

THRESHOLD MODEL FOR ANALYZING THE TRAIT IN YOUNG (BABY) NEW ZEALAND WHITE RABBITS

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Abstract

A total of 2590 records (1592 live and 998 dead rabbits) of livability (LIV), weaning weight (WWT) and average daily gain from birth till weaning weight (ADG) of rabbits as growth traits were obtained from 142 (96 dams and 46 does) exotic New-Zealand White (NZW) having 344 litters and 18 sires, raised at the experimental farm belonging to animal production research institute (APRI). Records were analyzed to obtain variance and (co) variance components of livability trait using Gibbs Sampling, WWT and ADG using MTDFREML procedures. The livability single trait analyzed using threshold animal model, while, WWT and ADG multi-traits were analyzed using animal model with the flat distribution. The Models included litter size at birth (lsb), weight of doe at conception, month of birth, year of birth and parity as fixed effects for (LIV) trait add to sex effect for WWT and ADG. The random effects in the models were additive genetic, maternal and permanent environmental effects.

Gibbs Sampling (GS) heritability estimate for binary trait (LIV) was 0.44. The variances due to maternal and permanent environmental effects were 0.48 and 0.001 as a proportion of phenotypic variance, respectively. The correlation between direct genetic and maternal effect was -0.25.

MTDFREML heritabilities estimates for (WWT) and (ADG) were 0.55 and 0.75, respectively. The variance due to maternal and permanent environmental effects as a proportion of phenotypic variance for WWT and ADG were 0.41, 0.30, .52 and .03, respectively. The correlation between WWT and ADG was 0.99.

INTRODUCTION

Statistical methodology for categorical data has only recently reached the level of sophistication achieved early in this century by methodology for continuous data. In animal breeding, many traits of economic importance are continuous response variables. Most quantitative genetics methodology have been developed to handle these types of traits Gianola, 1982. However, data may not always show a continuous phenotypic distribution. Some traits, such as livability of bunnies (from birth till weaning at four

weeks of age) are measured as binary data. Response is fitted into two discrete classes. Character of this sort as "threshold characters" may be analyzed by assuming a hypothetical, underlying normal distribution through a set of fixed threshold (Gianola, 1982).

This study aimed to obtain variance and covariance components for individual traits of bunnies using Gibbs Sampling and MTDFREML for analyzing the binary trait (LIV) and for two others continuous traits (WWT) and (ADG). There was a brief description of a general non-linear procedure to analyze binary variables often encountered in animal breeding.

MATERIALS AND METHODS

The experimental work of this study was carried out at the experimental farm belonging to animal production research institute (APRI), Agricultural research center (ARC), Saka, Kafr-El-Sheikh, Ministry of Agriculture.

The exotic New-Zealand White rabbit breed (NZW) was used in this study that lasted for two-production seasons 1995-1996 and 1996-1997.

Animals were fed a pelleted ration whose constitution is mentioned as 17 % crude protein, 12 % crude fiber, and 3 % fat and 2600 k.cal digestible energy. Berseem (*Trifolium alexandrinum*) was also fed daily ad-libitum.

Random mating, avoiding all full and half-sib mating was practiced.

Growth traits statistically analyzed were livability (LIV), weaning weight (WWT) and average daily gain (ADG) for individual rabbits from birth till weaning age at 4 weeks.

The MTDFREML programs of Boldman *et al.* (1993) and Gibbs Sampling Program of Van Tassell and Van Vleck (1995) were used for the estimation of variance components.

Principles of derivative - free restricted maximum likelihood (MTDFREML) have been described by Smith and Graser (1986) and Meyer (1989) and reviewed in Boldman *et al.* (1991).

Sorensen *et al.* (1995) applied GS to Bayesian analysis of single trait threshold model with multiple categories. Wang *et al.* (1997) developed GS algorithm that may be applied to an analysis of multiple level categorical traits with a continuous

trait. The result of Wang *et al.* (1997) is extended to completely general case of any combination of continuous and categorical data with missing data.

Derivation of the threshold model for this study was based on the model described by Sorensen *et al.* (1995).

