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CORRELATED RESPONSE TO SELECTION ON GROWTH CURVES IN RABBITS SELECTED FOR INCREASING GROWTH RATE.

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ABSTRACT

A hierarchical Bayes analysis of Gompertz growth curves was conducted using 137 rabbits from two groups, control (C) and selected (S). Animals came from a synthetic line selected for increased growth rate between 4 and 9 weeks of age. Embryos from generations 3 and 4 were frozen, and then thawed to be contemporary of rabbits of generation 10. Animals were weighed individually twice a week for the first four weeks, and then weekly until 20 weeks of age. Males were weighed weekly until 40 weeks of age. Correlated response to selection on Gompertz growth curve parameters was estimated as the difference between posterior means of groups C and S in a model ignoring relationships and in a model including relationships of individuals of groups S an C and their parents. Random samples from posterior distributions were drawn using Markov chain Monte Carlo methods. Body weight of S animals was higher throughout the entire growth curve. Adult weight, a parameter of the curve, was 7% higher in the selected line. Other parameters of the curve were affected mildly, if at all, by selection. The two methods of estimating response to selection gave similar results. When represented in a metabolic scale, all differences between growth curves of groups C and S disappeared, showing that the effect of selection on the growth curve was primarily a scale effect.

INTRODUCTION

Current commercial programs of rabbit selection normally include a terminal sire selected on growth rate from weaning to slaughter. Selection on growth rate can modify the whole growth curve of rabbits, changing the age at which commercial slaughter weight is raised. Growth curves are used as a way of expressing the whole growth process with few parameters having a biological interpretation. Live weight growth curves are needed to determine an economically acceptable age of slaughter, and to examine the consequences of selection on growth rate for further strategies and selection objectives. For example, an increment on adult weight is undesirable, since this increases the maintenance costs and makes the management of animals more difficult. Besides, a change in the slope of the curve makes the growth process more efficient. Growth curves have been fitted in rabbit before, but only BLASCO et al. (1990) examined the consequences of selection for growth rate in rabbit growth curves. However, this last study was made without any control population, limiting the validity of its results. In a previous report (BLASCO et al., 1996), Gompertz growth curves were fitted to a selected and a control population, but no comparisons were possible because the sampling distribution of the parameters is not known. A further difficulty comes from the existence of environmental effects that need to be corrected, or from the inclusion of the genetic relationships between individuals in the structure of the errors. The objective of this research is to examine the effect of selection for increased growth rate of rabbit on their growth curves by using a Bayesian procedure derived from the methodology of VARONA et al. (1997), that overcomes all these difficulties.

MATERIAL AND METHODS

Animals

Rabbits come from a synthetic line (R) selected for increased growth rate. This line was originated by mating animals from a California line with those from another synthetic line created by mating two commercial crossbred rabbits. Selection of parents was based on daily body weight gain between 4 and 9 weeks of age. Animals were reared in the farm of the Universidad Politécnica de Valencia. This farm has isolated roof and walls, controlled lightening and ventilation, and a cooling-system to avoid high temperatures in summer. After weaning, they were placed in flat-deck cages, 8 rabbits per cage, until they were 9 weeks old, and they were fed *ad libitum* with a commercial diet (16.0% crude protein, 15.5% fiber, 3.4% fat). Then they were placed in individual cages and the same food was restricted to approx. 140 g per day. At 20 wk of age they were placed in individual flat-deck reproductive cages, and a commercial diet with 17.5% crude protein, 14.5% of fiber and 3.4% of fat was provided. Data of animals with signs of illness were excluded from the analysis.

Embryos from generations 3 and 4 were frozen and thawed to be contemporary of rabbits born in generation 10th. Offspring from these thawed embryos constituted the control group (C), and they were contemporaries to offspring from parents born in the 10th generation of selection (selected group, S). Four males and two females from generation 3 and one male and three females from generation 4, all unrelated, produced group C, whereas 6 males and 15 females produced group S. The effect of selection for increased growth rate in the growth curve was estimated with 127 rabbits of group C and 141 of group S. A total of 137 animals from these groups were individually weighed twice a week the first four weeks and once a week until 20 weeks of age. Males were weekly weighed until 40 weeks of age. Data of females more of 20 wk old have not been included because they were later pregnant and this modified their growth curve. The number of animals measured per group were 27 males and 34 females for group C, and 27 males and 49 females for group S.

