku-Mensa, (2019); Argente *et al*. (2017); Ajayi *et al*. (2014) who documented negative correlation between parents and their offsprings in rabbit breeding in their respective studies in relation to genetic correlations of growth parameters of rabbits. Montes-Vergara *et al.* (2020) affirmed the existence of negative correlated values existed between New Zealand rabbits traits and body measurements. Hagan and Opoku-Mensa (2019) observed negative correlation among growth traits in rabbit crosses in New Zealand White, Blue Vienna and Chinchilla and their crosses. Argente *et al.* (2017) found negative correlation among the growth parameters measured in synthetic line created from commercial crossbred rabbits in Kenya which agreed with this current finding. Ajayi *et al.* (2014) claimed negative correlation among the growth parameters measured in heterogenous rabbit population in Nigeria. The implication of this finding is that when two traits are positively correlated, selection for one trait will automatically improve the other trait in a correlated response. However, the negative correlations seen among some traits show that selection for improvement of one trait leads to decreases in improvement of the other traits. The genetic correlation has revealed options for breeding programme for achieving economic traits like body weight. Some of the positive correlations between the growth traits studied were not also different from the findings of Chineke and Adeyemo (2001). However, the results were not consistent with Akano and Ibe, (2005) who reported strong genetic correlation between individual body weight and most of growth trait measured. This may be as a result of season effect and time of the collection of data on these experimental animals.

Meanwhile, the pattern of the heritability displayed by the pure and crossbred rabbits that signified that high estimates that there is a stronger additive gene effect in those traits considered compared to non-additive genes (Dominance, interaction, and environment). This agrees with the works of Donicer *et al*. (2021); Adeolu and Ogunnupebi, (2019); Abel *et al.* (2018); Argente *et al*. (2017) and Ajayi *et al.* (2014) who obtained a moderate to high heritability values for rabbits for their different studies. Heritability was able to be estimated in all of the traits due to positive progeny variance components in the analysis of covariance and usually, positive variance components indicated contribution of additive gene in the traits of interest. This is also in line with Dige *et al.* (2012) who encountered positive variance while working on genetic parameters in New Zealand White rabbit in Nigeria. Donicer *et al*. (2021) affirmed positive heritability estimate in New Zealand white rabbits in a tropical dry forest area of Nigeria. Khan *et al*. (2020) also reported positive heritability estimate in wool type Angora rabbits in an organized farm of Kashmir. Abel *et al.* (2018) reported positive heritability estimate for growth pattern in New Zealand White rabbit in Nigeria. Nagar *et al.* (2020) also affirmed positive heritability estimate for growth traits in five rabbit lines. Adeolu and Ogunnupebi, (2019) study on estimation of heritability and repeatability for pre-weaning body weights of domestic rabbits raised in the humid tropics Nigeria aligned with the obtained results on heritability. Ajayi *et al.* (2014) also found positive heritability estimate for growth traits in heterogenous rabbit population. The implication of these findings is that, for traits with high positive genetic correlation, selection for one trait may indirectly improve the other trait as a correlated response.

Conclusion

In this study, genetic parameters for different growth traits were estimated for pure and crossbred rabbits population. High genetic correlations between weaning weight and post-weaning weights suggest that the selection of animals at weaning can be a suitable criterion for the selection of the crossbred rabbits under sub-temperate conditions. Moderate heritability of growth traits indicates further scope for genetic improvement. Inbreeding was on the rise, which might lead to reduction in additive genetic variance and heritability while adopting crossbreeding. Opening the herd with new animals would help to increase the genetic variability and such as revealed for CAW x CHC crossbred rabbits. This study can help in carrying out similar studies to meet the demand for animal protein in developing countries.

Recommendation

The information obtained on the correlated responses could be used for optimization of mating strategies for non-additive genetic effects while the heritability estimates could be used to check the genetic progress or setbacks in different traits considered.

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