

## HERITABILITY AND REPEATABILITY ESTIMATES OF DOE AND LITTER TRAITS IN NIGERIA; DOMESTIC RABBIT

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This study was conducted to estimate genetic parameter of Doe and litter traits in a sub-population of Nigeria domestic rabbit. A total number 30 (thirty) rabbit (24 Does and 6 Bucks) were selected from a population of rabbits maintained at the rabbitry unit of the Teaching and Research Farm, Kogi State University, Anyigba. All the rabbits were housed in cages separately and fed *ad libitum* with pelleted rations.

In the mating plan, four Does were selected at random and assigned to one Buck each; mating were mostly carried out in the morning and evening. The Doe to be mated were first weighed with a top loader weighing balance in order to know the initial weight of each doe before being carried for mating, the mating was observed and number of time mating took place. A total number of 75 kits were produced from the study. Data were taken on sire effects on litter size (LS), Number of Time Mated (NTM), Doe Weight (DW), Total mortality (TM) and Litter weight (1-4 weeks) and were statistically analyzed using Analysis of Variance (ANOVA) appropriate for Completely Randomize Design. LS, NTM, TM were significant ( $P < 0.05$ ). DW was not significant ( $P < 0.05$ ), in terms of litter weight, LW1, LW2, LW4 showed significant ( $P < 0.05$ ) but LW3 was not significant. Repeatability and Heritability were estimated from the variance components, the Heritability estimates ( $\pm$  SE) for LS, NTM, DW TW, LW1, LW2, LW3 and LW4 varied generally from medium to high (0.04 to 0.60) and the Repeatability estimates ( $\pm$ SE) ranged from low to high (0.3 to 0.90). Individual selection of sire may lead to fast genetic

progress in traits that shows high heritability and or repeatability such as litter weaning weight.

**Keywords:** Litter weight, heritability, repeatability, genetic progress.

For the past two decades, meat production in Nigeria has failed to meet up with the ever increasing demand of the rapidly growing population. The gap between food requirement and supply with particular reference to protein of animal origin is widening at an alarming rate (Njoku, 2009). Biobaku and Ekpenyong (2008) indicated that to meet the increasing future demand for animal protein, non-traditional meat sources suitable for small-scale farmer need to be introduced. The inadequate supply of animal protein in Nigeria has been attributed to inadequate production and high cost of conventional sources of animal proteins (poultry, goatmeat, mutton and pork). The cost of other animal products apart from meat, milk and egg has also gone out of the reach of common man due to their staggering and intimidating prices. These common Nigerians however form up to 70% of the entire population (Onyimonyi and Ene, 2003). Therefore, if the increasing demand for animal protein is to be met, emphases must shift from expanded production of other livestock such as poultry, sheep, goat and cattle to other less conventional livestock. One of the cheapest producers of meat that can easily fit into a wider segment of populace but which has been neglected in Nigeria is the Rabbit. The need to improve rabbit production in Nigeria to increase supplies of animal protein is clear, due to the high cost of chicken and

beef. Also, the animal protein shortage facing Nigeria cannot be solved by large animals with their slow production cycle (Okpanachiet *al.*, 2010). This is why there is a need to source for a smaller animal with desirable traits, high prolificacy, having a short gestation period which can be reared with a relatively low cost of production. Rabbit production is a veritable way of alleviating protein deficiencies in Nigeria. This is as a result of such attributes it possesses like good conversion of forage to meat, short gestation period, and high nutritional quality of rabbit meat with low cholesterol and low sodium (Field, 2000). However, there is a need to improve the production system of rabbit and management using the approach of genetic parameter (Heritability and Repeatability). The knowledge of genetic improvement will help to boost the population of rabbit of any farm at a very short period of time. Parameters such as heritability and repeatability are necessary for designing an appropriate breeding plan for genetic improvement and the litter traits in Rabbit. Heritability (h) 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 (Cambelet *al.*, 2003). With the knowledge of this parameter, animal geneticist can determine whether or not a particular trait can be improved by selection by improvement of management practices or both (Meyer, 1995). Repeatability (r) is the ratio variance in Real Producing Ability. It can be estimated by obtaining repeated performance records for individuals, either in time or space (Monardes *et al.*, 2005). This study is therefore designed to determine the heritability and repeatability estimates of doe and litter traits in Nigerian domestic rabbits.

