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## Estimates of genetic parameters of litter size traits at birth and weaning in domestic rabbits (*Oryctolagus cuniculus*) raised in Anwai community, South Nigeria

<sup>1</sup>G. U. Sorhue, <sup>2</sup>P. O. Akporhwarho, <sup>2</sup>I. Udeh, <sup>2</sup>F. U. C. Mmereole

<sup>1</sup> Department of Agricultural Education, College of Physical Education, Mosogar, Delta State, Nigeria; <sup>2</sup> Department of Animal Science, Delta State University, Asaba, Delta State, Nigeria. Corresponding author: G. U. Sorhue, gtsorhue@yahoo.com

**Abstract.** Data on litter size traits of 224 bunnies obtained from a mating involving five sires and fifteen dams at three dams/sire were collected and analyzed to estimate genetic parameters in commercial domestic rabbits raised in Anwai, Delta State, Nigeria. Traits studied were: total litter size born (TB), number born Alive (BA), number born dead or still born (BD), and number weaned (NW). The analysis of variance was done in a nested or hierarchical design with equal number of sub-class. Heritability and correlations were calculated using standard expressions. Heritability estimates from sire component for TB, BA, BD and NW were 0.08, 0.02, 0.007 and 0.94 and 0.89, 0.55, 0.76 and 0.97 respectively using dam component of variance. Genetic correlations were generally positive and highly significant ( $P < 0.01$ ) for TB X NW. Environmental correlations ranged from negative to positive values and were highly significant ( $P < 0.01$ ) for TB X BD and BA X NW from dam component while estimates of phenotypic correlation were generally positive but mostly low. In conclusion heritability of litter size traits were mostly low from sire component and high from dam component while genetic and phenotypic correlations among the traits were generally positive. The low heritability for litter size (TB, BA and BD) suggest possible improvement of these traits by progeny selection or sib-testing while the trait with high heritability can be improved by record based on own performance while the positive correlations indicates that genes responsible for those traits are related.

**Key Words:** Correlation, dam component, heritability, hierarchical, sire component.

**Introduction.** The domestic rabbit (*Oryctolagus cuniculus*) presents favorable biological characteristics as most avian species because the rabbit is characterized by a short generation interval and a high fecundity and prolificacy (Beaumont et al 2003). One of the pre-requisite for genetic improvement is knowledge of genetic parameter for important economic trait (Akanno & Ibe 2005). Santacreu et al (2005) reported that litter size is easy and not expensive to measure. Some of the criteria used for selection of domestic rabbits are number of kits born alive or number of kits at weaning. Litter size has a low heritability, but is highly variable, significant genetic variation also exists between breeds and populations (Blasco et al 1993). The estimation of variance components and genetic parameters of litter size traits is very important to establish their breeding program, to predict how much we can improve these traits and for monitoring the process of selection along the time. Ibrahim et al (2007) reported that the effects of genotype, season, parity, gender and year interactions were not significant in estimating genetic parameters. The major objective of this study is to estimate the genetic parameters of litter size traits in domestic rabbits at birth and weaning.

### Material and Method

**Experimental Site.** The study was conducted at the rabbitry unit of the Department of Animal Science, Delta State University, Asaba Campus. Asaba campus is located at latitude  $06^{\circ}14'$  N and longitude  $06^{\circ}49'$  E. It lies in the tropical rainforest zone,

characterized by seven months of rainy season between April and October punctuated by a short break in August with annual rainfall of 1500 mm-1849 mm.

**Materials and stock used for the study.** Fifteen dams and five sires were sourced from J. J. Scot farms Sapele in Sapele Local Government area of Delta State and a commercial rabbit breeder from Agbor in Ika south Local Government Area of Delta State, Nigeria were used for the study. Sires and dams that died before the commencement of the breeding exercise were replaced. The experimental stocks were non-descript breeds of domestic rabbits (commercial rabbit). The parental stock produced 224 bunnies which were used for the study.

**Pen design and replication.** There were five pens of 90 x 80 x 65 cm for the five sires, fifteen pens of 100 x 80 x 65 cm for the fifteen dams and litters after kindling. The design was a balanced design with equal numbers of sub-class. It was a three way nested classification, dams were nested between sires and litters were weaned at 6 weeks (42 days).

