

Influence of additive and non-additive gene effects on body measurements in the domestic rabbit

V. N. Obasi and S N Ibe*

Department of Non-Ruminant Animal Production, Michael Okpara University of Agriculture, Umudike, P.M.B. 7267 Umuahia, Abia State, Nigeria.

* Corresponding Author: e-mail: sylvester_ibe@yahoo.com

Abstract

General Combining Ability (GCA) and Specific Combining Ability (SCA) were used to determine the influence of additive and non-additive gene effects on growth parameters, using 72 kits produced in full diallel crosses involving three breeds of rabbits namely, New Zealand White (NZW), Dutch (DT) and Chinchilla (CH). GCA was significant ($P < 0.05$) for four out of the twelve traits studied, namely Body length (BL), Heart girth (HG), Ear length (EL) and Tail Length (TL). GCA values ranged from -12.594 for body weight (BWT) to 0.041 for the length of the hind limb (LHL) for NZW, -3.836 for BWT to 0.123 for Head Circumference (HC) for DT and -0.035 for Head-to-shoulder (HS) and 16.431 for BWT for Chinchilla. SCA was significant ($P < 0.05$) for HS only. SCA estimates ranged from -0.016 (BWT) to 0.187 (HG), 1.018 (BL) to 10.22 (BWT) and -0.09 (LHL) to 7.354 (BWT), for NZW x DT, NZW x CH and DT x CH crosses, respectively. The significant GCA observed in the four growth parameters indicates that genes governing them act mainly additively. This implies that they may be genetically improved by selection and pure breeding. Significant SCA for HS is an indication that genes governing this character impart non-additive effects, suggesting that improvement could be brought about by exploiting crossbreeding and by improving the environment.

Keywords: Additive and non-additive genes, general combining ability, growth traits, rabbit, specific combining ability

Introduction

Genes could impart additive and non-additive effects on traits. While additive gene action is transmissible from parents to their offspring, non-additive gene action (dominance and epistasis) is not. Consequently, the proportion of total phenotypic variance that is additive is used as measure of heritability. Traits with high heritability may be improved by individual selection. On the other hand, traits with low

heritability may be improved genetically by family and other aids to individual selection and by exploiting heterosis through crossbreeding, and, non-genetically by improving the environment.

There is dearth of information in available literature on estimates of general and specific combining abilities for growth traits in rabbits. However, there are few studies on heritability

estimation and heterosis for growth traits. Ndjon and Nwakalor (1999) observed that gestation length, average daily gain at 56 days and individual weaning weight showed little or no heterosis, ranging from -1.4% for gestation length to 2.6% for average daily gain. They explained this to be an indication of the importance of additive gene effects on these traits and therefore, suggested that pure breeding and selection rather than crossbreeding might be the solution to the improvement of these traits and equally suggested that improvement of these traits could be sought by amelioration of management technique of the purebreds. Khalil and Soliman (1989) found that heritabilities for doe reproductive traits (number of service per conception and gestation length) were low in magnitude in Bauscat and Giza White rabbits. They also observed that estimates of heritability and repeatability of doe reproductive traits in Bauscat rabbits were generally lower than corresponding estimates in Giza White rabbits.

Some authors have reported some highly heritable traits in the rabbit. Chineke and Adeyemi (2001) reported 0.28, 0.99, 0.69, 0.43, 0.24 and 0.69 as heritability estimates of nose-to-shoulder, shoulder to tail pin bone, heart girth, withers height, length of ear and trunk length, respectively at 49 days of age in rabbits. Akanno and Ibe (2005) reported heritability estimates (from paternal half sibs) at 9 weeks of 0.30, 0.18, 0.45, 0.59 and 0.43 and at 12 weeks of 0.09, 0.35, 0.67, 0.06 and 0.03, for body width, body length, head-to-shoulder, shoulder-to-tail and length of leg, respectively. The indication is that some of the body measurements are governed by genes with additive effects, while some others are governed by genes with non-additive effects. Positive and high correlations have been reported between various linear body measurements and body weight (Tiamiyu *et al.*, 2000). Leplege (1970) reported heritability of the average weight