## MATERIALS AND METHODS

The study was carried out at the Rabbitry unit of the Teaching and Research Farm, Kogi State University, Anyigba. which is located between Latitude 7°15' and 7°29' N of the equator and Longitude 7°11' and 7°32' East, with average altitude of 420 metres above sea level. The area falls within tropical wet and

dry regions and the Guinea savanna (Ifatimehin *et al.*, 2015). The study lasted for about 3 months

### Experimental Animals and management

Twenty four does coded; T1, T2, T3, T4.....T24 and six bucks coded; M1, M2, M3....M6 totalling thirty (30) rabbits were randomly sampled from a population of rabbits maintained at the Rabbitry unit. All the rabbits were housed in cages separately and fed *ad libitum* with pelleted rations. *Panicum maximum* and *Centrosema pubescens* legume were also fed as supplementary ration. Cages of all the rabbits were cleaned and disinfected regularly with dettol and izal. All animals were given appropriate and regular medication.

### Experimental Design

In the mating plan, four Does were selected at random and assigned to one Buck each; mating were mostly carried out in the morning and evening. The Doe to be mated were first weighed with a top loader weighing balance in order to know the initial weight of each Doe before being carried for mating, the Does were carried to the buck cage, the mating was observed and the number of time the mating took place. Sire daughter, full and half sib mating were avoided. Pregnancy test was carried out on mated Doe on the tenth-day post mating using abdominal palpation. Non-pregnant does were immediately returned to the Doeshutch. A total number of 75 kits were produced from the research.

### Data collection

Data were collected during mating and after kindling on Doe Body Weight (DBW), Doe Production Efficiency (DPE), as well as on litter traits such as litter size, litter size, litter alive and dead, weekly litter weight (1,2,3, and 4).

### Statistical Analysis

Data were analyzed using Analysis of Variance (ANOVA) appropriate for a completely Randomized Design and mean that were significantly different were separated using Least Significant Difference (LSD). The variance components were estimated from the analysis of variance using the following formular;

$$\delta^2 e = MSE$$

$$\delta^2 W = \frac{MSW - \delta^2 e}{K}$$

Where K is the number of sire group  
 Repeatability and Heritability were estimated from the variance components as follows;

$$\text{Repeatability} = \frac{\text{Genetic variance}}{\text{Phenotypic variance}} = \frac{\delta^2 W}{\delta^2 W + \delta^2 e}$$

$$R = \frac{\delta^2 W}{\delta^2 W + \delta^2 e}$$

Heritability using the following formulae;

$$h^2 b = \frac{4\delta^2 s}{\delta^2 s + \delta^2 e}$$

Where  $h^2 b$ ,  $\delta^2 s$ , and  $\delta^2 e$  were heritability due to sire effect, variance due to sire and variance due to kits' effect, respectively. The mathematics model for determining the effects of sire is as follows

$$y_{ij} = \mu + \delta_j + \ell_{ij}$$

Where

$Y_{ij}$  = the record of  $j$ th litter mated to  $i$  sire,

$\delta_j$  = fixed effect if the  $i^{\text{th}}$  sire

$\ell_{ij}$  = random error with expectation equals to zero

## RESULTS AND DISCUSSION

Based on the result from Table 1, the litter size (LS), Number of time mated (NTM) and Total mortality are significant ( $P < 0.05$ ), but Doe weight is not significant. The litter size was significantly higher in M3 than M1, M2, M4, M5 and M6 while M4 had the least

litter size. Number of successful mating per Doe varies significantly ( $P < 0.05$ ) among the sire (Table 1), M6 is significantly higher than ( $P < 0.05$ ) other sires (M1, M3, M4, M5 and M6) and M5 shows the least mean value and there is no significant difference ( $P < 0.05$ ) between M2 and M6, but they significantly differ ( $P < 0.05$ ) from M1 and M5, this table shows that there is effect in the number of successful mating per sire, this may be different in the genetic makeup of the sire and time to mate in rabbit. Total mortality (TM) is significant ( $P < 0.05$ ), M3 and M6, while M4 showed a good reproductive performance

According to Table 2, Sire effect was significant ( $P < 0.05$ ) For Litter weight 1 (LW1), Litter weight 2 (LW2) and Litter weight 4 (LW4). M1 is significantly higher ( $P < 0.05$ ) in LW1, LW2, LW3 and LW4, while M4 had the least mean value in LW1 and LW2 and M6 had the least mean value in LW3 and LW4, this implies that M1 gives the best quality in litter trait while M4 and M6 gives the worst litter traits, this result is in contrast with Khalil (1994) who observed heavierweight in all of sires.

