ESTIMATES OF HERITABILITY AND REPEATABILITY FOR GROWTH TRAITS IN THREE BREEDS OF RABBIT

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ABSTRACT

Data on 169 progeny from 3 breeds {New Zealand white (NZW), Chinchilla (CHC) and Dutch (DUT)} of rabbits were used to estimate heritability and repeatability for growth traits. The growth traits considered were body weight (BW), ear length (EL), nose to shoulder (NTS), body length (BL), length of back leg (LBL), thigh length (THL), heart girth (HG) and thigh circumference (TC). The variance components used for estimation of heritability was obtained through VARCOMP procedure of SAS. Repeated records of dams were used to estimate repeatability. Estimates of heritability for growth traits were low - high for sire, dam and sire dam. The repeatability estimates for growth traits were from low to high. Low heritability traits can be improved upon by crossbreeding; moderately heritable traits however, can be improved by combining pedigree and individual selection. While individual selection can be adopted to improve highly heritable traits. The repetition of low repeatability trait in subsequent generation is no certainty; however, great reliability can be put upon selection of bucks and does with moderate to high repeatability traits.

Keyword: Heritability, Repeatability, Growth Traits, Breeds, Rabbit

INTRODUCTION

The domestic rabbit *(Oryctolagus cunniculus*) is a source of food in many countries. The potential benefit from rabbit production includes, boosting food security, raising farmer's income, creating employment opportunity and producing high quality meat (Mailafia *et al.*, 2010). Estimates of heritability for ear length at 6 week of age in the CHC (0.14), NZW (0.11) and CAW (0.22); while shoulder to tail , body length, length of front legs and length of back legs were moderate to high as reported by Kabir (2010). The traits with moderate to high repeatability imply that great reliability can be put on selection or culling of does and bucks for that trait, based on 1 or 2 record (Kabir, 2010).

MATERIALS AND METHODS

Study location

The research was conducted at the Rabbit Unit of the Department of Animal Science Research and Teaching Farm, Faculty of Agriculture, Ahmadu Bello University Zaria. The area is located in the Northern Guinea Savanna of Nigeria at latitude 11º 09' 06" and longitude 7º 38' 35" (Ovimaps, 2012).

Experimental animals and management

The stock comprised of {New Zealand white (NZW), Chinchilla (CHC) and Dutch (DUC)} purchased from Zaria environs, Kaduna State. Rabbits were kept in well ventilated pens with each individual ear-tagged in a separate hutch; each hutch was equipped with plastic rubber drinker and round bottom earthen pot feeder. Feed and water were provided *ad libitum*. They were fed twice daily and green forage *Tridax procumbens* was supplied to enhance digestion. The animals were raise to sexual maturity and mated (1:3 ratio) and weaning was done at 35 days of age.

Data collection and statistical analysis

Data collected on 169 progeny from New Zealand white (NZW) 58, Chinchilla (CHC) 58 and Dutch (DUT) 53 of 12 sire and 36 dam were used. Growth traits considered include the followings: Body weight (BW) measured in (kg) and *Ear length* (EL), *Body length* (BL), *Length of back leg* (LBL), *Thigh length* (THL), *Nose to shoulder* (NTS) and *Heart girth* (HG) all were measured in centimeters (cm). Data generated were subjected to analysis of variance (ANOVA) using General Linear Model (GLM) procedure of SAS (2002). The design of the experimental was nested type, in which a sire was mated to several dams with each mating producing several offspring. The significantly different means were separated using Duncan Multiple Range Test (DMRT) of SAS (Duncan, 1955).

The model equation for the study

$Y_{ijklm} = \mu + P_i + K_j + S_k + D_{kl} + \mathcal{E}_{ijklm}$

Where; Y_{ijklmn} = Observation on the mth progeny of the lth doe mated to the kth sire belonging to the jth sex and ith parity; μ = overall population mean; P_i = ith effect of the parity; K_j = jth effect of the sex; S_k= kth effect of the sire; D_{kl}= Random effect of dam within sire; and $\mathcal{E}_{ijklm}$ = Random error.

Heritability estimates

Heritability for growth traits due to sire model was then obtained using the standard expression given by Becker (1992) as follows: $h_s^2 = \frac{4\sigma_S^2}{\sigma_T^2}$ $h_D^2 = \frac{4\sigma_D^2}{\sigma_T^2}$

Where: h_s^2 = heritability based on sire variance component; h_D^2= heritability based on dam variance component; σ_w^2= the variance within offspring.