per rabbit at 56 days as 65.0%. Lukefahr *et al.* (1992) reported a value of 69.4% for total litter weight adjusted for litter size. Heritability of body weight at 60 days was 54.0% (Patras, 1985). Odubote and Somade (1992) reported moderate heritability estimates for litter size at birth, litter weight and litter weaning weight as 38.0, 32.0 and 16.0%, respectively. Lukefahr (1987) observed that productive traits relating to fertility, litter performance and those relating to health and/or survival are lowly heritable. This suggests that they are basically under the control of genes, which have non-additive effects.

The objective of this study is to estimate general and specific combining abilities for growth traits in domestic rabbits with a view to determining the contribution of genes with additive and non-additive effects on these characters. Knowledge of the type of gene action operating in a population enables a breeder to formulate breeding plans for genetic improvement of characters. Since much breeding work has not been done with rabbits in Nigeria, it is important to provide such baseline information, which could serve as basis for future research.

Materials and Methods

Study Area

This study was carried out at the Rabbitry Unit of Michael Okpara University of Agriculture, Umudike. The University is located at longitude 7°29'2" East and Latitude 5°21'2" North on an elevation of about 120 m above sea level. Umudike falls within the rainforest zone of Nigeria, with an average annual rainfall of about 220 mm distributed over eight months (March to November) with its peak in June or July and a dry spell usually in August. It has a humid climate and temperature that ranges from 28°C in the wet season to slightly over 35°C in the dry season

Experimental animals and matings

Three breeds of rabbits, namely New Zealand White (NZW), Dutch (DT) and Chinchilla (CH), were used in this study. The three breeds were used in complete diallel crosses, as indicated below.

Pure Crosses: NZW x NZW; DT x DT; CH x CH
 Main Crosses: NZW x DT; NZW x CH; DT x CH
 Reciprocal Crosses: DT x NZW; CH x NZW; CH x DT

One sire of each breed was mated to three dams, one each of the three breeds. There were two litters, with 35 and 37 kits in the first and second litters, respectively. Seventy-two kits were produced from the crosses. The numbers of sires, dams, litters and kits by breed type are given in Table 1.

Management of Experimental Animals

The rabbits were fed with compounded feed and forage (grass and legumes) between 0800 and 0900 hours and again between 1600 and 1700 hours. Water was given *ad libitum*. The does were placed on concentrates and forage during the

gestation period to help them have enough nutrients for embryonic and foetal development. The does were initially palpated to ensure that none was pregnant. They were then left for one week, during which period they were flushed and were served immediately thereafter. The does were taken to the bucks for mating between 0900 and 1100 hours and, after successful mating, the does were removed and new ones brought in. This was done three consecutive times and, thereafter, the bucks were left alone in their cages in case of failure and also for the second parity matings. Does were diagnosed for pregnancy and those diagnosed open were immediately returned to the appropriate buck for re-mating.

One week to the expected date of kindling, wooden kindling boxes were washed, disinfected, dried and placed inside the does' cages. This was to enable the does get used to them before kindling. After kindling, the kits were examined, and dead ones removed from the boxes. Litter weights were also taken.

Progeny that could not suckle were enabled to get colostrum by holding their does and taking the kits to the teat to suckle. The kindling boxes were removed when the kits were four to five weeks.

Table 1: Number of kits produced by each mating

Sire breed ^a	Dam breed ^a	Litter 1	Litter 2	Total No. of kits
NZW	NZW	4	5	9
NZW	DT	4	3	7
NZW	CH	3	4	7
DT	DT	5	5	10
DT	NZW	4	5	9
DT	CH	3	5	8
CH	CH	5	3	8
CH	NZW	3	4	7
CH	DT	4	3	7
Total		35	37	72

^a NZW = New Zealand White, DT = Dutch, CH = Chinchilla

Parameters Measured

The following parameters were measured from week one to week seven when the experiment was terminated in each parity: Body Length (BL), Body Width (BWH), Heart girth (HG), Height-at-withers (HW), Shoulder-to-tail drop (ST), Ear Length (EL), Head-to-shoulder (HS), Length of the forelimb (LFL), Length of the hind limb (LHL), Tail Length (TL), Body Weight (BWT) and Head Circumference (HC). All the parameters, with the exception of body weight (g), were measured in centimeter (cm). All the linear body parameters were measured using a tailor's tape while body weight was measured with a sensitive table weighing scale.

