

Estimation and evaluation of genetic parameters for body weight traits of New Zealand White rabbits in Egypt using different multivariate animal models

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Abstract

Records on 1265 New Zealand White rabbits for body weight at weaning (BW4), 8 (BW8) and 12 weeks (BW12), produced in the period from 2001 to 2003, were analyzed using four multi-trait animal models (three traits at the same time) to estimate genetic parameters (direct additive, maternal genetic, common litter effects and residual variances as well as heritabilities). Model 1 included only animal direct genetic effect, Model 2 the animal direct and common litter effects, Model 3 also included the effects included in the model 2 plus the animal maternal genetic effect, uncorrelated with the direct effect, and Model 4 included all the effects included in Model 3, but in this case the animal direct and maternal genetic effects were included correlated.

Percentages of variance component showed that direct additive genetic effects were the highest (ranged from 23.2 to 49.1%) when using Model 1, and then greatly decreased when using Models 2, 3 or 4 (ranged from 0.0 to 10.5%). Estimates of common litter effects were 80.5, 63.5 and 42.7% for BW4, BW8 and BW12, respectively. Estimates of maternal genetic variance were very low (ranged from 0.0 to 4.3%) for body weights. Estimates of direct additive heritability were 0.08, 0.06 and 0.0 (when using Model 4) for BW4, BW8 and BW12, respectively, while the corresponding maternal heritability values were 0.02, 0.0 and 0.04 for the same weights. Estimates of direct genetic correlation were very different (ranged from -0.25 to 0.56) when using the different multi-trait animal models. Most estimates of maternal genetic correlation were positive and higher than those of direct genetic correlation. Estimates of common litter, environmental and phenotypic correlations were positive and ranged from moderate to high between body weights.

The Qui-squared values show that differences between values of -2 LOG (Likelihood) of Model 1 and each of Models 2, 3 and 4 were highly significant. When comparing Model 2 with each of Models 3 and 4, the differences were non-significant. Furthermore, Model 4 should be used only if the correlation between direct and maternal genetic effects is supposed to be important.

Introduction

Rabbits have a number of characteristics that would make them particularly suitable as meat-producing animals, especially when compared with other herbivores. Rabbits could contribute significantly in solving the problem of meat shortage (Taylor 1980; Lebas 1983). Meat of rabbits has a low cholesterol level (50 mg 100 gm⁻¹), high protein/energy ratio and is relatively rich in essential fatty acids.

The New Zealand White rabbits as a foreign breed are the most prevailing and wide spread over all the world. Genetic evaluation for economic traits in rabbits is required and genetic parameters should be estimated without any bias. Some authors have made studies on genetic parameters of several traits of rabbits. Khalil et al (1986) made an important review article on this subject. However, most of these studies have used the sire or dam model of analysis. Moreover, most of these studies have neglected the effects of common litter and/or maternal genetic effects on post weaning growth traits in rabbits, although, those effects may be more important than additive genetic effects (Ferraz et al 1992; Ferraz and Eler 1996; Iraqi et al 2002). Several other studies have used mixed models, like Baselga et al (1992) and Lukefahr et al (1992). Nowadays, the multi-variate animal model is the best model because it increases the accuracy of selection when the genetic and environmental correlations between traits as well as other relevant information are included.

The main objectives of the present study were to: (1) estimate genetic parameters (e.g. variance components, direct heritability, maternal genetic heritability and all genetic and non-genetic correlations) for body weights at weaning (4-weeks), 8 and 12 weeks of age in New Zealand White rabbits using four multi-variate animal models, and (2) determine the best model of the four multivariate animal models that can be used as selection criteria of rabbits.

Materials and methods

This experiment was carried out at the Rabbit Farm of the Department of Animal Production, Faculty of Agriculture at Moshtohor, Zagazig University, Banha Branch, Egypt in the period from 2001 to 2003. Locally born rabbits of the New Zealand White breed were used in this study. This breed came from Bank El-Nil rabbitry since 1994. Twelve bucks and 55 does were used as the base population for this work. Bucks and does were individually housed in wire cages with standard dimensions arranged in one-tire batteries allocated in rows along the rabbitry with passages suitable for service. Each buck was mated to 4 or 5 does (at 6 month of age).

