

**ORIGINAL RESEARCH ARTICLE****Heritability estimates and genetic correlations of some reproductive traits in heterogeneous rabbit population in South-west Nigeria****\*<sup>1</sup>Ajayi, B. A., <sup>2</sup>Oseni, S. O. and <sup>3</sup>Popoola, M. A.**<sup>1</sup> Department of Animal Science Landmark University Omu-Aran, Kwara State, Nigeria<sup>2</sup> Department of Animal Sciences Obafemi Awolowo University, Ile-Ife, Nigeria<sup>3</sup> Federal College of Animal Health and Production Technology, P.M.B.5029 Moor Plantation Ibadan, Nigeria\*Corresponding author: [ajayi.bababunmi@lmu.edu.ng](mailto:ajayi.bababunmi@lmu.edu.ng); +234 (0) 803 800 1269**ABSTRACT**

Litter records of fifty six adult rabbits from heterogeneous rabbit population were used to estimate heritability ( $h^2$ ) and genetic correlations of some litter traits at birth, weaning and at 12- weeks of age. Forty-nine does were randomly allocated to seven sire families and the sire component of variance with unequal numbers of offspring per family was used to estimate heritability. Data were analysed using the General Linear Mixed Model procedure of SAS via Restricted Maximum Likelihood Method. Variance and Covariance Component Estimation Procedure were used to calculate  $h^2$  and genetic correlation respectively. Results showed that, Heritability estimates ( $h^2$ ) for body weight (BWT), litter birth weight (LBW) and litter size at birth (LSB) were 0.02, 0.19 and 0.20 respectively. The corresponding estimates at weaning were 0.02, 0.09 and 0.23 respectively. The  $h^2$  for individual weight and litter size at 12- week ( $LS_{12}$ ) were 0.46 and 0.06 respectively. Genetic correlation coefficients were generally positive for weekly body weight from birth to 12-week and ranged from low (0.09) to very high (1.00). The LBW and litter weaning weight (LWW), LBW and litter size at weaning (LSW) and LSW and LWW had genetic correlation coefficients of 0.87, 0.57 and 0.86 respectively. It was concluded that, this heterogeneous rabbit population showed high variability in reproductive traits, indicating a high degree of heterogeneity. Heritability estimates indicated that various outbreeding mating systems and family selection will be effective for the improvement of these traits with low heritability estimates by taking advantage of heterosis (hybrid vigour) while individual selection will be effective for the improvement of body weight at 12-week for this rabbit population. Strong genetic correlations between LWW and LBW in this rabbit population showed that, selection for increased LBW will lead to a correlated increase in LWW.

**Keywords:** Heterogeneous rabbit population, Heritability and Genetic correlation.**INTRODUCTION**

Heterogeneous rabbit populations are products of many decades of planned and indiscriminate crossbreeding among different exotic domestic rabbit breeds (*Oryctolagus cuniculus* L.) at government research stations and backyard farms in Nigeria. Present day rabbit breeds evolved from the European wild rabbit and Archaeological records indicate that this species of rabbit may have originated in the Mediterranean region (Lukefahr and Cheeke, 1991). The domestication is believed to have taken place in European monasteries probably during the sixteenth century before their movement to other parts of the world including sub-Saharan African countries. These occurred during the pre-colonial era by sailors and by the activities and movements of the colonial masters and Christian missionaries. This trend continued till the post-independence period (1960 to 1980s) when further importations were made by United States Agency for

International Development (USAID) and other Non-Governmental Organisations (NGOs) such as Heifer Project International formerly (HPI now HI), World Neighbours and Winrock International (Price and Regier, 1982; Lukefahr and Cheeke, 1991). Among the pre-requisites for genetic improvement is the knowledge of reproductive performance and genetic parameters such as heritability and genetic correlations of important economic traits. Unfortunately, information on these parameters is scanty in available literature for rabbits raised in the tropics (Akanno and Ibe, 2005). Although there had been previous efforts in genetic improvement programmes in Nigeria, these have been largely unsustainable because these were based on specific crosses (two or three-way crosses) among the most common commercial meat rabbit breeds which include New Zealand White, California, Chinchilla and Flemish Giant under on-station

conditions (Somade and Adesina, 1990; Odubote *et al.*, 1995).

The stocks of rabbits used in many developing countries are heterogeneous or composite populations derived either from crosses between local breeds and exotic rabbits or from crosses among exotic rabbit breeds (Lukefahr and Cheeke, 1990; Lukefahr, 2000). At the moment, pure breeds are scarce and can only be available on research farms and few commercial rabbit farms in Nigeria. Therefore, the objective of this study was to estimate heritability and genetic correlations of some litter traits at birth, weaning and at 12-weeks of age with the view of providing information for the genetic improvement of this rabbit population which is the most prevalent in South-west Nigeria. Such information would assist rabbit breeders to decide genetic improvement methods that will be appropriate for the genetic improvement of the heterogeneous rabbit populations.