The general representation of the animal model used is:

$$Y = Xb + Z_a a + Z_m m + Z_c c + e_i$$

Where:

- Y is a n by 1 vector of records,
- b denotes the fixed effects in the model with association matrix X;
- a is the vector of direct animal effect with association matrix Z_a ;
- m is the vector of maternal genetic effect with association matrix, Z_m ;
- c is the vector of permanent environmental effects with the association matrix, Z_c ; and
- e denotes the vector of residual effects.

The variance co-variance structure for model is as follows:-

$$V = \begin{bmatrix} a \\ m \\ c \\ e \end{bmatrix} = \begin{bmatrix} A\sigma^2 a & \sigma_{am} & 0 & \\ \sigma_{am} & A\sigma^2 m & & \\ & & I\sigma^2 c & \\ 0 & & & I\sigma^2 e \end{bmatrix}$$

Fixed effects included in the model were litter size at birth (lsb), weight of doe at breeding, season of birth, year of birth and parity for livability trait adding to sex for weaning weight and average daily gain analysis.

Random effects were additive genetic effect, maternal genetic effect, permanent environmental effect and residual effect.

Livability at weaning (4 weeks) has two phenotypic classes with one threshold separating them. The two classes will be referred to as 1 and zero. The first class is assigned if the bunny is survival at weaning, while the zero class is assigned otherwise.

For the binary trait, the variable y_i is observed for each individual taking on value of $y_i = 1$ or $y_i = 0$.

The variable y_i is the expression of an under continuous random variable u_i , the livability of individual, Φ

Let the model of livability be:

$$u_i = X_i'b + Z_a'a_i + Z_m'm_i + Z_c'c_i + e_i = w_i'\theta + e_i \quad (1)$$

Where $\theta = (b, a, m, c)$ and w' is a row of incidence vector linking θ to the observation, b is a vector of fixed effects, a is the vector of additive genetic random effect, c is the vector of uncorrected permanent environmental effect and m is the vector of maternal genetic effect, X_i' , Z_i' are row vector of known design matrices X and Z and e_i is the residual term.

When u_i exceeds an unknown fixed threshold t , then $y_i = 1$, and if not, $y_i = 0$.

We assume that the liability is normal distributed, with the mean value indexed by a parameter θ , and without loss of generality, that it has unit variance (Curnow and smith, 1975).

$$(u_i / \theta) \sim N(w_i' \theta, 1) \quad (2)$$

So for the vector $u = \{ u_i \}$ given θ , the joint density is

$$p(u / \theta) = \prod_{i=1}^n \phi(u_i / w_i' \theta, 1) = \phi(u / w_i' \theta, 1) \quad (3)$$

Where $\phi(\cdot)$ normal density with parameters as indicated in the argument. Given the model, we have :-

$$P(y_i = 0 / w_i' \theta) = P\{u \leq t_j / w_i' \theta\} =$$

$$P\{w_i' \theta + e_j \leq t_j / w_i' \theta\} =$$

$$P\{e_j \leq t_j - w_i' \theta / w_i' \theta\} =$$

$$\int_{-\infty}^{t_j - w_i' \theta} P(e_j) de_j = \Phi(-(t_j - w_i' \theta)) \quad (4)$$

where $\Phi(\cdot)$ is the cumulative distribution function of standardized normal

variate, can be set to zero and reduced to

$$P(y_i = 0 / w_i' \theta) = \Phi(w_i' \theta)$$

So

$$P(u / w_i' \theta, y_i = 0) = \frac{\phi(w_i' \theta, 1)}{\phi(w_i' \theta)} \text{ when } \mu_i \leq 0 \quad (5)$$

While when $u > 0$

$$P(y_i = 1 / w_i' \theta) = \{P \mu > \tau_j / w_i' \theta\} =$$

$$P\left\{\omega_i' \theta + e_i > \tau_j / \omega_i' \theta\right\} = P\left\{e_i > \tau_j - \omega_i' \theta / \omega_i' \theta\right\} = \int_{\tau_j - \omega_i' \theta}^{-\infty} P(e_i) de_i = 1 - \phi\left(-(\tau_j - \omega_i' \theta)\right) = 1 - \phi\left(-\omega_i' \theta\right) \quad (6)$$

and

$$\left(\mu / \omega_i' \theta, \gamma = 1\right) = \frac{\phi\mu(\omega_i' \theta)}{1 - \phi(\omega_i' \theta)} \quad (7)$$