The does were assigned randomly according to the available numbers. Does were mated in the bucks' cage and logged individually. Sire-daughter, full and half sib matings were avoided. Each doe was palpated 10 days thereafter to detect pregnancy. Those which failed to conceive were returned to the same mating-buck at the day of test. Metal nest boxes were provided at 27 days after fertile mating. Within 24 hours of kindling, does and their litters were weighed and recorded. At weaning age (28 days after kindling), the young rabbits were separated from their dams' cage, sexed, weighed, ear-tagged and lodged in collective cages in groups having automatic water fountains. Breeding animals and young litters were fed *ad libitum* a pelleted rabbit ration containing 17.7 % crude protein, 13 % crude fiber and 2.54 % fat. In winter and early months of spring berseem (*Trifolium alexandrinum*) was supplied at midday. Cages of all animals (breeding animals) were cleaned and disinfected before each kindling regularly. Manure was collected daily and removed outside the rabbitry. All animals were treated and medicated similarly throughout the work period under the same managerial and climatic conditions.

Data and models of analysis

Data of 1265 individual body weights of animals were recorded at weaning (BW4), 8 (BW8) and 12 weeks (BW12) of age, which were produced from 12 bucks and 55 does (base population) of New Zealand White rabbits (Table 1).

Table 1. Structure of the data analyzed

Item	New Zealand White
No. of sires (in the base population)	12
No. of sires with records	28
No. of dams (in the base population)	55
No. of dams with records	56
No. of animals weaned	1265
Total number of animals in the pedigree file	1332

Data were analyzed using four multi-trait animal models (three traits at the same time) using MTDFREML programs of Boldman et al (1995). Variances and covariances obtained by REML method of VARCOMP procedure (SAS 1996) were used as starting (guessed) values for the estimation of variance and covariance components. Analyses were done according to the general model:

$$y = Xb + Za + Zm + Zc + e,$$

where:

y = vector of observation;

X= incidence matrix of fixed effects;

b = vector of fixed effects including sex (2 levels) and year-season (7 levels);

Z_a , Z_m and Z_c = incidence matrices corresponding to random effects of direct additive, maternal genetic and common litter (dam x litter size at birth x parity combination), respectively;
 e = vector of random errors.

The difference between the four models used refers to the number of random effects included. Model 1 included only animal direct genetic effect, Model 2 the animal direct effect and common litter effects, Model 3 also included the effects included in the model 2 plus the animal maternal genetic effect, uncorrelated with the direct effect and Model 4 considered all the effects included in Model 3, but in this case the animal direct and maternal genetic effects were correlated.

All estimates of BLUP were derived by the four multi-trait animal models (MTAM) using the MTDFREML program (Boldman et al 1995) adapted to use the sparse matrix package, SPARSPAK (George and Ng 1984). The MTAM considered the relationship coefficient matrix (A^{-1}) among animals in the estimation (Korhonen 1996). Convergence was assumed when the variance of the log-likelihood values in the simplex reached $<10^{-12}$. Occurrence of local maxima was checked by repeatedly restarting the analyses until the log-likelihood did not change beyond the first decimal. The MTAM was used to estimate direct additive genetic, maternal genetic, common litter effect, error, phenotypic variances and direct heritability and maternal genetic heritability as well as all genetic and non-genetic correlations. Direct (σ_a^2) and maternal genetic (σ_m^2) heritabilities were computed as:

$$h_a^2 = \frac{\sigma_a^2}{\sigma_p^2} \quad \text{and} \quad h_m^2 = \frac{\sigma_m^2}{\sigma_p^2},$$

where σ_a^2 , σ_m^2 and σ_p^2 are the variances due to effects of direct additive genetic, maternal genetic and phenotypic ($\sigma_a^2 + \sigma_m^2 + \sigma_c^2 + \sigma_e^2$), respectively.

To compare animal models, it was made of a property of the mixed model that the higher the likelihood function, the more the model explained the data. Likelihood function is higher when new parameters are included in the model. So, all comparisons between models were tested based on methodology described by Rao (1973) and Mood et al. (1974). This method is based on in fact that the difference $-2 \log \Lambda_i - \log \Lambda_j$ has a Qui-squared distribution function, after the convergence criteria of the iterative process has been reached in the different models. The number of degrees of

freedom of this comparison is equal to the number of parameters that were added to the model. Significance was tested not only at level of $P < 0.05$ and $P < 0.01$, but also a “practical” significance, based on variation of values of genetic parameters, was considered in the choice of the “best” model.

Results and discussion

Means, standard deviations and coefficient of variability for body weight traits in New Zealand White rabbits are given in Table 2 to characterize the population used.

