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Application of Best Linear Unbiased Predictor (BLUP) in Estimating Breeding Value for Rabbit Bucks Raised in Humid Tropics

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Target Audience: *Animal Geneticists, Rabbit breeders, Researchers*

Abstract

Best Linear Unbiased Predictor (BLUP) procedures to estimate the breeding value of bucks among three rabbit breeds namely; Chinchilla (CHI), Dutch (DUT) and New Zealand White (NZW) were systematic followed for the selection of sire breed. Records of 604 kits produced through nested (hierarchical) design of 9 sires mated to 27 dams over a period of three parities were used in the estimation of heritability for kits weight at weaning (KWW) and computation of Least Squares Equation (LSE) and Mixed Model Methodologies (MMM). CHI had significantly ($P<0.05$) highest kit weight at weaning (KWW) when compared to the other two breeds, DUT and NZW. Coefficient of variation for KWW was generally low (4.00% to 19.73%). Heritability from sire components (h^2_s) for pre-weaning body weights were moderate to high. As economic trait (Yi), heritability value (0.64±0.26) for KWW were used to compute LSE and MMM accordingly. The predicted breeding values/ranking of individual sire ($\hat{S}$), using LSE and MMM showed $\hat{S}_3 > \hat{S}_4 > \hat{S}_2 > \hat{S}_5 > \hat{S}_6 > \hat{S}_1$ and $\hat{S}_3 > \hat{S}_4 > \hat{S}_6 > \hat{S}_5 > \hat{S}_2 > \hat{S}_1$ respectively. This study therefore presents the theory of BLUP and its practical applications in sire evaluation for rabbit bucks raised in humid tropics.

Keywords: *Rabbit, BLUP, Heritability, Mixed Model Methodology, Breeding Value*

Description of Problem

The goal of the animal breeder is to achieve rapid genetic improvement, for which accurate estimation of breeding value is crucial. Estimation of breeding value of sire for pre-weaning body weight and litter traits in rabbits will provide useful information to breeders in selecting good stocks and individuals for optimum production. Availability of such genetic information to the breeder will help to rank the bucks, cull those with poor performance indices while those with the best performance in ranking are selected as replacement. Best Linear unbiased prediction (BLUP) is a procedure which predicts breeding values (BV's) of animals and adjusts simultaneously for fixed effects of the model. Mixed Model Methodology (MMM) on the other hand is a useful tool for obtaining estimates of breeding values specific for populations and for ranking. Flint and Williams (1) reported that this statistical method uses matrix algebra to solve the large number of simultaneous equations generated for estimating BVs and for identifying environmental effects simultaneously. Implementation of BLUP required considerable computing power and skill to solve the matrices generated. In particular, the complexity of the genetic information used dictates the amount of computer space or time required.

Ferraz and Johnson (2) asserted that progress in animal selection could easily be achieved when breeding values are estimated with parameters specific for a particular population. By knowing BVs, changes can be made in traits without knowing what gene(s) are responsible, and this is what has been exploited throughout domestication- the heritability of traits and the similarity of relatives. The development of this process has produced the advanced methods available today, of which BLUP is the finest package for now.

BLUP is the current method of choice for evaluation of breeders in all farm animal stock and is widely implemented. This study therefore, was designed to revalidate the theory of BLUP and its applications in sire evaluation of rabbits and subsequently other larger animals (e. g. cattle) in the humid tropics.

Table 1: Descriptive Statistics for Economic Yield (*Y*i), KWW as influenced by breeds and Parity

Breed	Sire (Ŝ)	Parity (p̂)	Mean (KWW)	SD	Range		CV (%)
					Min.	Max.	
DUT	1	1	405.68	10.23	328.75	488.75	12.99
	2	2	441.44	9.94	381.67	476.25	9.85
CHI	3	1	561.59	9.57	407.50	660.00	12.67
	4	2	511.54	10.18	472.00	534.00	8.44
NZW	5	1	436.39	11.04	417.00	463.75	4.00
	6	3	426.42	10.59	402.50	445.00	3.44

DUT=Dutch, CHI= Chinchilla, NZW= New Zealand White
SD= Standard Deviation
CV= Coefficient of Variation

Table 2: Heritability estimates for pre-weaning growth traits of rabbit

Pre weaning body weight	h^2_s
KWB	0.59±0.24
KW2	0.55±0.24
KW4	0.93±0.31
KW6	0.28±0.17
KWW	0.64±0.26

h^2_s = heritability fromsire components of variance
KWB, KW2, KW4, KW6 and KWW = kit weight at birth, 2nd, 4th, 6th and 8th week (weaning) respectively