Table 1  
Experimental layout and design

<i>Sires</i>	<i>Dams</i>	<i>Progenies</i>		
Sire <sub>A</sub>	Dam <sub>1</sub>	Progeny1	Progeny2	Progeny3
	Dam <sub>2</sub>	Progeny1	Progeny2	Progeny3
	Dam <sub>3</sub>	Progeny1	Progeny2	Progeny3
Sire <sub>B</sub>	Dam <sub>1</sub>	Progeny1	Progeny2	Progeny3
	Dam <sub>2</sub>	Progeny1	Progeny2	Progeny3
	Dam <sub>3</sub>	Progeny1	Progeny2	Progeny3
Sire <sub>C</sub>	Dam <sub>1</sub>	Progeny1	Progeny2	Progeny3
	Dam <sub>2</sub>	Progeny1	Progeny2	Progeny3
	Dam <sub>3</sub>	Progeny1	Progeny2	Progeny3
Sire <sub>D</sub>	Dam <sub>1</sub>	Progeny1	Progeny2	Progeny3
	Dam <sub>2</sub>	Progeny1	Progeny2	Progeny3
	Dam <sub>3</sub>	Progeny1	Progeny2	Progeny3
Sire <sub>E</sub>	Dam <sub>1</sub>	Progeny1	Progeny2	Progeny3
	Dam <sub>2</sub>	Progeny1	Progeny2	Progeny3
	Dam <sub>3</sub>	Progeny1	Progeny2	Progeny3

Table 1 presents the experimental layout and design showing the numbers of sires, number of dams per sire and the number of progeny per dam. It was a hierarchical design having three dams per sire and three parities per dam (equal number of sub-class), it is a three way nested classification, and dams were nested between sires and progenies cross classified between dams.

**Management of the experimental rabbits.** Feed and water were provided *ad libitum* throughout the period of the experiment. The rabbits were raised in wooden cages with wire mesh. The feed used was commercial pellets with forages and grasses supplied to meet the nutrient required by the experimental animals.

**Data collection.** Litter size trait at birth and weaning were collected from progeny of a particular dam, mated to a particular sire separately. The kits of a certain litter from a certain dam mated to a certain sire were marked. The litter sizes were counted at birth and weaning at 42 days of age. There were three parities per dam. The collected data includes:

1. Total born litter size at birth (TB)
2. Born alive (BA)
3. Born dead (BD)
4. Litter size at weaning (NW)

**Data analysis.** All data collected were subjected to analysis of variance in a nested or hierarchical design using SAS (2001). Heritability and correlations were estimated using standard expressions given by Becker (1984).

**Statistical model.** The statistical model used for the analysis of variance was

$$Y_{ijk} = \mu + S_i + D_{ij} + e_{ijk}$$

Where:

$Y_{ijk}$  - record of the k-th progeny of the Jth dam mated to the I-th Sire;

$\mu$  - the overall population mean;

$S_i$  - the random effect of the i-th sire;

$D_{ij}$  - the random effect of the jth dam mated to the i-th sire;

$E_{ijk}$  - the error term.

**Heritability estimated from sire and dam components.**

$$h^2_s = 4\sigma^2_s / (\sigma^2_s + \sigma^2_d + \sigma^2_w)$$

$$h^2_d = 4\sigma^2_d / (\sigma^2_s + \sigma^2_d + \sigma^2_w)$$

Where:

$h^2_s$  - heritability from sire;

$h^2_d$  - heritability from dam;

$\sigma^2_s$  - sire variance component;

$\sigma^2_d$  - dam variance component;

$\sigma^2_w$  - within progeny variance component.

**Results and Discussion.** The genetic group means and standard errors of litter size TB, BA, BD and NW are presented in table 2.

Table 2  
Means and standard errors for litter size traits of domestic rabbits

Traits	No. of observations	Mean	SEM
TB	224	4.98	0.04
BA	195	4.33	0.02
BD	29	0.64	0.12
NW	174	3.87	0.02

TB - total born, BA - born alive, BD - born dead, NW - number weaned.

