ESTIMATION OF GENETIC PARAMETERS FOR LITTER SIZE AND WEIGHT TRAITS IN NZW RABBITS RAISED IN HUNGARY

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ABSTRACT

The genetic parameters of litter size and weight traits were estimated in the New Zealand White (NZW) breed raised in a rabbit farm that belongs to the Institute for Small Animal Research, Godollo, Hungary. Using Multi-Trait Derivative-Free Restricted Maximum Likelihood (DF-REML) procedure applied to a multiple trait animal model, five traits were analyzed: litter size at birth (LSB), litter size at weaning (LSW) at 6 weeks, litter size at marketing (LSM) at 10 weeks, litter weight at weaning (LWW) and litter weight at marketing (LWM). The genetic parameters were then used to estimate genetic trends between 1992 and 1997, using the BLUP methodology. The data consisted of 3956 litters from 525 dams and 212 sires. Heritability of LSB, LSW, LSM, LWW and LWM were: 0.03, 0.03, 0.03, 0.09, and 0.07 respectively. LSW was strongly correlated with LWW and LSM, as well as LWW with LSM while the correlations between LSB and LSW or LWW were positive but low. The number of sires having positive transmitting ability (TA) records reached less than 50% at all traits while the number of dams having positive TA records reached <50% at all traits studied. The ranks of sire TA were generally low 46.2, 45.2, 44.3, 45.7 and 46.6 while 56.1, 60.3, 61.1, 62.1 and 62.8 considerable high of dams for LSB, LSW, LSM, LWW and LWM traits of NZW rabbits.

Key words: Litter size, Heritability, Correlation, Transmitting ability.

INTRODUCTION

Best linear unbiased prediction (BLUP) is an approach to predict breeding values of animals and to adjust simultaneously for fixed effects of the model (Lukefahr, 1992). Mixed-model procedures are useful means for obtaining estimates of genetic parameters specific for populations and for monitoring and then improving industry selection programs and most progress in industrial selection can be achieved when breeding values are estimated with parameters specific for the population (Ferraz and Johnson, 1993). The objectives of the present study were to estimate variance components and to predict the sire proofs as well as their rank using the BLUP procedure under mixed model equations (MME) pertaining to doe reproductive traits of New Zealand White (NZW) rabbits. In addition to, study the correlations among those traits.

MATERIALS AND METHODS

Data of litter size at birth (LSB), litter size at weaning (LSW) at 6 weeks of age, litter size at marketing (LSM) at 10 weeks of age; litter weight at weaning (LWW) and litter weight at marketing (LWM) of NZW rabbits were recorded. These records were collected from 1992 to 1997 in the rabbit farm that belongs to Rabbit Production Department, Institute for Small Animal Research, Godollo University, Hungary. The structure of the data is shown in Table 1.

Table 1: Structure of the data analyzed

Litters	3956
Traits	5
Number of sires	212
Number of dams	525
Number of does	1506
Total number of animals in the pedigree file	1718

An animal model accounting for relationship was used as follows:

$$y = Xb + Z_a u_a + Z_c u_c + e$$

where y = vector of observations on animal; b = vector of unknown fixed effects peculiar to year-season, (23 levels for LSB, LSW, LWW and 22 levels for LSM and LWM), farms (9 levels) and LSB (12 levels). u_a = vector of random additive genetic effect of the animal for the iᵗʰ trait; u_c = vector of random common litter effect (doe x parity combination with 3841 levels); e = vector of random error; X, Z_a and Z_c are incidence matrices relating records of iᵗʰ trait to the fixed, random animal and random common litter effects, respectively. Where; expectation and variances are defined as:

$$E\begin{bmatrix} \delta \\ \varepsilon \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix} \qquad \text{var}\begin{bmatrix} \delta \\ \varepsilon \end{bmatrix} = \begin{bmatrix} G..........0 \\ 0..........R \end{bmatrix}$$

The mixed model equations are:

$$\begin{bmatrix} X'R^{-1}X..........X'R^{-1}Z \\ Z'R^{-1}X..........Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} r \\ a \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix}...................(2)$$

where r and a are estimates of $\Re$ and δ. Let n denote the number of animals and t the number of traits. Data are ordered traits within animals and missing observation are accounted for by zero columns in X and Z (Merey, 1983). Occurrence of local maxima was checked by repeatedly restarting the analyses until the log-likelihood did not change beyond the fourth decimal. The Multi-trait Animal Model (MTAM) was used to estimate additive genetic, common litter effect, error, co-variance matrices and heritability. Predicted breeding values (PBV), the (co)variances estimated using MTAM analysis were used for the prediction of breeding values.

RESULTS AND DISCUSSION

Additive genetic variance

Variance components [direct additive genetic (σ_a^2), error (σ_e^2), common litter effect (σ_c^2) and phenotypic (σ_p^2)] and heritabilities for litter traits in NZW rabbits are presented in Table 2. The additive genetic variances constituted 0.01–0.64% of the phenotypic variance. The percentage of direct additive genetic variance was higher at litter weights at weaning and marketing than all litter sizes ages. This indicated that selection in the herd under consideration, preferably (though of the elongated generation interval) may be made during earlier ages after weaning, to allow individuals to express their full potential. The relative low magnitude of the additive genetic variance LSB and LSW is quite in agreement with Su *et al.* (1999), which could be attributed to the rather high common litter effect variance at this age.