Table 2. Means, standard deviations (SD) and coefficients of variation (V%) for body weights at weaning, 8 and 12 weeks of age in New Zealand White rabbits

Body weight	New Zealand White		
	Mean	SD	V%
At weaning (BW4)	589	217	36.9
At 8 weeks (BW8)	1227	365	29.8
At 12 weeks (BW12)	1903	419	22.0

Variance components

Variance component estimates in Table 3 show that percentages of direct additive genetic variance (σ_a^2) were the highest (ranged from 23.2 to 49.1 %) when using Model 1, and then greatly decreased when using Models 2 or 3 or 4 (ranging from 0.0 to 10.5 %). These reflect the importance of both common litter and maternal genetic effects on post weaning body weights in rabbits. Ferraz et al (1992), Ferraz and Eler (1996) and Iraqi et al (2002) reported that maternal or common litter influences might be more important than additive genetic effects for post-weaning growth in rabbits. On the other hand, percentage of σ_a^2 in the present study was low at a young age (at 4 weeks) and then slightly increased at 8 week. This may be due to high non-genetic effects (e.g. common litter and non genetic maternal effects), which is in agreement with Su et al (1999). Iraqi et al (2002) found that percentages of σ_a^2 were 9.8 and 24.9% for body weight at 8 and 12 weeks of age in Z-line rabbits, respectively. Comparison of variance component percentages from Models 2, 3 and 4 showed that there were very little changes in the direct additive genetic variances for the studied traits.

Maternal genetic variance (σ_m^2) estimates (Table 3) show that the effects on body weight traits were very low (ranged from 0.0 to 1.8%), when the correlation between direct and maternal genetic effects was ignored (Model 3), and somewhat increased (range from 0.0 to 4.3%) when that effect was considered (Model 4). When considering the correlation between direct and maternal genetic effects, estimates of σ_m^2 were increased by 22.4% and 138% for body weights at 4 and 12 weeks of age, respectively as calculated from Table 3. This indicates that the correlation between the two

effects affected the maternal genetic variance estimates. On the other hand, these estimates were lower than the corresponding estimates of direct additive genetic variance (except for body weight at 12 weeks). Using a single trait animal model, Ferraz et al (1992) obtained percentages of σ_m^2 were 9.1, 16.8 and 3.3% for body weight at 4, 8 and 11 weeks, respectively, for pooled data collected on Californian and New Zealand White rabbits.

Table 3. Variances components estimates [direct additive genetic (σ_a^2), maternal genetic (σ_m^2), common litter effect (σ_c^2), error (σ_e^2) and phenotypic (σ_p^2)], direct heritability (h_a^2) and maternal heritability (h_m^2) for body weights in New Zealand White rabbits.

Model of analysis ⁺⁺	Trait ⁺	σ_a^2	%	σ_m^2	%	σ_c^2	%	σ_e^2	%	σ_p^2	h_a^2	h_m^2
1	BW4	14697	36.1	--	--	--	--	26033	63.9	40731	0.36	--
	BW8	60925	49.1	--	--	--	--	63118	50.9	124043	0.49	--
	BW12	38482	23.2	--	--	--	--	127534	76.8	166017	0.23	--
2	BW4	3739	7.4	--	--	40536	80.5	6075	12.1	50350	0.07	--
	BW8	14124	10.5	--	--	85361	63.5	34931	26.0	134416	0.11	--
	BW12	0.033	0.0	--	--	73837	42.7	98899	57.3	172736	0.00	--
3	BW4	4507	8.8	718	1.4	40012	78.6	5696	11.2	50934	0.09	0.01
	BW8	14675	10.9	0.0012	0.0	85851	63.5	34709	25.7	135236	0.11	0.00
	BW12	0.0082	0.0	3089	1.8	71771	41.2	99191	57.0	174053	0.00	0.02
4	BW4	4139	8.2	879	1.7	39606	78.4	5884	11.7	50510	0.08	0.02
	BW8	8512	6.5	0.0082	0.0	85076	64.8	37633	28.7	131221	0.06	0.00
	BW12	0.0076	0.0	7367	4.3	66232	38.4	99051	57.4	172652	0.00	0.04

⁺Traits as defined in table 2.

⁺⁺Model 1 = direct additive + error; Model 2 = direct additive + common litter effect + error; Model 3 = direct additive + genetic maternal effect + common litter effect + error (when ignored covariance between direct additive and genetic maternal effects); Model 4 = direct additive + genetic maternal effect + common litter effect + error (when considered covariance between direct additive and genetic maternal effects).