Means and standard errors for litter size traits are presented in table 2. The mean values ranged from  $0.64 \pm 0.12$  for total number born dead (BD) to  $4.98 \pm 0.04$  for total number born (TB). The mean values were lower than those reported by Mohammed & Baselga (2009) with values ranging from 7.79 for NW to 9.80 for TB but were comparable to reports from Ogah & Ehiobu (2004) with values of 2.86 to 5.44 for TB and NW. These discrepancies could be due to the fact that the animals were reared in different environment, breeds as well as the breeding season.

Table 3  
Variance components for litter size in domestic rabbit

Traits	$\sigma_s^2$	$\sigma_d^2$	$\sigma_e^2$	$\sigma^2_p$
TB	0.0086	0.0925	0.3111	0.4122
BA	0.0012	0.0407	0.2555	0.2974
BD	0.0002	0.0185	0.0778	0.0965
NW	0.1148	0.1185	0.2556	0.4889

$\sigma^2_s$  - sire component of variance,  $\sigma^2_d$  - dam component of variance,  $\sigma^2_e$  - variance error,  $\sigma^2_p$  - total phenotypic variance.

Table 3 shows the variance components of litter size traits. Sire component of variance was lower than the corresponding dam and progeny component of variance for all the traits studied.

Heritability estimates and standard errors for litter size traits

Table 4

<i>Traits</i>	$h^2_{\sigma s} + se$	$h^2_{\sigma d} + se$
TB	0.08 ± 0.60	0.8971 ± 0.15
BA	0.02 ± 0.59	0.5477 ± 0.54
BD	0.01 ± 0.58	0.7638 ± 0.22
NW	0.94 ± 0.10	0.9695 ± 0.05

$h^2_{\sigma s}$  – heritability from sire component of variance,  $h^2_{\sigma d}$  – heritability from dam component of variance.

Heritability estimates were presented in table 4. Heritability estimates from dam component were higher than the corresponding heritabilities from sire components for the traits studied. This was due to the lower variance component from sire since heritability depends on the variance in the population. Values ranging from 0.01 (0.55) to 0.94 (0.97) were obtained when heritabilities were estimated from sire (dam) component. Heritability estimates from sire component were low except for NW with values of 0.08, 0.02, 0.01, and 0.94 for TB, BA, BD and NW. Heritability from dam component were generally high with values of 0.89, 0.55, 0.76 and 0.97 for TB, BA, BD and NW. The low heritability estimates obtained for litter size (TB) 0.08 in the present study is lower than estimates reported by Lukefahr & Hamilton (1997), Mohammed & Baselga (2009) and Piles et al (2006), with values of 0.24, 0.14 and 0.13 respectively. However similar values of 0.09, 0.09 and 0.07 have also been reported by Lukefahr & Hamilton (1997), Rastogi et al (2000) and Abou Khadiga et al (2008).

The values of 0.08 obtained in this study is higher than values reported by Iraqi (2008) 0.04 and Baselga et al (1992) 0.03 using different kinds of animal models. The estimated values of heritability 0.02 for number of kits born alive (BA) in this study is lower than heritability values reported from literatures, with values of 0.08, 0.13, 0.12, 0.07, and 0.09, as reported by Cifre et al (1998), Rastogi et al (2000), Garcia & Baselga (2002), Abou Khadiga et al (2008) and Mohammed & Baselga (2009) respectively. While heritability for number of kits born dead (BD) in this study showed the lowest estimate of heritability of 0.01 which is lower than estimates of 0.070 reported by Baselga et al (2003) for still born using a repeatability animal model. The very low heritability estimates from sire component of variance shows that sire contribution to heritability of these traits is very minimal and suggest improvement of these traits by progeny testing or sib-analysis. Estimated values of heritability from dam component were high with values of 0.89, 0.55, 0.76 and 0.97 for TB, BA, BD and NW respectively. These values are higher than estimates reported in literatures with value of 0.16 and 0.14 as reported by Cifre et al (1998) and Piles et al (2006) for TB, BA and NW respectively. Discrepancies between the estimates in this study and those reported in literature is as expected since heritability values depends on the genetic make up of the stocks, management and climatic conditions and period of study as well as differences in data size and method of analysis (Khalil et al 1986). Moderate to high heritability values imply that selection would be efficient to improve these traits and the characters are susceptible to genetic influence and could be improved by simple selection methods such as one based on individual performance as reported by Khalil et al (1987). Moderate to high heritability indicate strong contribution of additive genes in the expression of these traits and suggest possible improvement of litter size trait in rabbits in Asaba Delta State Nigeria by use of either pedigree or individual selection method.