Repeatability estimates

Repeatability estimates were obtained using the following formula:

$R = \frac{\sigma_I^2}{\sigma_I^2 + \sigma_e^2}$ Where: σ_I^2= fixed effect of each animal and σ_e^2 = within individual records variance

RESULTS AND DISCUSSION

Heritability estimates for growth traits

The heritability estimates for NZW from sire and dam variance component for growth traits presented in Table 1. The estimate values from sire and dam variance component ranged from (0.01 to 0.84) and (0.02 to 0.91). The low h^2 for BW at 6 week of age (0.05±0.04) disagreed with the findings of Nwagu (2004) who reported high heritability from the sire component of variance for body weight. The dam estimates for BW 0.02±0.16 at 10 week of age were lower than 0.43, 0.11 and 0.36 reported by Akanno and Ibe (2005) at 6, 9 and 12 weeks of age.

CONCLUSION

The heritability and repeatability values for growth traits in three breeds were low to high. Low heritability traits can be improved upon by crossbreeding; moderate heritability traits however, can be improved by combining pedigree and individual selection. While individual selection can be adopted to improve highly heritable traits. The repetition of low repeatability trait in subsequent generation is no certainty; however, great reliability can be put upon selection of bucks and does with moderate to high repeatability traits.

Table 1: Heritability estimate for sire (h^2_S±SE) and for dam (h^2_D±SE) variance component for growth traits in New Zealand White

	Sire (h^2_S±SE)			Dam (h^2_D±SE)		
	Age (weeks)			Age (weeks)		
Traits	6	10	20	6	10	20
BW	0.05±0.04	0.67±0.03	0.45±0.09	0.38±0.11	0.02±0.16	0.21±0.36
EL	0.10±0.07	0.04±0.12	0.40±0.08	0.03±0.02	0.86±0.06	0.45±0.08
NTS	0.13±0.15	0.34±0.06	0.84±0.13	0.80±0.18	0.61±0.23	0.70±0.37
LBL	0.31±0.19	0.22±0.07	0.60±0.24	0.91±0.12	0.61±0.27	0.89±0.29
HG	0.62±0.12	0.01±0.48	0.17±0.06	0.24±0.11	0.42±0.05	0.08±0.04
THL	0.79±0.01	0.14±0.25	0.11±0.25	0.27±0.07	0.31±0.05	0.17±0.07
BL	0.07±0.17	NE	0.77±0.21	0.07±0.15	0.31±0.16	0.34±0.18
TC	0.47±0.17	0.54±0.5	0.11±0.06	0.89±0.12	0.34±0.28	0.27±0.10

h^2_S= sire heritability, BW = body weight, EL=ear length; BL=Body length; LBL= length of back legs; THL=thigh length,

NTS= nose to shoulder, HG= heart girth, TC=thigh circumference, NE=not estimable

Table 2: shows heritability estimates from sire (h^2_S±SE) and dam (h^2_D±SE) variance component in Chinchilla. The h^2 components from sire ranged from (0.01-64) and (0.2-0.86) for dam. The low to

moderate h^2 estimates for BW for sire and for dam agreed with the findings of Ferraz and Eler (1994) who reported direct heritability of 0.26 and 0.17 for individual body weight at 11 weeks of age in New Zealand White and Californian fryers, whereas maternal heritability were 0.00 and 0.08 respectively. The estimates for dam were moderate this corroborates with the report of Elamin *et al*. (2011) who recorded 0.211 to 0.372 based on paternal half-sib analyses.

Table 2: Heritability estimate of sire (h^2_S±SE) and for dam (h^2_D±SE) variance component in Chinchilla

	Sire (h^2_S±SE)			Dam (h^2_D±SE)		
	Age (weeks)			Age (weeks)		
Traits	6	10	20	6	10	20
BW	0.19±0.12	0.23±0.07	0.05±0.06	0.04±0.02	0.13±0.08	0.01±0.03
EL	0.44±0.09	0.29±0.09	0.07±0.02	0.27±0.07	0.20±0.07	NE
NTS	0.01±0.21	0.05±0.60	0.07±0.05	0.05±0.39	0.08±0.76	0.86±0.17
LBL	0.56±0.28	0.06±0.10	0.30±0.10	0.43±0.25	0.26±0.21	0.43±0.12
HG	0.46±0.10	0.16±0.10	0.26±0.18	0.81±0.13	0.02±0.03	0.24±0.08
THL	0.11±0.03	0.28±0.09	0.64±0.10	0.45±0.06	0.21±0.08	0.14±0.04
BL	0.08±0.08	0.01±0.03	0.04±0.06	0.60±0.23	0.03±0.08	0.21±0.14
TC	0.36±0.06	0.05±0.03	0.21±0.06	0.04±0.02	0.10±0.04	0.43±0.09

h^2_S= sire heritability, BW = body weight, EL=ear length; BL=Body length; LBL= length of back legs;THL=thigh
length, NTS= nose to shoulder, HG= heart girth, TC=thigh circumference, NE=not estimable.