## MATERIALS AND METHODS

### Location

The study was conducted at the Rabbit Unit of Obafemi Awolowo University Teaching and Research Farm, Ile-Ife, Nigeria, at an altitude of 240 m above sea level, located at latitude 7° 28' N and longitude 4° 34' E (Wikipedia.org.). Ile-Ife ecologically typifies the hot humid tropical rain forest zone.

### Experimental animals

Rabbits used for this study were obtained from heterogeneous populations reared in Ibadan, Osogbo and Ile-Ife in South-west Nigeria. Heterogeneous rabbit stocks are products of non-specific crosses of New Zealand White, California, Chinchilla and Flemish Giant breeds.

### Animal management and housing

Before the commencement of the experiment all the animals were injected with ivomec® to treat both internal and external parasites at a recommended dosage of 0.2 ml per animal. Pen and hutches were thoroughly cleaned and disinfected with izar® and used engine oil was applied periodically around the pen to keep away Soldier Ants which constitute a perennial problem around the experimental site. Animals were housed in hutches made of wood and wire mesh with each cell measuring 76 × 62 × 42 cm and raised with wooden stands 90 cm high from concrete floor. The pen house was covered with wire mesh at three of the sides and planks at one end, and roofed with asbestos roofing sheets. Two clay pots for feed and water were placed in

each hutch. Other feeding details are as stated by Oseni and Ajayi (2010). Animals were identified by ear tattoo on their left ears using a tattooing set and by means of cage labels on every hutch for primary records.

### Reproductive management

Forty-nine does were randomly allocated to sire families with the use of Table of Random Numbers using a balanced design (Falconer and Mackay, 1996). The statistical design was sire component of variance design in which each of the seven bucks was mated to seven does and each mating resulted in a number of kits. The death of two does from two families changed the design to unbalanced design. Matings were routinely done in the morning before the weather gets hot usually between (8.00 - 9.00 A.M.). Females were usually taken to the males for mating in the bucks' cages. Gravidity test was carried out on each doe at 12<sup>th</sup> to 14<sup>th</sup> day after mating by abdominal palpation. Does that were not gravid were re-mated immediately. For all gravid does, kindling boxes were placed in their cages on day 25 of their gestation period and daily checking of nest boxes were done to ascertain the date of kindling. Weaning was done 42 days post-partum.

### Data collection and preparation

Data were collected from all kits arising from the matings forming a population of half-sibs and full-sibs. Records of 682 progeny from across three parities were used in this study. Litter sizes at birth, weaning and 12-week were done through counting of kits from the same doe. While litter weight at birth and at weaning and body weight at birth, weaning and 12-week of age were taken with the aid of top loading weighing scale graduated in 25 grammes. Data were recorded within sire families to generate performance record for families as well as for dams within families. The data was edited using PROC SORT and PROC FREQ of SAS (2004). Outliers were not included in the data for heritability estimate in order to eliminate biases. Animals with records that were not up to week 12 were not included in the estimation of variances and covariances, thus, there was a considerable reduction in the number of observations from birth through to 12<sup>th</sup> week.

### Statistical model:

Model used for heritability was

$$Y_{ij} = \mu + B_i + e_{ij} \dots \dots \dots (1)$$

i = 1, 2, \dots \dots \dots 7<sup>th</sup> sire

$Y_{ij}$  = the observed trait of individual animal

$\mu$  = the overall mean;

$B_i$  = random effect of the  $i^{\text{th}}$  buck;

$e_{ij}$  = uncontrolled environmental and genetic deviations attributable to individuals within sire groups. All effects were random, normal and independent with expectations equal to zero (Becker, 1984).

$$h_s^2 = \frac{4\sigma_s^2}{\sigma_s^2 + \sigma_w^2} \dots\dots\dots (2)$$

Where  $h_s^2$  = heritability estimate from sire component  
 $\sigma_s^2$  = Sire component of variance

$\sigma_w^2$  = within progeny component of variance (for heritability estimates)

Se ( $h_s^2$ ) = standard error of heritability estimates.