Growth model

Individual growth curve is described using the Gompertz function:

$$y_{ij} = a_i \cdot \exp\left[-b_i \cdot \exp\left(-k_i \cdot t_j\right)\right] + \varepsilon_{ij}$$

where y_{ij} is the observed weight of the individual i on time j; a_i, b_i, k_i, are the parameters of the Gompertz function for the i^{th} animal, and ε_{ij} the residual. We assume that the data are Normally distributed, the residuals are independent and all animals have the same residual variance at the same time j, but the residual variance increases with time until the adult weight is raised, and then remains constant. This can be represented in several manners, we assume here that the standard deviation of the residuals increases according to a Gompertz law; i.e., for each individual

$$\sigma_j = a_0 \cdot \exp\left[-b_0 \cdot \exp\left(-k_0 \cdot t_j\right)\right]$$

We name $\mathbf{p}_\varepsilon$ the vector with the Gompertz curve parameters for the s.d. of the residuals. Each parameter of the curve of an animal is determined by an effect of sex (male or female) and group (C or S), a genetic effect and a random environmental component that we assume Normally distributed:

$$\mathbf{p} \sim \mathrm{N}(\mathbf{X}\boldsymbol{\beta}+\mathbf{Zu}\ ,\ \mathbf{R} \otimes \mathbf{I})$$

where $\boldsymbol{\beta}$ is the vector with all sex-group effects, **u** is the vector of the genetic effects, and **p** is the vector with the Gompertz curve parameters for each animal. $\mathbf{R}\otimes\mathbf{I}$ is the (co)variance matrix of the random environmental effects, where **R** is the (co)variance matrix between these effects within individual. We have thus assumed that the random effects are independent between individuals, but the random effect of the Gompertz curve parameters are correlated within individual. We consider that the sex-group effects and the genetic effects have Normal prior distributions:

$$(\boldsymbol{\beta} \mid \mathbf{m}, \mathbf{V}) \sim N(\mathbf{m}, \mathbf{V}) \qquad\qquad (\mathbf{u} \mid \mathbf{G}) \sim N(\mathbf{0}, \mathbf{G}\otimes\mathbf{A})$$

where **m** and **V** are the subjective mean and variance for the prior beliefs about systematic effects, **G** the genetic (co)variance matrix between growth curve parameters and **A** the relationship matrix. We propose, according to SORENSEN et al. (1994), an inverted Wishart distribution for prior distributions of **R** and **G**. Prior distributions for the parameters $\mathbf{p}_\varepsilon$ of the residual standard deviation are assumed to be flat with limits that guarantee the property of the distribution. We will name this model as ‘Model B’. We also fitted a model without genetic effects (‘Model A’). Proper prior distributions were always used in order to guarantee all the posterior distributions to be proper.

Bayesian inference

The joint posterior distribution is

$$f(\mathbf{p}, \boldsymbol{\beta}, \mathbf{u}, \mathbf{G}, \mathbf{R}, \mathbf{p}_\varepsilon \mid \mathbf{y}) = f(\mathbf{y} \mid \mathbf{p}, \mathbf{p}_\varepsilon)\, f(\mathbf{p} \mid \boldsymbol{\beta}, \mathbf{u}, \mathbf{R})\, f(\boldsymbol{\beta})\, f(\mathbf{u} \mid \mathbf{G})\, f(\mathbf{G})\, f(\mathbf{R})\, f(\mathbf{p}_\varepsilon) \,/\, f(\mathbf{y})$$

Prior distributions represent the state of knowledge before the results of the experiment become available. For the group effects $\boldsymbol{\beta}$ we have used vague priors, taking **m** and **V** from a previous experiment of BLASCO and GÓMEZ (1993), who estimated the growth curve of this line in the base generation. Since there is no information on residual (co)variances for the growth curve in rabbits, we used first flat priors (with limits that guarantee the property of the distribution) as reference priors. Univariate marginal posterior distributions are derived from the multivariate posterior distribution in order to make the statistical inferences. Marginalization requires a high dimensional multivariate integration, not feasible in this case. An alternative is to approximate this solution by using Monte-Carlo Markov Chain (MCMC) techniques. Details of how we used these techniques can be found in PILES (2000).