Dutch breed recorded heritability estimates which ranged from low - high for sire and dam (Table 3). High estimates were observed in sire or BW, EL and LBL at 6 and 10 week, HG at 10 week, BL at 6 week, NTS and TC at 6, 10 and 20 week of age. High estimates were observed for DUC sire for BW, EL and LBL at 6 and 10 week, HG at 10 week, BL at 6 week, NTS and TC at 6, 10 and 20 week of age, this suggests that, the animals have not been previously subjected to selection over time. The high BW obtained in this study disagreed with the report of Iraqi *et al*., (2002) who estimated heritability using multi-trait animal model as 0.34, 0.30 in NZW and 0.10, 0.25 in Z line rabbits for BW8 and BW12 respectively.

Table 3: Heritability estimate of growth traits for sire (h^2_S±SE) and for dam (h^2_D±SE) Component for Dutch

	Sire (h^2_S±SE)			Dam (h^2_D±SE)		
	Age (weeks)			Age (weeks)		
Traits	6	10	20	6	10	20
BW	0.62±0.10	0.83±0.21	0.16±0.12	0.09±0.03	0.18±0.13	0.22±0.13
EL	0.86±0.16	0.72±0.11	0.34±0.06	0.34±0.10	0.06±0.03	0.28±0.06
NTS	0.53±0.33	0.63±0.37	0.70±0.14	0.29±0.24	0.03±0.07	0.54±0.12
LBL	0.91±0.04	0.79±0.04	0.02±0.63	0.36±0.28	0.21±0.23	0.04±0.30
HG	0.34±0.11	0.63±0.40	0.25±0.12	0.13±0.07	0.15±0.20	0.85±0.23
THL	0.33±0.12	0.29±0.11	0.06±0.08	0.48±0.15	0.42±0.13	0.16±0.14
BL	0.49±0.24	0.06±0.21	0.03±0.09	0.14±0.13	0.04±0.40	0.14±0.21
TC	0.43±0.13	0.77±0.20	0.53±0.15	0.03±0.04	0.36±0.19	0.31±0.12

h^2_S= sire heritability, BW = body weight, EL=ear length; BL=Body length; LBL= length of back legs; THL=thigh length,
NTS= nose to shoulder, HG= heart girth, TC=thigh circumference.

Repeatability estimates for growth traits

Table 4: shows the repeatability estimates for growth traits in three breeds of rabbit. The estimates of repeatability for NZW were moderate to high except HG and THL at 6 weeks which had low estimates. CHC estimates were moderate to high except for THL and TC at 6 weeks which also had low values. The repeatability estimates for DUC breed were low to high. The moderate to high repeatability estimate in NZW observed in this study agreed with the findings of Chineke *et al.* (2001) for body weight and linear measurement at various ages. The CHC repeatability estimates ranged from moderate to high in some age

corroborate with (Ndjon and Nwakalor, 1998). DUC gave low to moderate estimates for some trait at various age agreed with the range of 0.00 to 0.26 (Khalil, 1994).

Table 4: Repeatability (R±SE) estimate for growth traits in three breeds of rabbit

Breed	Age \ Traits	BW	EL	NTS	LBL	HG	THL	BL	TC
NZW	6	0.67±0.11	0.89±0.03	0.77±0.22	0.35±0.11	0.09±0.02	0.12±0.05	0.91±0.06	0.56±0.12
	10	0.90±0.09	0.54±0.22	0.36±0.11	0.33±0.13	0.69±0.05	0.70±0.02	0.56±0.12	0.69±0.05
	20	0.37±0.03	0.71±0.09	0.54±0.21	0.37±0.13	0.75±0.20	0.55±0.23	0.60±0.30	0.73±0.11
CHC	6	0.64±0.09	0.54±0.26	0.60±0.13	0.91±0.20	0.32±0.13	0.14±0.08	0.34±0.05	0.14±0.03
	10	0.84±0.09	0.71±0.22	0.66±0.20	0.78±0.13	0.59±0.11	0.55±0.10	0.45±0.06	0.70±0.21
	20	0.75±0.09	0.34±0.14	0.75±0.32	0.88±0.30	0.57±0.21	0.89±0.32	0.38±0.12	0.51±0.20
DUC	6	0.91±0.05	0.34±0.11	0.06±0.02	0.43±0.30	0.67±0.14	0.20±0.12	0.09±0.01	0.45±0.17
	10	0.50±0.23	0.16±0.02	0.34±0.11	0.67±0.23	0.30±0.11	0.18±0.03	0.03±0.01	0.34±0.10
	20	0.67±0.06	0.70±0.10	0.70±0.23	0.32±0.05	0.25±0.04	0.23±0.11	0.03±0.01	0.53±0.23

R=repeatability, SE= standard error, BW = body weight, EL=ear length; BL=Body length; LBL= length of back legs; THL=thigh length, NTS= nose to shoulder, HG = heart girth, TC = thigh circumference

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