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ARTICLE

Estimating Additive and Dominance Variance for Litter Traits in Purebred California White Kits Using Different Models

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SUMMARY

Reproductive and growth records of 82 purebred California white kits were used to estimate additive and dominance genetic variances using BULPF90 PC-PACK. Estimates were obtained for litter size at birth (LSB) and at weaning (LSW); litter weight at birth (LWB) and at weaning (LWW); individual kit weight at birth (IKWB) and at weaning (IKWW) as well as neonatal (NM) and mortality at weaning (WM). Two mixed model equations were adopted The first model included fixed effects and random effects identifying inbreeding depression, additive gene effect and permanent environmental effects. The second model was similar to the first model, but included the dominance genotypic effect. Estimates of heritability from sire component of variance for LSB, LSW, LWB, LWW, IKWB and IKWW were 0.48/0.53, 0.41/0.44, 0.50/0.55, 0.49/NA, 0.44/0.47 and 0.48/0.56 from model 1 and 2 respectively. Proportions of dominance effect to total phenotypic variance from the dominance model were 0.222, 0.453, 0.206, 0.349, 0.417 and 0.521 for LSB, LSW, LWB, LWW, IKWB and IKWW respectively. Dominance effects, which are not transferable through gametes (haploid entities) but are recreated at random in the offspring, were found to influence the litter traits analyzed. Therefore, genetic evaluation with the dominance model (Model 2) was found more appropriate than the animal model (Model 1).

KEY WORDS: Additive, Dominance, Heritability, Inbreeding, Rabbit.

INTRODUCTION

Mixed model methodologies for genetic evaluations in rabbits currently use an additive genetic model (Culbertson *et al.*, 1998). Production and reproduction traits in rabbit may have a substantially higher heritability in the broad sense relative to the narrow sense. Under these conditions the selection accuracy is reduced under an additive model as stated by Falconer and Mackay, (1996). The prediction of additive and dominance genetic effects concurrently should allow for a more precise prediction of total genetic merit and breeding value, and may prove beneficial in the estimation of the dominance effects for a mate selection program (Henderson, 1989). These conditions are particularly valid in fullsib populations with a large number of dominance relationships that use specialized sire and dam lines (DeStefano and Hoeschele, 1992). Since rabbits are litter bearing species with a large expression of dominance relationships and possibly useful magnitude of dominance effects in reproductive traits, genetic evaluation in rabbits seems well suited for dominance models. However, before such genetic evaluation, the relative importance of the dominance genetic effects must be characterized. Therefore, the objective of this study was to estimate the dominance variance for litter traits in purebred

Californian breed of rabbits.

MATERIALS AND METHODS

Location of the study

The study was conducted at the rabbitry unit of the Experimental and Research Farm of the Department of Animal Science, Ahmadu Bello University, Zaria. Zaria is located between latitude 11° and 12° N and on altitude of 640m above sea level. The area falls within the Northern-Guinea Savannah zone of Nigeria, having an average annual rainfall of 1100mm which starts from late April and early May to mid October (Encarta Encyclopedia, 2009 PC version). The peak of rainy season is between June and September, followed by the harmattan period of cool and dry weather which starts from October to January. This is then followed by hot-dry weather from February to April (otherwise called the pre-rain period). The maximum temperature varies from 26.2° C to 35.7° C depending on the season, while the mean relative humidity during the harmattan period and the wet season are 21% and 72% respectively, as reported by Kabir *et* al. (2006).

Experimental animals and management

The stock of rabbit used for this study was purchased from the National Veterinary Research Institute (NVRI), Vom near Jos, Plateau State. They were housed in well ventilated pens and small metallic ear-tags were used for their identification and proper record keeping. Feed and clean drinking water were provided *ad libitum*. They were raised on a mixed feeding regime and fed twice daily at 8:00am and 4:00pm with concentrates given in the morning and forage (*Panicum maximum* grass and/or *Centrosema pubescence* legume)in the evening to enhance intake (Aduku and Olukosi, 1990).

The animals were raised to sexual maturity and mating began when they were 5 months of age. The does were mated to intact bucks by introducing them to the bucks and allowed to remain until mating was assured after which the does were returned to their pens and observed for pregnancy. Pregnancy diagnosis was done 14 days post coitus by palpation of the abdominal region between the thighs. Ten days to kindling, nest-boxes were provided and placed into individual pen in preparation for kindling. The kindling dates were noted, litter size and litter weight were also taken and recorded immediately kindling was discovered. Weaning of kits was done at 35 days and dry does were remated within 7 days after weaning their kits.