Heritability estimates ( $\pm$ SE) for LS, NTW, DW, TW, LW1, LW2, LW3, and LW4 are presented in Table 3, heritability varies generally from medium to high (0.04 to 0.60) for all the traits measured. Similar results were reported for litter size, number born

Table 1: Sire effect on litter size, Number of time mated, Doe weight and Total Mortality

Parameters	M1	M2	M3	M4	M5	M6	LOS	SEMS
LW1	6.00 <sup>a</sup> ±2.71	5.30 <sup>ab</sup> ±1.71	6.50 <sup>a</sup> ±2.40	2.30 <sup>c</sup> ±0.96	4.50 <sup>ab</sup> ±1.30	5.30 <sup>ab</sup> ±2.22	*	0.45
NTM	1.25 <sup>c</sup> ±0.50	2.80 <sup>a</sup> ±0.50	2.00 <sup>ab</sup> ±0.82	2.00 <sup>ab</sup> ±0.82	1.00 <sup>c</sup> ±0.00	3.00 <sup>a</sup> ±1.41	*	0.20
DW	1.80±0.40	1.94±0.31	1.81±0.63	1.81±0.13	1.69±0.24	1.65±0.24	NS	0.06
TM	1.75 <sup>c</sup> ±1.50	1.50 <sup>ab</sup> ±1.30	3.50 <sup>a</sup> ±1.0	0.75 <sup>c</sup> ±0.96	1.25 <sup>ab</sup> ±0.96	3.50 <sup>a</sup> ±2.40	*	0.34

Footnotes: LS=litter size, NTM=Number of time mated, DW=Doe weight, TM=Total mortality, M1= sire 1, M2= sire 2, M3= sire 3, M4=sire 4, M5=sire 5, M6=sire 6. LOS= level of significant. Mean in the row having different superscript and significantly different ( $P < 0.05$ )

Table 2: Sire effects on weekly litter weights

Parameters	M1	M2	M3	M4	M5	M6	LOS	SEM
LW1	428.75±99.86	422.50±149.14	218.75±80.03	195.00±82.76	338.75±130.41	232.25±157.67	*	29.56
LW2	601.25±156.92	516.50±109.43	331.25±92.14	268.00±59.07	435.00±140.77	327.50±226.00	*	35.25
LW3	681.25±106.80	636.25±142.91	561.25±224.18	373.75±71.92	575.00±238.92	368.75±330.92	NS	44.87
LW4	1006.25±171.24	743.75±168.79	681.75±224.18	406.25±71.92	565.50±238.92	391.25±330.92	*	77.78

Footnote:LW1:Litter weight week 1, LW2=Litter weight week 2, LW3= Litter weight week 3, LW4= litter weight week 4, LOS=Least of significant. Meaning the same row having different superscript and significantly different.

Table 3: Repeatability and heritability Estimate of LS, NTM, DW, LW1, LW2, LW3, LW4

Traits	R±SE	h <sup>2</sup> ± SE
LS	0.10±0.10	0.04±0.33
NTM	0.42±0.31	0.48±1.20
DW	0.14±0.15	0.56±0.01
LW1	0.03±0.00	0.35±0.00
LW2	0.31±0.00	0.45±0.00
LW3	0.19±0.00	0.56±0.00
LW4	0.21 ±0.04	0.60±0.05

Footnote: SE: R= Repeatability, h= Heritability, SE= Standard Error

alive and litter weight by Akano and Ibe (2005). This implies that these traits were under the strong influence of additive genes that individual selection would successfully improve them. However, the present result is in contrast with the submission of Ferraz and Eler (1996) who reported low heritability in LS, TM and LW. The differences in the two studies may be due to variation in reproductive performance of Sire used for the research.

The repeatability estimates of the traits studied as presented in Table 3, the repeatability of estimates ranges from low to high value (0.03 to 0.09), this is in agreement with Iraqi (2006) who reported low to high (0.15 to 0.80) repeatability estimates for LW, LS, TM, and GL in rabbits. As repeatability sets the upper limit of heritability, it is likely that these traits are lowly heritable. Because of low repeatability for most traits, it is very advantageous to consider more litters and parities before selecting a Doe for these traits.

## CONCLUSION

It can be concluded that the heritability and repeatability for reproductive traits ranged from low to high. The individual selection of sire may lead to fast genetic progress in traits that shows high heritability and or repeatability such as litter weaning weight. From this research, it is recommended that only proven bucks should be used for breeding. Furthermore, heritability and repeatability estimates for reproductive traits using higher number of animals is suggested as estimates of these genetic parameters rest heavily on the sample size used for the estimation.

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