The estimate of common litter effects (σ_c^2) for body weight at weaning was higher (80.5%) compared to that at later ages (63.5% at 8 weeks and 42.7% at 12 weeks). The same trend was observed by Ferraz et al (1992) and Iraqi et al (2002). However, percentages of σ_c^2 in this study were higher than those reported by Ferraz et al (1992) and Iraqi et al (2002) with New Zealand White rabbits, which ranged from 25.4 to 49.6% for body weight at different ages. This indicates that the weights of the New Zealand White rabbits in this study were subjected to a high variability in common litter effects, because individuals in the same litter were being nursed by the same dam and reared in the same cage. Lukefahr et al (1996) found that σ_c^2 accounted for 72% of the total variance for weaning weight of rabbits. Su et al (1999) also found that σ_c^2 accounted for 60% of the total variance for daily litter gain during the period from one to 35 days of age in Danish White rabbits. On the other hand, estimates of σ_c^2 were higher than those of direct additive, maternal genetic and residual variance (except for body weight at 12 weeks). Also,

Lukefahr et al (1996) reported that common environmental variances for weaning weight and mature weight were considerably larger than either additive or residual environmental variance. From this study, one can conclude that the common litter effect of post-weaning growth should be considered in genetic evaluation of breeding programs.

Estimates of experimental error variance (Table 3) were very high when using Model 1 for all the studied body weights, while these variances were reduced when using Models 2, 3, and 4. Therefore, common litter and maternal genetic effects should be considered in the model (Ferraz et al 1992).

Heritability

Estimates of h_a^2 were 0.08, 0.06 and 0.0 (when using Model 4) for body weights at 4, 8 and 12 weeks, respectively, while the corresponding maternal heritability estimates were 0.02, 0.0 and 0.04 for the same weights (Table 3). Ferraz et al (1992) found that estimates of direct and maternal heritabilities were 0.007 and 0.091; 0.043 and 0.168; 0.082 and 0.033 for body weight at weaning, 8 and 11 weeks of age, respectively. Based on animal model estimates, Lukefahr et al (1996) and McNitt and Lukefahr (1996) reported direct and maternal heritabilities of 0.04 and 0.08 for weaning weight, respectively. Also, Khalil et al (2000) and Iraqi et al (2002) found direct heritabilities of 0.09 and 0.256; 0.10 and 0.25 for body weight at 8 and 12 weeks, respectively. Comparison of direct heritability values from models 2, 3 and 4 showed that there were very few changes in the variance component estimates for the studied traits.

Correlations

Estimates of direct genetic (r_G), maternal genetic (r_M), common litter (r_C), environmental (r_E) and phenotypic (r_P) correlations between body weight traits are given in Table 4.

Estimates of r_G were very different (range from -0.25 to 0.56) when the different multi-trait animal models were used. Actually, this trend makes little sense, and probably can only be best explained by the paucity of data. Similarly, there are wide variations in estimates of r_G between body weight traits reviewed by Khalil et al (1986). Mostageer et al (1970) reported a similar estimate of 0.046 for r_G between body weights at 6 and 8 weeks. Nossier (1970) found that the estimate of r_G was 0.033 between body weights at 8 and 12 weeks. Estimates of r_M were positive and higher than the estimates of r_G . This indicates that the maternal genetic effect is more important than the direct additive effect. On the other hand, when the correlation between direct and maternal genetic effects (Model 3) was ignored, estimates of r_M were higher compared to those

estimates when the correlation was included (Model 4). The highest direct (0.56) and maternal genetic (1.0) correlations were obtained between body weight at 4 and 12 weeks of age (Model 3). Thus, one can conclude that selection for body weight is more effective at early ages (4 weeks) to improve post weaning growth in rabbits. Estimates of r_M are not available in the literature, since previously the maternal genetic effect was included only in single trait rabbit models.

Table 4. Direct genetic correlation (r_G), maternal genetic correlation (r_M), common litter correlation (r_C), environmental correlation (r_E) and phenotypic correlation (r_P) estimates for the two body weights in New Zealand White rabbits

Model of analysis ⁺⁺	Traits correlated														
	BW4 and BW8				BW4 and BW12				BW8 and BW12						
	r_G	r_M	r_C	r_E	r_P	r_G	r_M	r_C	r_E	r_P	r_G	r_M	r_C	r_E	r_P
1	0.28	---	---	0.58	0.45	0.43	---	---	0.36	0.37	0.29	---	---	0.67	0.51
2	-0.18	---	0.57	0.66	0.51	0.18	---	0.50	0.46	0.42	0.55	---	0.66	0.59	0.58
3	0.12	0.94	0.57	0.61	0.51	0.56	1.00	0.50	0.48	0.42	0.14	0.92	0.68	0.60	0.58
4	-0.25	0.42	0.56	0.65	0.50	0.30	0.64	0.50	0.47	0.41	0.05	-0.04	0.68	0.57	0.57

⁺Traits as defined in table 2.