Table 5

## Covariance between litter size traits at birth and weaning

<i>Traits</i>	<i>TB</i>	<i>BA</i>	<i>BD</i>	<i>NW</i>
		0.0009	0.0001	0.0295
TB	-----	0.0245	0.0196	0.0524
		0.0926	0.0286	0.1240
			0.0003	0.0086
BA	-----	-----	0.0058	0.0537
			0.0002	0.0513
				0.0006
BD	-----	-----	-----	0.0043
				0.0097
NW				-----

First, second and third values are sire, dam and progeny covariance respectively.

Table 5 shows the estimates of covariance between litter size traits. The covariance values ranged from 0.0001 for TB X BD to 0.1240 for TB x NW, highest covariance from sire component was 0.0295 for TB X NW, while lowest covariance sire component was 0.0001 for TB X BD. Values of 0.0043 for BD X NW to 0.0537 for BA X NW was obtained for dam covariance.

Table 6

## Genetic correlations from sire and dam covariance between litter size traits

<i>Traits</i>	<i>TB</i>	<i>BA</i>	<i>BD</i>	<i>NW</i>
TB	-----	0.2863	0.1031	0.9367**
		0.2992	0.0305	0.5006
BA	-----	-----	0.6693	0.7226*
			0.2120	0.0773
BD	-----	-----	-----	0.1402
				0.091
NW				-----

First value and second values for sire and dam components respectively, \* - significant ( $p < 0.05$ ), \*\* - significant ( $p < 0.01$ ).

Table 6 shows the estimate of genetic correlations between litter size and body weight traits. Estimates of genetic correlations were generally positive and mostly non-significant ( $p > 0.05$ ). Estimated values ranged from 0.03 for TB X BD to 0.94 for TB X NW. However highly significant genetic correlations ( $p < 0.01$ ) was obtained for TB X NW. Genetic correlations observed between TB (total born) and other litter size traits were positive and ranges from 0.03 for TB X BD to 0.94 for TB x NW which is in line with estimates of genetic correlations reported by Mohammed & Baselga (2009) with value of 0.80 for total born and other litter size traits using repeatability animal model. Genetic correlation estimates for number of kits born alive (BA) and other litter size traits were also positive ranging from 0.08 for BA X NW to 0.72 for BA X NW from sire and dam component which were lower than estimates from Mohammed & Baselga (2009) with estimates of 0.90 for BA and other litter size traits. Piles et al (2006) also reported positive genetic correlation ranging between 0.54 to 0.94 for TB and other litter size traits. The range of positive genetic correlation reported by Piles et al (2006) for these traits is higher than report in the present study of 0.03 to 0.94 while estimates of 0.09 for BD X NW to 0.72 for BA x NW were lower than values ranging from 0.011 - 0.91 obtained by Piles et al (2006) for the same traits. Genetic correlation is independent of heritability meaning traits with low heritability can have a high positive genetic correlation (Falconer 1989) as recorded for some of these traits. The implication of positive genetic correlation is that selection for one trait will lead to improvement of the other. This is a phenomenon of correlated response, Falconer (1989) ascribed genetic

correlations among traits to effect of linkage between genes and pleiotropy, linkage causes temporary genetic correlations while pleiotropy causes permanent genetic correlation. Falconer (1989) ascribed genetic correlation among traits to the effect of linkage between the genes controlling them (particularly in populations derived from crosses between divergent strains) and pleiotropy (a situation whereby a gene influences the expression of more than one trait).

Table 7

Environment correlations between litter size traits

<i>Traits</i>	<i>TB</i>	<i>BA</i>	<i>BD</i>	<i>NW</i>
TB	-----	0.33	0.38	0.74*
	-----	0.29	0.80**	0.40
BA	-----	-----	-0.003	0.42
	-----	-----	-0.14 <sup>n*</sup>	0.71**
BD	-----	-----	-----	0.03
	-----	-----	-----	0.04
NW	-----	-----	-----	-----

n\* (P>0.05), \* (P<0.05), \*\* (P<0.01), First value - sire component, Second value - dam component.