Common litter effect variance

Variances of common litter effect (σ_c^2) for LSB, LSW and LSM recorded a very low estimates while a high one was recorded for LWW and LWM 23 and 1% respectively (Table 2). The estimate of σ_c^2 was the highest for litter weight at weaning at 6 weeks, this may be due to mothering ability, which is continued to the end of suckling period. Estimates of σ_c^2 for litter size at birth, weaning and at marketing were of low, this is comparable with Hassan (2005) who indicated that bunnies started to have its expression along with increasing its variances and also declining the effects of mothering ability.

Genetic parameters

Heritability estimates (h_a^2) for litter traits (Table 2) recorded a Low heritability estimates for sizes at different ages (0.03) and for LWW as well as LWM (0.09 and 0.07, respectively). Low h^2 for litter traits may be due to that maternal variation and non-additive genetic effects were large and could mask any additive genetic variance. In agreement with Youssef *et al.* (2000), Hassan (2005) mentioned that system of culling may be the main causes for reducing the sire component of variance.
The genetic correlation between LSB and LSM was moderate (0.41) but high with LWM (0.67); LSW with both LSM (0.87) and LWW (0.76) was very high which is similar between LSM (0.87) and LWW (0.45). Litter size and weight traits, are presented in Table 3.

Table 2: Estimates of genetic, error (between brackets, as a proportion of the phenotypic variance), permanent environmental variance covariance components for LSB, LSW, LSM, LWW and LWM. and heritability (on the diagonal and correlation (above diagonal) estimates

	LSB	LSW	LSM	LWW	LWM
Genetic and environmental (between brackets as a proportion of total variance) variance-covariance					
LSB	0.12 (0.97)	0.001	0.04	0.02	0.18
LSW	0.001	0.10 (0.97)	0.07	0.13	0.11
LSM	0.04	0.07	0.08 (0.97)	0.1	0.11
LWW	0.02	0.13	0.10	0.22 (0.68)	0.27
LWM	0.18	0.11	0.11	0.27	0.64 (0.91)
Permanent environmental variance-covariance as a proportion of total variance					
LSB	0.00047				
LSW	0.19199	0.00273			
LSM	0.05658	0.05461	0.00426		
LWW	0.43187	0.89511	- 0.04596	0.23008	
LWM	0.24851	0.64111	- 0.19688	0.83569	0.0165
Heritability and genetic correlations estimates					
LSB	0.03				
LSW	0.01	0.03			
LSM	0.41	0.87	0.03		
LWW	0.13	0.92	0.76	0.09	
LWM	0.67	0.45	0.5	0.72	0.07

LSB=litter size at birth; LSW=litter size at weaning; LSM=litter size at marketing; LWW=litter weight at weaning and LWM=litter weight at marketing

Transmitting ability (TA)

It concerns the genetic merit that an individual transmits to his offspring, BLUP estimated by animal model procedures can be used to predict their breeding values (twice their transmitting abilities) of animals and to adjust simultaneously for the fixed effects of the model (Lukefahr, 1992). Minimum and maximum litter size and weight traits (LSB, LSW, LSM, LWW and LWM) regarding animals TA are presented in Table 3.

When evaluations consider sires only the respective figures were 0.89, 1.12, 1.06, 1.92 and 2.87 while those for females were 1.19, 1.68, 1.47, 2.88 and 3.97. The trends of results reveal a general

superiority of does over that of bucks that reveals the higher intensity of selection imposed on sires because of the relatively fewer replacements needed as compared to does especially with the application of artificial insemination techniques using fresh semen. In this respect, sires would be further selected efficiently, using TA when frozen semen introduced to these rabbit farms. However, combining these results with the low figures of heritabilities reported in Table 2 may reveal a proportional easier selection response of females for individual selection. Moreover, results of Table 3 exhibited an obvious trend for the percentage of animals that possess positive values (% PR); which amounted approximately to 50%. Furthermore, females acquired a relatively higher percentage of those animals with positive records when compared to males.

Table 3: Minimum and maximum transmitting abilities estimates (TA) for all data, sires and dams as well as those extrapolated for the superior 25% animals in addition to number and percentage of positive records

Traits	Sires			Upper 25%		Positive records	
	Maximum	Minimum	Range	Minimum	Range	# Positive records	% of positive records
LSB	0.41	-0.48	0.89	0.06	0.35	98	46.2
LSW	0.45	-0.67	1.12	0.11	0.34	96	45.2
LSM	0.41	-0.65	1.06	0.09	0.32	94	44.3
LWW	0.73	-1.19	1.92	0.18	0.56	97	45.7
LWM	0.99	-1.88	2.87	0.22	0.78	99	46.6
	Dams			Upper 25%		Positive records	
	Maximum	Minimum	Range	Minimum	Range	# Positive records	% of positive records
LSB	0.66	-0.53	1.19	0.15	0.51	295	56.1
LSW	0.76	-0.92	1.68	0.22	0.54	317	60.3
LSM	0.67	-0.8	1.47	0.21	0.46	321	61.1
LWW	1.35	-1.53	2.88	0.39	0.96	326	62.1
LWM	1.96	-2.01	3.97	0.59	1.37	330	62.8

LSB=litter size at birth; LSW=litter size at weaning; LSM=litter size at marketing; LWW=litter weight at weaning and LWM=litter weight at marketing

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