Materials and Methods

This study was conducted in the Rabbitry Unit of the Teaching and Research farm of the Ebonyi State University, Abakaliki. Animals used in this study consisted of three (3) rabbit breeds [Dutch (DUT), Chinchilla (CHI) and New Zealand White (NZW)]. Three bucks and nine does (between 8 – 10 weeks of age) of each breed were used in the experiment. These were obtained from random-bred selected population of male and female (parent stock) of each breed from Emmpina Livestock Farms and Goddy Veterinary Services, Uyo, Akwa-Ibom State. All animals were treated and given medication throughout the study period under the same managerial and climatic conditions.

The rabbits were housed in an open sided building, covered with chicken wire mesh. Breeding animals were kept individually in three – tier rectangular cages, measuring 60cm x 38cm x 48cm with aluminum feeders and drinkers attached to the cage with a hook in order to avoid toppling. Additional wooden cages were also provided for mating. The cages were partitioned into seven (7) individual pens, each measuring 62cm x 44cm x 48cm for easy individual mating activities. Cages and nest boxes were regularly cleaned and disinfected before kindling. Urine and faecal droppings beneath the cages were removed in the morning every day.

Rabbits of all ages were fed commercial pelletized growers diet obtained from Vital Feed Company. The chemical analysis of the diet as provided by the company was: crude protein (15% minimum); fat (7% maximum); crude fiber (10% maximum), calcium (1% minimum); phosphate (0.35% minimum) and metabolisable energy (2550kcal minimum). They were also provided with supplementary diet of grass/legume forage. Feed and clean drinking water were provided *ad-libitum.*

Table 3: Estimates of the fixed factors and sires breeding values for rabbit.

$$\begin{array}{ccccc} & & \text{LS} & & \text{MMM} \\ \begin{pmatrix} \hat{p}_1 \\ \hat{p}_2 \\ \hat{p}_3 \\ \hat{S}_1 \\ \hat{S}_2 \\ \hat{S}_3 \\ \hat{S}_4 \\ \hat{S}_5 \\ \hat{S}_6 \end{pmatrix} & = & \begin{pmatrix} 0 \\ 0 \\ 0 \\ 405.66 \\ 441.44 \\ 561.59 \\ 511.54 \\ 436.39 \\ 426.42 \end{pmatrix} & = & \begin{pmatrix} 467.91 \\ 476.49 \\ 426.42 \\ -10.04 \\ -5.61 \\ 14.99 \\ 5.61 \\ -5.04 \\ 0.00 \end{pmatrix} \end{array}$$

Data Collection and Analysis

The kits were weighed at birth (KWB); and at 2 weeks (K2W); 4 weeks (K4W); 6 weeks (K6W) and at weaning (KWW). These were measured using sensitive Mettler toled top pan weighing balance with 1000g capacity and 0.001g error. The measurements were taken while the animals were held in a standing position on top of the pan.

The following descriptive statistics: mean (x), standard deviation (s), standard error of the mean (SEM) and coefficient of variation (CV) were used to describe the data obtained for pre weaning body weights in each breed group. The x, s, SEM and CV were computed as $x = \sum Xi/n$; $s = \sqrt{\text{variance}}$; $SEM = s/\sqrt{n}$ and $CV = s/x$

* 100. For the purpose of this study, the results of economic trait (*Y*i) were extracted and presented in Table 1. In order to determine if differences exist among breeds, data were further subjected to Analysis of Variance (ANOVA) using General Linear Model (GLM) of (3) version 22.0. Significant mean differences observed among breeds were separated by (4).

By equating the mean square of each random effect to its expectation, variance component for sire (σ^2_s), dam (σ^2_d), and error (σ^2_e) were obtained. Similarly, by equating mean cross products for pairs of traits to their expectations, covariance components for sire (COV_s), dam (COV_d) and error (COV_e) were also obtained. These were used to estimate heritability for pre-weaning body weights, which is one of the parameters needed to compute BLUP

BLUP Procedures

Best linear unbiased prediction (BLUP) procedure was employed to predict breeding values of individual sires based on their breeds in reference to the three parities. The mixed effects linear model, in matrix notation is:

$$P = X\,\underline{b} + Z\,\underline{u} + e$$

where;

P= a vector of n observable random variables,
$\underline{b}$= fixed effects of parity (p= 3 levels)
$\underline{u}$= random effects of sire (s= 6 levels)
e = vector of residual error
X and Z = are design (known) matrices