Data collection and analysis

The data comprised of 82 California White (CAW) purebred kits born in 13 litters obtained from June 2007 to October 2008. Litter traits considered included litter size at birth (LSB), litter size at weaning (LSW) determined by counting the number of kits alive at birth and at weaning; litter weight at birth (LWB), litter weight at weaning (LWW) determined by weighing all the kits in a litter at birth and at weaning (in grams) using a digital scale (Mettler Toledo, Top Pan Sensitive Balance, J. Liang Int. Ltd. U.K.); individual kit weight at birth (IKWB) and individual kit weight at weaning (IKWW) obtained by dividing the litter weight by the number of kits that made-up the litter at birth and also at weaning (in grams); neonatal mortality (NM) and weaning mortality (WM) were obtained by counting the total number of kits that died within 24 hours of birth and those that died at weaning.

The litter records were then adjusted for parity and age of dam according to Culbertson *et al.* (1997). The dominance relationship matrix was formed using the method of Hoeschele and Van Raden (1991). In this method, dominance effects are defined and predicted as specific mating pair or parental dominance class. LSB, LSW, LWB, LWW, IKWB, IKWW, NM and WM were analyzed separately using two mixed models as follows:

$y = X\beta + Zb\lambda + Za + Zp + e$ Model 1

$y = X\beta + Zb\lambda + Za + Wf + Zp + e$ Model 2

Where **y** is the vector of records, **β** is the vector of fixed effects, λ is the regression of **y** on inbreeding coefficient, **b** is the vector of inbreeding coefficients, **a** is the vector of additive animal effects, **f** is the vector of parental dominance effects, **p** is the vector of animal permanent environmental effects, **e** is the vector of residuals, and **X**, **Z** and **W** are known matrices that relate records to respective effects.

The variances of the two mixed models are;

$$\mathrm{Var}\begin{pmatrix} a \\ p \\ e \end{pmatrix} = \begin{pmatrix} A\sigma^2_a & 0 & 0 \\ 0 & 1\sigma^2_p & 0 \\ 0 & 0 & 1\sigma^2_e \end{pmatrix} \qquad \text{Model 1 (Animal model)}$$

$$\mathrm{Var}\begin{pmatrix} a \\ d \\ p \\ e \end{pmatrix} = \begin{pmatrix} A\sigma^2_a & 0 & 0 & 0 \\ 0 & F\sigma^2_f & 0 & 0 \\ 0 & 0 & 1\sigma^2_p & 0 \\ 0 & 0 & 0 & 1\sigma^2_e \end{pmatrix} \qquad \text{Model 2 (dominance model)}$$

Where $\boldsymbol{\sigma}^2_a$ is the additive variance, $\boldsymbol{\sigma}^2_f$ is the parental dominance variance and thus 1/4 of the total dominance variance, σ^2_p is the animal permanent environmental variance, σ^2_e is the residual variance, **A** is the additive relationship matrix, and **F** is the parental dominance relationship matrix. The estimations were done using BULPF90 PC-PACK (Duangjinda and Misztal, 2001).

Variance component for sire (σ^2_S), dam (σ^2_D) and error (σ^2_E) were calculated by equating computed mean squared of each random effect to its expectations and solving the components. These estimates were then used to compute heritability from sire component of variance, using the standard expression given by Becker, (1992) as follows:

$h^2_S =$

Where; h^2_S = heritability based on sire variance component; h^2_D = heritability based on dam variance component. The standard errors for heritability estimates were calculated using the formula described by Becker, (1992).

RESULTS

Heritability estimates

Estimates of heritability from sire variance components (h^2_s) for litter traits at birth and at weaning from models 1 and 2 are given in Table I. The values obtained for litter traits at birth ranged from 0.44 to 0.50 in model 1 and from 0.47 to 0.55 in model 2. However, litter traits at weaning ranged from 0.41 to 0.49 in model 1 and from 0.44 to 0.56 in model 2.

Inbreeding depression

Estimates of inbreeding depression and variances for LSB, LSW, LWB, LWW, IKWB and IKWW are presented in Table II. All variances are expressed as percentage of the phenotypic variance.