Table 7 shows the environmental correlations between litter size traits. Estimate of environmental correlations varied from negative to positive with values ranging from -0.003 for BA X BD to 0.74 for TB X NW when environmental correlations were estimated from sire covariance components. Environmental correlations were mostly non-significant (p>0.05) while highly significant environmental correlations (p<0.01) were obtained for TB X BD and BA X NW from dam covariance component. These positive environmental correlations ranged between 0.29 for TB x BA to 0.80 for TB x BD which is higher than the range of 0.083 to 0.563 reported by Piles et al (2006) for values of environmental correlations between TB and other litter size traits. Positive environmental correlations ranging from 0.29 to 0.71 obtained for TB x BA and BA x NW were lower than the range of 0.069 to 0.856 recorded by Piles et al (2006) for BA and other litter size traits.

Value ranging from 0.03 to 0.74 obtained for NW and other litter size traits in this study is similar to reports by Piles et al (2006) with values ranging from 0.025 to 0.856 for NW and other litter size traits using repeatability versus multi-trait animal models. The negative environmental correlations obtained for BA x BD means that the both traits are influenced by common environmental factors and is inline with the correlations obtained by Akanno & Ibe (2008) with value of -0.12 for IBW x HS. The negative environmental correlations ranging from -0.003 to -0.05 is inline with reports by Mohammed & Baselga (2009) for kindling interval and other litter size traits with values of -0.03 respectively.

Table 8

Phenotypic correlations between litter size traits in domestic rabbits

<i>Traits</i>	<i>TB</i>	<i>BA</i>	<i>BD</i>	<i>NW</i>
TB	-----	0.3265	0.3646	0.4460
	-----	0.3387	0.3912	0.4540
BA	-----	-----	0.0036	0.1943
	-----	-----	0.0357	0.1701
BD	-----	-----	-----	0.061
	-----	-----	-----	0.074
NW	-----	-----	-----	-----

(P>0.05) First value - sire component, Second value - dam component.

Table 8 shows the estimates of phenotypic correlation between litter size traits in domestic rabbits. Values ranging from 0.004 for BA X BD to 0.45 for TB X NW were recorded from both sire and dam components. The estimate of phenotypic correlation

were positive but generally non-significant ( $p > 0.05$ ) for all the traits studied from sire and dam component of covariance. The values of 0.06 and 0.07 for BD x NW is in line with values reported by Ibrahim et al (2007) for 21 day body weight x 42 day body weight using paternal half-sib and maternal half-sib methods with values of 0.08 and 0.09 respectively.

**Conclusions.** The implication of these findings is that traits having high heritability such as those from dam component can be improved by simple selection method such as one based on individual performance or pedigree records while the low heritability estimates from sire component can be improved by progeny records or sib testing. For traits with strong positive genetic correlation, selection for one trait will lead to improvement in the other. This is the phenomenon of correlated response, however the negative correlations observed in some cases indicate that selection for one of the traits could lead to the improvement in the other if a reduction of the second trait is desired. Genetic correlation coefficients are helpful as guides to selection. For example, selection for litter size at birth in the experimental population could be effective in a breeding program aimed at achieving increased litter size at weaning since traits were positively correlated. Secondly, the high positive environmental correlation observed indicates strong environmental influence on the traits.

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Authors:

G. U. Sorhue, Delta State University, College of Physical Education Mosogar, Department of Agricultural Education, Nigeria, Delta State, Sapele, Asaba, Asaba Campus, P. M. B. 4085, e-mail: gtsorhue@yahoo.com

P. O. Akporhwarho, Delta State University, College of Physical Education Mosogar, Department of Animal science, Nigeria, Delta State, Sapele, Asaba, Asaba Campus, P. M. B. 4085.

I. Udeh, Delta State University, College of Physical Education Mosogar, Department of Animal science, Nigeria, Delta State, Sapele, Asaba, Asaba Campus, P. M. B. 4085, e-mail: drudeh2005@yahoo.com

F. U. C. Mmereole, Delta State University, College of Physical Education Mosogar, Department of Animal science, Nigeria, Delta State, Sapele, Asaba, Asaba Campus, P. M. B. 4085.

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