Mathematically, BLUP was used to estimate $\underline{b}$ and $\underline{u}$ as solutions to the general MME:

$$\begin{pmatrix} X' R^{-1}X & X' R^{-1}Z \\ Z' R^{-1}X & Z'R^{-1}Z + G^{-1} \end{pmatrix} \begin{pmatrix} \underline{b} \\ \underline{u} \end{pmatrix} = \begin{pmatrix} X' R^{-1}X \\ Z' R^{-1}Y \end{pmatrix}$$

Henderson (5, 6) described the efficient computational procedures to solve the mixed model equations (MME) for simultaneous estimation of the fixed effects and prediction of breeding values. Therefore, in reference to equation above, mixed model methodology (MMM) permits the estimation of $\underline{b}$ by the generalized least squares procedure and the prediction of $\underline{u}$ by the BLUP procedure. Looking into large data set obtained in our experiment and in line with the procedures of (6), the least square equation (LSE) was thus derived as:

$$\left|\begin{array}{ccc|cccccc} 3 & 0 & 0 & 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 2 & 0 & 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 \\ \hline 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 \end{array}\right| \left|\begin{array}{c} P_1 \\ P_2 \\ P_3 \\ S_1 \\ S_2 \\ S_3 \\ S_4 \\ S_5 \\ S_6 \end{array}\right| == \left|\begin{array}{c} 1403.64 \\ 952.98 \\ 426.42 \\ 405.66 \\ 441.44 \\ 561.59 \\ 511.54 \\ 436.39 \\ 426.42 \end{array}\right|$$

We observed that the least squares coefficient matrix is singular, because row 1= row 4 + row 6 + row 8; row 2= row 5 + row 7, and row 3 = row 9. Therefore, to obtain a solution to the unknown parameter vector, three constraints was imposed. By imposing three constraints $P_1 = P_2 = P_3 = 0$ the solutions to the ranking of sires according to LSE was

$$\left|\begin{array}{c} P_1 \\ P_2 \\ P_3 \\ S_1 \\ S_2 \\ S_3 \\ S_4 \\ S_5 \\ S_6 \end{array}\right| == \left|\begin{array}{l} 0 \\ 0 \\ 0 \\ 405.66 \\ 441.44 \\ 561.59 \\ 511.54 \\ 436.39 \\ 426.42 \end{array}\right|$$

With LSE, the ranking of the sires is: $S_3 > S_4 > S_2 > S_5 > S_6 > S_1$
In order to calculate MME, we added k to the diagonal elements of the random portion of the LSE having assumed existence of zero covariance among the sires. Cameron (7) described a relation for k as $k = 4 - h^2/ h^2$ and from the heritability estimates for pre-weaning growth traits of rabbit in Table 2, $h^2_{(s)}$ for KWW = 0.64±0.26.
Then k = 4 – 0.64/0.64 = 5.25
Addition of 5.25 to the diagonal elements of the random portion of the LSE gives MME as follows:

$$\left|\begin{array}{ccc|cccccc} 3 & 0 & 0 & 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 2 & 0 & 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 \\ \hline 1 & 0 & 0 & 6.25 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 6.25 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 6.25 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 6.25 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 6.25 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 6.25 \end{array}\right| \left|\begin{array}{c} P_1 \\ P_2 \\ P_3 \\ S_1 \\ S_2 \\ S_3 \\ S_4 \\ S_5 \\ S_6 \end{array}\right| == \left|\begin{array}{l} 1403.64 \\ 952.98 \\ 426.42 \\ 405.66 \\ 441.44 \\ 561.59 \\ 511.54 \\ 436.39 \\ 426.42 \end{array}\right|$$

The modified coefficient matrix above will have the following generalized inverse:

$$Z := \begin{bmatrix} 3 & 0 & 0 & 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 2 & 0 & 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 6.25 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 6.25 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 6.25 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 6.25 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 6.25 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 6.25 \end{bmatrix}$$