The conditional underlying distribution of additive genetic value given the additive genetic variance is multivariate normal distribution.

$$a/\sigma^2 a \quad N(0, \sigma^2 a) \quad (8)$$

where A is the known g by g matrix of additive genetic relationships among animals and $\sigma^2 a$ (a scalar) is unknown additive genetic variance.

$$m/\sigma^2 m \quad N(0, \sigma^2 m) \quad (9)$$

Where:-

$\sigma^2 m$ is a scalar unknown variance and m is a vector of maternal genetic value with variance, $\sigma^2 m$ and

$$C/\sigma^2 c \quad N(0, \sigma^2) \quad (10)$$

Where:-

$\sigma^2 c$ is a scalar unknown variance and C is a vector of uncorrelated permanent environmental value with variance, $\sigma^2 c$

The vector b will be assumed to have a proper uniform distribution:-

$$P(b) \propto \text{Constant} \quad (11)$$

RESULTS AND DISCUSSION

Preliminary least squares analysis using PROC GLM option of SAS (1996) showed that livability of bunnies was affected ($P < 0.001$) by month of birth and parity. Weaning weight (WWT) and average daily gain from birth to weaning (ADG) were affected ($p < 0.001$) by litter size at birth, month of birth, year season and parity. Detailed results are shown in Table1.

The mean of weaning weight at 4 weeks of age being 382.69 g with standard deviation 116.36 g was the same with those reported by Hassan (1995), and lighter than those reported on the same breed and same age by Khalil *et al.* (2000) and Khalil (1986) who reported that the differences in mean weaning weight may be due to rearing rabbit at different management levels and differences in the models used for

analysis. The high estimate of CV % recorded in this study (116.3 %) for the post-weaning weight trait, may be due to the high sensitivity of the weaned rabbits to the non-genetic maternal effect.

The mean of ADG was 13.67 ± 4.16 with C.V. 30.41. The percentage of survival bunnies livability at weaning in the present study was 65.27% comparable to that obtained by Shower (1963) of 60.70 % on BAL rabbit at 4 weeks of age and 58.70% on NZW rabbit by Hassan (1995). The increase of (c.v.%) from 28.10 for WWT and ADG to 71.08 for LIV turn mean that improvement of these traits through phenotypic selection is quite possible with high and moderate h^2 estimates.

Table 1. Analysis of variance of WWT, ADG and LIV traits.

S.O.V.	Df	WWT&ADG	LIV
Sex	1	34858.92	-
LSB	4	49608.61**	0.23
Weight of doe	3	30816.37	0.43
Month of birth	9	119624.69**	1.60**
Year-season	2	74772.2707**	0.50
Parity	2	905693.84**	2.96**
X		382.69±16	.65±.05
C.V.		28.10	71.08

MTDFREML estimates of variance components for (WWT) and (ADG) and GS estimate for (LIV) of NZW are shown in Table 2. The variances due to permanent environmental effect (c^2), coded as an effect of the dam (possibly due to uterine capacity, feeding level at late gestation, and maternal behaviour of doe) were 0.001, .03 and 0.003 for LIV, WWT and ADG, respectively. The genetic correlation between WWT and ADG was 0.99. Heritability estimates for WWT fall within the range of the value reported in the literature. Heritability estimate of WWT was larger than those observed by Johanson *et al.* (1988) for the NZW, whose estimate of h^2 was 0.44, and Khalil *et al.* 2000 who recorded an estimate of (0.349). Hassan (1995) working on NZW bunnies, obtained estimate which was 0.622. High, moderate and low negative genetic correlations between direct genetic and maternal effects were observed for ADG, LIV and WWT, respectively (Table3). This may be due to the higher expression of doe effect than the direct effect, especially during the pre-weaning period.