Standard errors of heritability estimate (Se $h_s^2$ ) was approximated according to the formula of Becker (1984).

$$r_G(x_1x_2) = \frac{Cov_s(x_1x_2)}{\sqrt{\sigma_s^2x_1 \times \sigma_s^2x_2}} \dots\dots\dots (3)$$

Where

$Cov_s(x_1x_2)$  = sire component of covariance of the 1st trait and the 2nd trait,

$\sigma_s^2(x_1)$  = sire component of variance of trait  $x_1$  ;

$\sigma_s^2(x_2)$  = Sire component of variance of trait  $x_2$  and

$r_g$  = Genetic correlations

**Data analysis**

Data were analysed using the General Linear Mixed Model procedure (PROC MIXED) of SAS (2004) following the Restricted Maximum Likelihood (REML) method. The Sire component of variance with unequal numbers of offspring per sire family was used to estimate heritability estimates ( $h^2$ ) following the procedure of Becker (1984).

**RESULTS AND DISCUSSION**

Table 1 showed that heritability estimates were low to moderately high for the traits under study. Estimate of  $h^2$  for Individual body weight at weaning and at 12 weeks were within the range  $0.03 \pm 0.22$  -  $0.74 \pm 0.45$  reported by Akanno and Ibe (2005). Birth weight (BWT), litter birth weight (LBW), litter size at birth (LSB), weaning weight (WWT), litter weaning weight (LWW) and litter size at weaning (LSW) were  $0.02 \pm 0.23$ ,  $0.19 \pm 0.15$ ,  $0.20 \pm 0.01$ ,  $0.02 \pm 0.05$ ,  $0.09 \pm 0.12$ , and  $0.23 \pm 0.23$ , respectively. Others were  $0.46 \pm 0.26$  for individual weight and  $0.06 \pm 0.38$  for litter size at 12

weeks (LS<sub>12</sub>). Lukefahr *et al.* (1992) reported paternal half sib estimates of heritability (pooled estimate) of 0.42 for body weight at 90 days in Ghana. It is also, in agreement with the estimate for individual body weight at 12 weeks (0.46) obtained in this study. This suggests that this trait is controlled by genes and additive gene effects and thus, individual selection will be effective in the improvement of individual 12-week body weight through crossbreeding. Lukefahr and Cheeke (1991) suggested that selection emphasis should be applied to traits of moderate to high heritability. The heritability estimate of individual body weight at six weeks age (0.02) is close to the report of Ferraz and Eler (1994) that reported an estimate of 0.03 at the same age but a lower estimate of 0.26 for body weight at 12 weeks of age. All the estimates for individual body weight at birth, weaning and 12<sup>th</sup> week showed that the estimate at birth and weaning were low and close to zero when compared with that of 12<sup>th</sup> week body weight, indicating that individual selection method at birth and at weaning will not be effective for this rabbit population. However, baseline culling levels (independent culling technique) for low to average productivity should be established as suggested by Lukefahr and Cheeke (1991) for traits with low heritability estimates. For litter size at birth, the estimate of 0.19 from this study was higher than 0.09 reported by Krogmeier *et al.* (1994) for litter size at birth but lower than the range of 0.32 to 0.53 in three different breeds (Chinchilla, New Zealand White and California White) in Northern Guinea Savana zone of Nigeria reported by kabir *et al.* (2012). This indicates 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.

Table 1: Heritability estimates ( $h_s^2$ ) based on sire component of variance for litter size and body weight at birth, weaning and 12<sup>th</sup> week

Traits	$h_s^2$	SE
Birth weight	0.02	0.23
Litter birth weight	0.19	0.15
Litter size at birth	0.20	0.01
Weaning weight	0.02	0.05
Litter weaning weight	0.09	0.12
Litter size at weaning	0.23	0.23
Weight at 12 wks	0.46	0.26
Litter size at 12 wks	0.06	0.38

SE – Standard error of  $h_s^2$ s, Wks-weeks

The estimate for litter size at weaning (0.23) compared favourably with 0.25 reported by Krogmeier (1994). Odubote and Somade (1992) reported estimates of  $0.33 \pm 0.08$ ,  $0.38 \pm 0.02$ ,  $0.03 \pm 0.02$  and  $0.16 \pm 0.05$  for

Table 2: Genetic correlations of body weight from birth to twelve weeks of age for a composite rabbit population