Additive and dominance variance

Table II presents the estimates of inbreeding depression and variance components for litter traits from additive model (1) and dominance model (2). The estimates of dominance variance from model 1 were 0.222, 0.453, 0.206, 0.349, 0.417, 0.521, 0.028 and 0.023 for LSB, LSW, LWB, LWW, IKWB, IKWW, NM and WM respectively.

DISCUSSION

The heritability estimates obtained from model 2 for all litter traits studied were higher than those from model 1 (Table I). This was an indication that model 2 (dominance model) seemed more appropriate for estimation of heritability for litter traits than model 1 (additive model), having higher h^2_a estimates. High heritability estimates indicates that individual selection could be adopted if improvement of such traits is desired. Moderately heritable traits on the other hand could be improved upon by combining pedigree and mass selection (Akanno and Ibe, 2005). Litter traits otherwise called reproductive traits are influenced by dominance factors (Odubote and Somade, 1992). The heritability estimates obtained in this study were higher than 0.33±0.08 for litter birth weight reported by Odubote and Somade (1992). Khalil and Soliman (1988) reported lower h^2_a estimate of 0.24±0.15 in Bouscat breed of rabbit. Similar values for litter traits had been reported by other workers (Ndjon and Nwakalor, 1998). Differences in estimates of heritability could arise from differences in breeds, environment, management as well as method of estimation used (Lukefahr *et al.*, 1992).

Estimates of inbreeding depression for the eight traits showed small values. Although there are no available literature on rabbits for comparison, the results are in general agreement with a previous work on reproductive traits in swine (Culbertson *et al.*, 1998), which is a litter bearing species. Estimates of additive and permanent environmental variances are also in general agreement with swine studies (Mabry *et al.*, 1988; Kaplon *et al.*, 1991; Ferraz and Johnson, 1993). Dominance variance for LSB, LSW, LWB, LWW, IKWB and IKWW traits were found to be 63.06%, 41.72%, 11.65%, 33.23%, 23.98% and 17.08% of the additive variance.

CONCLUSION

These results indicated that dominance effects may be important for reproductive and growth traits in rabbits as was reported in other litter bearing species (swine). Additive genetic effect measures the extent to which phenotypic individual differences are predicted from the additive effects of alleles. Dominance effects are associated with dominant gene action. Therefore, specific mating systems may allow for selection of dominance effects for these traits and subsequently increase the phenotypic performance. Additional studies are needed to analyze the relative improvements in prediction of additive effects by accounting for dominance and inbreeding effects in both purebred and crossbred kits.

TABLE I. Estimates of heritability (h^2_a±SE) for various litter traits at birth and weaning

Period	Traits	Model 1	Model 2
Birth	Litter size	0.48±0.38	0.53±0.45
	Litter weight	0.50±0.46	0.55±0.49
	Individual Kit Weight	0.44±0.42	0.47±0.49
Weaning	Litter size	0.41±0.47	0.44±0.40
	Litter weight	0.49±0.47	NA
	Individual Kit Weight	0.48±0.51	0.56±0.49

TABLE II. Estimates of inbreeding depression and variance componentsfor litter traits from additive model (1) and dominance model (2)

Traits	Models	Inbreeding Depression	Variance (% phenotypic)		-2LogL
			Additive	Dominance	
LSB	1	0.0017	0.132	0.069	208
	2	0.0013	0.140	**0.222**	217
LSW	1	0.0015	0.152	0.199	212
	2	0.0012	0.189	**0.453**	223
LWB	1	0.0015	0.111	0.108	357
	2	0.0012	0.024	**0.206**	364
LWW	1	0.0000	0.144	0.217	389
	2	0.0000	0.116	**0.349**	402
IKWB	1	0.0012	0.099	0.333	275
	2	0.0011	0.100	**0.417**	289
IKWW	1	0.0000	0.132	0.382	333
	2	0.0000	0.089	**0.521**	351
NM	1	NA	0.171	NA	173
	2	NA	0.148	**0.028**	177
WM	1	NA	0.118	NA	200
	2	NA	0.101	**0.023**	190

LSB = litter size at birth; LSW = litter size at weaning, LWB = litter weight at birth; LWW = litter weight at weaning; IKWB = individual kit weight at birth; IKWW = individual kit weight at weaning; NM = neonatal mortality; PWM = pre-weaning mortality

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