Statistical Analysis

Firstly, the data were analyzed by analysis of variance to test the null hypothesis that there were no significant differences among the various genetic groups (the crosses), with respect to all the body measurements studied. Before the analysis, however, the data were adjusted for fixed effects, namely parity and age, using derived additive constants (C_i), which were added as appropriate to the unadjusted data. The adjustment factor was derived with expression (1).

$$C_i = -(P_i + A_i) \quad (1)$$

where C_i = adjustment factor

P_i = Least-squares constant for parity, and

A_i = Least-squares constant for age

P_i and A_i were derived following analysis of variance for unbalanced data, using Harvey's (1990) Mixed Model Least-Squares and Maximum Likelihood Program.

The statistical model for analysis of variance for the adjusted data is given in Expression (2)

$$Y_{ij} = \mu + g_i + e_{ij} \quad \dots (2)$$

where Y_{ij} = j^{th} observation on the i^{th} genetic group (cross)

μ = Overall mean

g_i = Effect of the i^{th} genetic group

e_{ij} = random error, identically and independently normally distributed, with zero mean and constant variance, i.e. $iind(0, \sigma^2)$.

The method of Griffing (1956) was used for diallel analysis of the adjusted data. The statistical model is given in expression (3).

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + r_{ij} + 1/n \sum e_{ijk} \quad (3)$$

where Y_{ij} = mean of ij^{th} cross between line i (as sire) and line j (as dam).

μ = overall mean

g_i/g_j = General Combining Ability (GCA) of the $i^{\text{th}}/j^{\text{th}}$ breed.

s_{ij} = Specific Combining Ability (SCA) of the ij^{th} combination

r_{ij} = Reciprocal Effect

e_{ijk} = Error associated with k^{th} individual observation.

Expressions (4) and (5) were used to estimate GCA and SCA, respectively.

$$GCA, \mu_i = 1/2p(Y_i + Y_j) - 1/p^2 Y_{ij} \quad \dots (4)$$

$$SCA, s_{ij} = 1/2 (Y_{ij} + Y_{ji}) - 1/2p(Y_i + Y_j + Y_i + Y_j) \quad \dots (5)$$

where p = number of lines/breeds involved in the crosses.

Table 2. Least squares means and standard errors of different parameter for different genetic groups