	BWT	WK												
		1	2	3	4	5	6	7	8	9	10	11	12	
BWT	1.00													
WK 1	0.73	1.00												
WK 2	0.68	0.78	1.00											
WK 3	0.65	0.78	0.99	1.00										
WK 4	0.61	0.72	0.97	0.98	1.00									
WK 5	0.58	0.72	0.86	0.87	0.97	1.00								
WK 6	0.48	0.82	0.77	0.84	0.91	0.97	1.00							
WK 7	0.39	0.72	0.75	0.82	0.90	0.91	0.97	1.00						
WK 8	0.30	0.65	0.67	0.76	0.88	0.86	0.93	0.99	1.00					
WK 9	0.21	0.58	0.61	0.71	0.85	0.84	0.90	0.96	0.99	1.00				
WK 10	0.17	0.54	0.56	0.67	0.83	0.83	0.86	0.93	0.97	0.99	1.00			
WK 11	0.11	0.46	0.48	0.60	0.78	0.80	0.81	0.88	0.94	0.97	0.99	1.00		
WK 12	0.09	0.41	0.43	0.48	0.73	0.78	0.79	0.84	0.90	0.95	0.97	0.99	1.00	

BWT – Birth weight, WK – Week

litter birth weight, litter size at birth, litter size at weaning and litter weaning weight respectively, when compared with the corresponding values of  $0.19\pm 0.15$ ,  $0.19\pm 0.01$ ,  $0.23\pm 0.23$  and  $0.09\pm 0.12$  from this study. The variations from other reports might have resulted from differences in genotypes, location, environmental factors and different sample sizes. Heritability estimate for litter size at birth ( $0.19\pm 0.01$ ) is higher and more reliable than the estimates for litter size at weaning and at 12-week which are  $0.23\pm 0.23$  and  $0.06\pm 0.38$  respectively, on account of the higher standard errors associated with the latter which might be as a result of high variability of the population in this study.

The pattern in Table 2 showed that genetic correlation coefficients decreased as the age of the rabbit increased. This indicates that selecting for individual body weight at early ages i.e. at birth or during the pre-weaning period will lead to correlated responses in weight gain in the immediate age brackets. Individual birth weight has a strong genetic correlation coefficient of 0.73 with bodyweight at one week and genetic correlation between subsequent weeks till weaning were strong and positive but a low genetic correlation with weekly bodyweight at 10, 11 and 12<sup>th</sup> week which are 0.17, 0.11 and 0.09 respectively. This might be as a result of the effect of non-genetic factors such as nutrition and housing on body weight after weaning than pre-weaning period. This observation is in agreement with the conclusion of Khalil *et al.* (1986) who reported that selection for heavy weight of litters at birth has usually been associated with genetic improvement in the corresponding trait at subsequent ages. Genetic correlations among litter traits in this study (Table 3) showed that litter birth weight was highly and positively

correlated with litter weaning weight with an estimate of 0.87 indicating that selection for either of the traits will lead to a correlated response. Litter birth weight was moderately correlated with litter size at weaning with a value of 0.57 and litter size at weaning had a high and positive correlation coefficient (0.86) with litter weaning weight which is expected since the higher the number weaned per litter, the higher the overall weight will be. Positive genetic correlations indicate the effect of same gene or pair of genes controlling both correlated traits. The zero coefficients for litter size at birth and litter birth weight, litter weaning weight and litter size at birth, and litter size at birth and litter size at weaning, in Table 3 showed that the genetic correlation coefficients cannot be calculated for this trait in this study. Genetic correlations were generally positive for weekly body weight from birth to week 12 ranged from low (0.09) to very high (1.00) The results also indicate that various outbreeding mating systems will be effective in the improvement of these traits with low heritability estimates by taking advantage of heterosis (hybrid vigor) based on the premise that the lower the heritability of a trait, the greater the heterotic response.

## CONCLUSION AND RECOMMENDATIONS

Heritability estimates were low for individual birth weight, individual weaning weight, litter weaning weight and litter size at 12<sup>th</sup> week. This indicates a low genetic influence but a high environmental influence for reproductive traits and suggests that non-genetic factors (environmental factors) affect the expression of these traits. Thus, various outbreeding mating systems and family selection will be appropriate for the genetic improvement of these litter traits. Traits with moderate heritability estimates (LBW, LSAB, LSAW and

Individual weight at 12 weeks) would be improved upon by combination of family and individual selection

Table 3: Genetic correlations among litter traits in heterogeneous rabbit population at birth and at weaning

	LBWT	LSAB	LWW	LSAW
LBWT	1.00			
LSAB	0.00	1.00		
LWW	0.87	0.00	1.00	
LSAW	0.57	0.00	0.86	1.00

Litter birth weight (LBWT), Litter size at birth (LSAB), Litter weaning weight (LWW) and Litter size at weaning (LSAW).

to achieve genetic improvement in these traits. Extra efforts should be put into selection of individual body weight at 12 weeks. Genetic correlations decreased as the age of the rabbit increased. Furthermore, the strong genetic correlation between Litter weaning weight (LWW) and Litter birth weight (LBW) in this rabbit population showed that, selection for increased LBW will lead to a correlated increase in LWW.

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