⁺⁺**Model 1** = direct additive + error; **Model 2** = direct additive + common litter effect + error; **Model 3** = direct additive + genetic maternal effect + common litter effect + error (when ignored covariance between direct additive and genetic maternal effects); **Model 4** = direct additive + genetic maternal effect + common litter effect + error (when considered covariance between direct additive and genetic maternal effects)

Estimates of r_C were positive and ranged from moderate (0.56 between body weights at 4 and 8 weeks) to high (0.64 and 0.68 between body weights at 4 and 12 weeks and between 8 and 12 weeks, respectively). Iraqi et al (2002) found that estimate of r_C between body weights at 8 and 12 weeks were 0.49 and 0.64 in New Zealand White and Z-line rabbits, respectively. This also indicates the importance of common litter effect on body weights in rabbits (Ferraz et al 1992; Iraqi et al 2002). All estimates of environmental and phenotypic correlations were positive and they had the same trend for r_C between the studied body weights.

Comparison between models:

The computed Qui-square value and its significance for the likelihood ratio test for comparisons between different animal models are given in Table 5. Differences between values of -2 LOG (Likelihood) of Model 1 and each of Models 2, 3 and 4 were highly significant. Therefore, results obtained from Model 1 are greatly biased and should not be used in any evaluation of breeding programs. This indicates that both common litter effects and genetic maternal effects strongly affected the estimation of (co)variance components for body weights. Ferraz and Eler (1996) and McNitt and Lukefahr (1996) noted that common litter effects were important for growth traits, and they recommended that they should be considered in animal models of such traits.

When comparing Model 2 with each of Models 3 and 4, the differences between values of -2 LOG (Likelihood), obtained with the largest likelihood when convergence criterion were attained,

were non-significant. Meanwhile, the differences between Models 2 and 4 are large comparable to differences between Models 2 and 3 because the likelihood function is higher when more random parameters are included in the model. The difference between Model 3 and 4 was non-significant. Thus, estimates obtained from Model 3 or Model 4 (the most nearly complete or complete models) were chosen for reporting of both variance components and heritabilities as that model had the largest logarithm of the likelihood function for multi-trait animal models. Furthermore, Model 4 should be used only if the correlation between direct and maternal genetic effects is supposed to be important.

Table 5. Computed Qui- square value for likelihood ratio test used to compare different animal models used for (co)variance components estimation in body weight traits in New Zealand White rabbits.

Comparison ⁺	d.f.	Computed Qui-square value	Critical Qui-square value	Significant
Model 1 and 2	1	1440	3.84	**
and 3	2	1438	5.99	**
and 4	3	1438	7.81	**
Model 2 and 3	1	1.348	3.84	ns
and 4	2	1.867	5.99	ns
Model 3 and 4	1	0.519	3.84	ns

⁺Model 1 = direct additive + error; Model 2 = direct additive + common litter effect + error; Model 3 = direct additive + genetic maternal effect + common litter effect + error (when ignored covariance between direct additive and genetic maternal effects); Model 4 = direct additive + genetic maternal effect + common litter effect + error (when included covariance between direct additive and genetic maternal effects)

Conclusions

- Since the estimate of heritability was higher for body weight at 4 weeks than other ages (when using Model 4), selection for animals is more effective at this age for improvement in post weaning growth in New Zealand White rabbits.
- Because the common litter effect is very important for post-weaning growth, one can conclude that the common litter effect should be included in genetic evaluation of breeding programs. Furthermore, estimates of experimental error variance were markedly high when using Model 1 for all the studied body weights, while that variance was reduced when using Models 2, 3, and 4. Therefore, common litter and maternal genetic effects should be included in the model.
- Estimates obtained from Model 3 or Model 4 were chosen for reporting for both variance components and heritabilities as that model had the largest logarithm of the likelihood function for multi-trait animal models. Furthermore, Model 4 should be used only if the correlation between direct and maternal genetic effects is supposed to be important.
- The correlation between direct and maternal genetic effects affected the maternal genetic variance estimates.

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