Genetic group/code	HS (cm)	BWT (gm)	BL (cm)	BWT (cm)	HG (cm)	Trails*		ST (cm)	EL (cm)	HC (cm)	LFL (cm)	TL (cm)	LHL (cm)
						HW (cm)	HL (cm)						
NZW x NZW (1)	4.84 ^a	335.12 ^b	22.08 ^{cd}	17.60 ^{bc}	15.58 ^b	10.84 ^b	22.20 ^b	6.57 ^b	12.34 ^{bc}	8.43 ^{bc}	4.58 ^b	11.86 ^{bc}	
	±0.40	±8.33	±0.25	±0.20	±0.20	±0.10	±0.24	±0.10	±0.10	±0.09	±0.08	±0.12	
NZW x DT (2)	4.99 ^a	351.90 ^{ab}	22.56 ^{bc}	17.50 ^{bc}	16.10 ^b	11.35 ^b	22.48 ^{bc}	6.91 ^{bc}	12.55 ^{bc}	8.52 ^{bc}	4.68 ^{bc}	11.63 ^{bc}	
	±0.04	±9.59	±0.28	±0.23	±0.23	±0.11	±0.28	±0.11	±0.12	±0.10	±0.09	±0.14	
NZW x CH (3)	4.72 ^{bc}	359.52 ^{ab}	22.18 ^{cd}	16.89 ^{cd}	15.52 ^b	11.43 ^b	22.19 ^b	6.92 ^{bc}	12.43 ^{bc}	8.08 ^{bc}	4.71 ^{bc}	12.37 ^b	
	±0.04	±9.59	±0.28	±0.23	±0.23	±0.11	±0.28	±0.11	±0.12	±0.10	±0.09	±0.14	
DT x NZW (4)	4.80 ^{abc}	311.55 ^c	21.14 ^d	16.71 ^{cd}	15.45 ^b	10.79 ^b	20.96 ^c	6.70 ^c	12.24 ^{bc}	7.74 ^c	4.64 ^{bc}	11.55 ^c	
	±0.04	±8.59	±0.25	±0.20	±0.20	±0.10	±0.25	±0.10	±0.11	±0.09	±0.08	±0.13	
DT x DT (5)	4.72 ^{bc}	335.16 ^{bc}	22.40 ^{bc}	16.51 ^d	15.34 ^b	11.08 ^{bc}	21.66 ^{bc}	6.46 ^c	12.52 ^{bc}	8.52 ^{bc}	4.91 ^{bc}	11.45 ^c	
	±0.04	±7.93	±0.23	±0.19	±0.19	±0.09	±0.23	±0.09	±0.10	±0.08	±0.08	±0.12	
DT x CH (6)	4.77 ^{bc}	357.34 ^{ab}	24.22 ^{ab}	18.74 ^d	17.94 ^c	11.23 ^{bc}	23.40 ^b	7.65 ^c	13.45 ^b	8.40 ^{bc}	5.58 ^c	11.53 ^c	
	±0.04	±9.04	±0.27	±0.22	±0.21	±0.11	±0.26	±0.10	±0.11	±0.09	±0.09	±0.13	
CH x NZW (7)	4.61 ^c	326.25 ^c	21.17 ^d	17.74 ^d	15.93 ^b	10.66 ^c	20.52 ^c	6.52 ^c	11.99 ^c	8.30 ^{bc}	4.82 ^{bc}	11.63 ^{bc}	
	±0.04	±9.30	±0.27	±0.22	±0.22	±0.11	±0.27	±0.11	±0.12	±0.10	±0.09	±0.14	
CH x DT (8)	4.92 ^{ab}	380.90 ^b	23.44 ^b	18.05 ^{bc}	16.21 ^b	11.20 ^{bc}	22.80 ^{bc}	7.22 ^{bc}	12.33 ^{bc}	8.06 ^{bc}	5.49 ^c	12.03 ^{bc}	
	±0.04	±9.30	±0.27	±0.22	±0.22	±0.11	±0.27	±0.11	±0.12	±0.10	±0.09	±0.14	
CH x CH (9)	4.76 ^b	384.80 ^b	25.05 ^b	18.10 ^{bc}	17.41 ^a	11.12 ^{bc}	23.64 ^b	7.57 ^b	12.46 ^{bc}	8.52 ^{bc}	5.00 ^b	11.93 ^{bc}	
	±0.40	±9.03	±0.27	±0.22	±0.21	±0.11	±0.26	±0.10	±0.11	±0.09	±0.09	±0.13	

a-d Means in the same column with different superscripts are significantly different (P<0.05)
 * HS = Head-to-shoulder, BWT = Body weight, BL = Body length, BWH = Body width, HG = Heart girth, HW = Height at withers, ST = Shoulder-to-tail dry EL = Ear length, HC = Head circumference, LFL = Length of the forelimb, TL = Tail length, LHL = Length of hind limb

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Table 3. Estimates of General and Specific Combining Abilities for growth traits ^a