MTDFREML procedure was not attended to convergence when applied to analyzing the livability trait even after 20 times restarting rounds and gave poor estimates. The problem mentioned may be due to a flat likelihood with data and structure, so that rounding error in likelihood means that distinguishing between different estimates is impossible.

Applied Gibbs Sampling for binary trait (LIV) was useful because the MTDFGS is prepared to handle this kind of trait performance. GS improved the estimate of heritability than reported in literature. The estimate of heritability was 0.44 which is larger than reported by Hassan (1995) using sire linear model with the same trait and breed (0.14).

Table 2. Estimates from variance component analysis for weaning weight (WWT), average daily gain (ADG) and livability (LIV).

Trait	σ_a^2	h^2	m^2	c^2
WWT	11145.17	0.55	0.41	0.03
ADG	13.48	0.75	0.52	0.003
LIV	8.29	0.44	0.48	0.001

Table 3. Estimates of environmental variance (σ_e^2), additive variance ($\sigma_a^2 + 1/2\sigma_m^2$), and genetic correlation between animal effect and maternal effect (σ_{am}) for WWT, ADG and LIV.

Trait	σ_e^2	$\sigma_a^2 + 1/2\sigma_m^2$	σ_{am}
WWT	255.87	9454.99	-0.04
ADG	6.70	13.67	-0.47
LIV	1.00	6.74	-0.25

Conclusion

Selection could be effective for ADG, WWT and LIV, respectively.

Maternal genetic component was important for ADG, LIV and WWT, respectively. Genetic correlation between ADG and WWT was high and positive; indicating that selection for any of the trait should result in genetic improved in the other trait. Permanent environmental effects seem to have influence on WWT, ADG and LIV, respectively. Gibbs sampling improved the estimate of h^2 , this means that information about distribution could be important to increase the estimate of h^2 and the trait becomes available for selection.

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النموذج غير المفصل (المتقطع) لتحليل الصفات المزدوجة في صغار الأرناب النيوزيلندي

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أجريت هذه الدراسة في مزرعة الأنتاج الحيواني بسخا - محافظة كفر الشيخ ، والتابعة لمعهد بحوث الأنتاج الحيواني - مركز البحوث الزراعية - وزارة الزراعة. تم إجراء البحث علي عدد ٢٥٩٠ أرنبا عمر الفطام أحياء وناقفة وذلك بهدف الحصول علي التباين والتغاير ومكوناته لصفات النمو، باستخدام برنامجين إحصائيين:

- برنامج نموذج الحيوان لدراسة صفتي وزن الجسم عند الفطام ومتوسط الزيادة اليومية.
 - برنامج النموذج السلمي الغير خطي لدراسة وتحليل صفة الحيوية.
- والمقارنة بينهما والتعرف علي مدي الدقة في حالة استخدام هذين النوعين من الصفات.
- تم الحصول علي تأثير معنوي علي جميع الصفات محل الدراسة بالنسبة لشهر الميلاد وترتيب البطن بالإضافة لنفس التأثير المعنوي لعدد الخلفة عند الميلاد وتأثير السنة وفصولها علي صفة معدل الزيادة اليومية. كذلك أعطي وزن الجسم عند الفطام متوسطا قدره ٣٨٢ جرام وسجل ١٣ جرام كمتوسط للزيادة اليومية.
- بالنسبة للصفات المستمرة، كان العمق الوراثي ٠,٥٥ و ٠,٧٥ علي الترتيب.
- وكان التباين الأمي الدائم والمؤقت ٠,٤١ و ٠,٣ لكل من صفة الوزن عند الفطام و معدل الزيادة اليومية علي الترتيب. وكان الارتباط الوراثي بين هاتين الصفتين ٠,٩٩ .
- أما بالنسبة للصفة غير الخطية فكان العمق الوراثي لها ٠,٤٤ وكل من التباين الأمي الدائم والمؤقت ٠,٤٨ و ٠,٠١ علي الترتيب.
- وكان الارتباط بين تأثير الحيوان كتأثير مضيف والتباين الدائم للأم -٠,٢٥ .