$$Z^{-1} = \begin{bmatrix} 0.397 & 0 & 0 & -0.063 & 0 & -0.063 & 0 & -0.063 & 0 \\ 0 & 0.595 & 0 & 0 & -0.095 & 0 & -0.095 & 0 & 0 \\ 0 & 0 & 1.19 & 0 & 0 & 0 & 0 & 0 & -0.19 \\ -0.063 & 0 & 0 & 0.17 & 0 & 0.01 & 0 & 0.01 & 0 \\ 0 & -0.095 & 0 & 0 & 0.175 & 0 & 0.015 & 0 & 0 \\ -0.063 & 0 & 0 & 0.01 & 0 & 0.17 & 0 & 0.01 & 0 \\ 0 & -0.095 & 0 & 0 & 0.015 & 0 & 0.175 & 0 & 0 \\ -0.063 & 0 & 0 & 0.01 & 0 & 0.01 & 0 & 0.17 & 0 \\ 0 & 0 & -0.19 & 0 & 0 & 0 & 0 & 0 & 0.19 \end{bmatrix}$$

$$Y := \begin{bmatrix} 1403.64 \\ 952.98 \\ 426.42 \\ 405.16 \\ 441.44 \\ 561.59 \\ 511.54 \\ 436.39 \\ 426.42 \end{bmatrix}$$

and;

$$B := Z^{-1}\, Y$$

$$B = \begin{bmatrix} 467.912 \\ 476.49 \\ 426.42 \\ -10.04 \\ -5.608 \\ 14.989 \\ 5.608 \\ -5.043 \\ 0 \end{bmatrix}$$

The values of B = - 10.04, - 5.608, 14.989, 5.608, - 5.043 and 0 represent BLUP breeding values for sire 1, 2, 3, 4, 5 and 6 respectively.

Results and Discussion

The descriptive statistics of an economic yield (KWW) as influenced by breeds and parities is as shown in Table 1. Chinchilla (CHI) had significantly ($P<0.05$) highest kit weight at weaning (KWW) when compared to the other two breeds [Dutch (DUT) and New Zealand White (NZW)].

Generally, the superiority of CHI over NZW and DUT for KWW in the present study was consistent with the findings of (8). The variations obtained in the present study and other earlier investigations may be due to breed differences, age and size of parents stock, location and management system during rearing.

Heritability estimates for pre-weaning body weights from sire component (h^2_s) are presented in Table 2. Moderate to high heritability (0.28±0.17 to 0.93±0.31) obtained in the present study are consistent with those estimates obtained in some studies in Egypt (9, 10), Spain (11, 12), Brazil (13) and Nigeria (14, 15). Akanno and Ibe (16) studied body weight traits in NZW and DUT and reported moderate to high heritability estimates (0.43 and 0.36 for 6 and 12 week body weights respectively). The results obtained in the present study indicate the strong influence of additive genes in the expression of these traits and at the same time suggest possible improvement of the rabbit breeds through individual selection method.

In contrast, (17) and (18) studied pre-weaning growth traits in Gabali rabbits in North – western coast of Egypt and reported low heritability estimates of 0. 00, 0.05 and 0.07 for pre- weaning body weight at birth, 21 and 28 days using animal model and 0.11, 0.10 and 0.00 for body weight at 4, 8 and 12 weeks respectively. Nevertheless, the difference between heritability estimates in the present study and those reported in the literature could be attributed to the method of estimation/analysis, strain, environmental effects and sampling error due to a small data set or sample size.

The predicted breeding values of the sires, using Least Squares (LS) and Mixed Model Methodologies (MMM) are presented in Table 3 and this shows the respective ranking of sires with the two methods. The ranking based on LS is $S_3>S_4>S_2>S_5>S_6>S_1$ while that of MMM (Best Linear Unbiased Predictor) is $S_3> S_4> S_6> S_5> S_2 > S_1$.

Both the Least Squares and BLUP ranked sires 3 and 4 highest. Both are Chinchilla and they performed better than the other two breeds of sires. This confirms the earlier better performance of CHI rabbits in other parameters measured over DUT and NZW rabbits in the present study. There are scanty information on estimates of sire breeding values for rabbits in available literature. However, (19) as cited by (20), reported that BLUP estimated by mixed model methodology (MME) can be used to predict animal breeding values and adjust simultaneously for the fixed effect of the model. Ibe (21) stated that BLUP estimations are more reliable than LS estimations of breeding values.

Conclusion and Applications

The findings of this study revealed that:

1. Chinchilla bucks ranked highest in breeding value, indicating that they are the sire of choice in crossbreeding aimed at exploiting non-additive genetic variance for the improvement of growth and litter traits.
2. The present study also made an attempt to presents the theory of BLUP and its practical applications in sire evaluation of rabbit bucks raised in humid tropics and subsequent application in larger animals like-Nigerian Indigenous Cattle, Muturu.
3. Results from our investigation certainly warrant further research. Future studies should look into evaluation of different

rabbit breeds at DNA levels through molecular marker techniques.

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