Combining Ability ^b	HS	BWT	BL	BVH	HG	HW	ST	EL	HC	LFL	LHL	TL
GCA (NZW)	0.008	-12.594	-0.825*	-0.198	-0.475*	-0.093	-0.448	-0.248*	-0.164	-0.036	0.041	-0.266*
GCA (DT)	0.028	-3.836	0.000*	-0.200	-0.099*	0.044	0.046	-0.047*	0.123	0.008	-0.169	0.101*
GCA (CH)	-0.035	16.431	0.825*	0.399	0.575*	0.049	0.492	0.295*	0.041	0.028	0.128	0.164*
SCA ¹²	0.067*	-1.016	-0.018	-0.034	0.187	0.041	0.008	0.153	-0.043	-0.128	-0.167	-0.106
SCA ₁₃	0.100*	10.122	-1.018	5.541	0.674	-0.989	-0.896	-0.273	-0.146	-0.088	-0.053	-0.069
SCA ₃₃	0.060*	7.354	0.312	0.660	0.437	0.044	0.448	0.240	0.247	-0.091	-0.063	0.334

* Significant (P<0.05)

^a HS = Lead-to-shoulder BWT = body weight BL = body length BVH = body width HG = heart

girth HW = height at withers ST = shoulder-to-tail drop EL = ear length HC = head circumference LFL = length of fore

limb LHL = length of hind limb TL = tail length

^b GCA = General Combining Ability SCA = Specific Combining Ability

1 = New Zealand White (NZW), 2 = Dutch (DT), 3 = Chinchilla (CH)

Results and Discussion

Effect of genetic group on growth traits

Least squares means and standard errors for different body traits are presented in Table 2. Genetic group differences were significant ($P < 0.05$) for all the traits. This necessitated the diallel analysis that was carried out for all the traits.

General Combining Ability (GCA)

Estimates of General Combining Ability for the twelve growth traits are given in Table 3. GCA was significant ($P < 0.05$) for BL, HG, EL and TL but not for HS, BWT, BWH, HW, HC, LFL and LHL. The indication is that additive gene action operates for BL, HG, EL and TL and not for the other traits, which are probably governed by genes with non-additive effects. Those characters governed by genes with additive effects are expected to respond to selection for their genetic improvement, since their heritability values are expected to be moderate to high. GCA estimates were highest for Chinchilla in ten out of twelve traits studied. The highest GCA was for body weight in Chinchilla, although GCA for this trait was not significant. Dutch was highest in two traits while NZW has the lowest estimates in all the traits studied. This suggests that Chinchilla has the highest preponderance of genes, which impart additive effects on the growth traits. The indication is that Chinchilla rabbits could possibly increase growth performance because of their higher GCA values. Afifi *et al.* (1987) used four breeds of rabbits and observed that Baladi was highest in GCA for birth weight.

Specific Combining Ability (SCA)

SCA was significant ($P < 0.05$) for only HS (Table 3). The significant SCA is an indication of non-additive gene action for this trait. The implication

is that HS can be improved genetically through appropriate crossing, utilizing non-additive gene effects for example dominance and epistasis involving dominance. Improving the environment may also bring about improvement in the character. The highest, although non-significant, SCA was for BWT in NZW x CH, followed by BWH in the same cross. This cross also had the highest SCA for HS, which was significant.

SCA for NZW x CH crosses was highest for six traits, namely BWT, HS, BWH, HG, LHL and TL, while estimates for DT x CH were highest for the remaining six traits, namely BL, HW, ST, EL, HG, and LFL. The indication is that non-additive gene effects could be exploited to genetically improve HS, BWT, BWH, HG, LHL and TL in NZW x CH and the remaining six traits in DT x CH. Improvement in the environment could also be useful. The result indicates that Chinchilla performed generally well in crosses with either NZW or DT. Cross performance was poor for NZW x DT, implying poor manifestation of non-additive gene action. The non-significant negative SCA suggests that crossing to utilize non-additive gene effects will result in depression of such traits.

Conclusion

There was significant General Combining Ability (GCA) for four traits, namely body length (BL), heart girth (HG), ear length (EL) and tail length (TL), indicating that additive gene effects are important for these characters, which may, consequently, be genetically improved by selection and pure breeding. Specific Combining Ability (SCA) was significant for head-to-shoulder (HS) only, an indication of the influence of non-additive gene effects on this trait. This suggests that improvement in this character may

be brought about by crossbreeding and by improving the environment.

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(Received 5th July 2005; Accepted 20th Sept. 2007)