Preliminary analyses were conducted to detect the presence of outliers or atypical growth patterns. An observed weight was declared to be an outlier if the standardized absolute value of the residual posterior mean was larger than three standard deviations from the standard normal distribution. An atypical growth pattern was declared when the Mahalanobis distance between the individual growth curve parameters and the average of its group was high. With three parameters, the square of this distance $D^2 = (\mathbf{p}_i - \mathbf{X}_i\boldsymbol{\beta})' \mathbf{R}^{-1} (\mathbf{p}_i - \mathbf{X}_i\boldsymbol{\beta})$ is distributed as a χ^2_3. We checked how many individuals had a value of D^2 laying in the area of p(<0.01). The goodness of fit was checked by the square of the correlation coefficient between the predicted and observed values. This global criterion, like the coefficient of determination of the fit, has the disadvantage of depending more of the last part of the curve than on the first part due to a scale problem, because the absolute value of the errors are higher at the adult weight than at the beginning of the growth. Moreover, nonlinear models require examining the whole growth trajectory, since a growth curve can fit well in some parts but not in others. Due to this, we used cross-validation predictive densities to assess the goodness of fit of the model. Observed values y_r were compared with their prediction Y_r

obtained using all the other data $\mathbf{y}_{-r}$. We used one of the checking functions proposed by GELFAND et al. (1992),

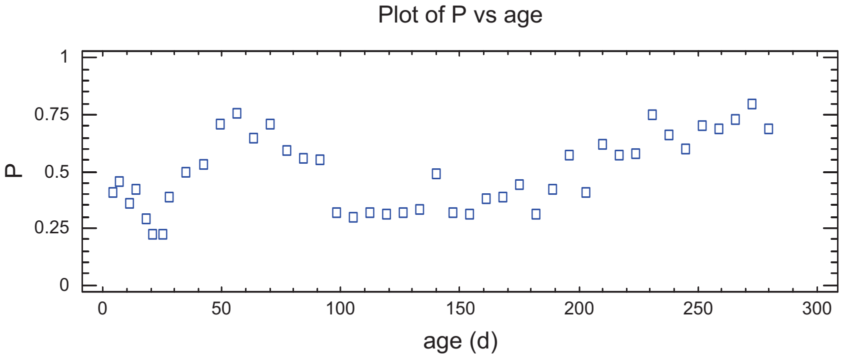
$$g = 1 \text{ if } Y_r < y_r$$
$$g = 0 \text{ if } Y_r \geq y_r$$

We obtained $E(g|\mathbf{y}_{-r})$ for each observed value r. This expectation shows the probability of a predicted value of being higher or lower than the observed one. If the model fits properly the data, $E(g|\mathbf{y}_{-r})$ should be close to 0.5, thus a global criterion for goodness of fit is to calculate the average of these expectations for all individuals in each point t_j of the growth curve. A graph with these averages shows whether the fit is good along the curve or there are parts of the curve that fit better than others. This technique has the advantage of being free of the scale effect. The expectation of the checking function $E(g|\mathbf{y}_{-r})$ is computed using MCMC methods.

RESULTS AND DISCUSSION

The square of the correlation coefficient between the predicted and observed values was 0.99. Figure 1 shows the averages of the expectations of the GELFAND et al. (1992) checking function for each point of the growth curve. Although all of them lay near 0.5 (none of the predicted values show a high probability of being lower or higher than the observed value), it can be seen that at the beginning there is a trend of obtaining predictions higher than the observations, and at the end of the growth curve there is a certain trend of obtaining predictions that are lower than the observations. Adult weight is raised very slowly and the asymptotes of growth curves tend to slightly underestimate the final adult weight. Nine observations were declared to be outliers and were removed. No animals presented an atypical growth pattern.

Figure 1. Goodness of fit: Average of the expectations of the GELFAND et al. (1992) checking function for all individuals in each point of the growth curve.



No other authors have studied hitherto the effect of selection for growth rate on the growth curve in rabbits. BLASCO et al. (1990) fitted rabbit growth curves in an unselected population, and in the same population ten generations later, but the absence of control population makes their results merely indicative. Even in other species, the studies of the effect of selection on the growth curve has been approached only indirectly, based in the estimation of the genetic parameters of the growth curve more than in direct comparisons of the effect of selection in these parameters. We have exemplified here a way of comparing growth curves using a procedure to assess the differences between the curve parameters.

Table 1 shows the means and standard deviations of the posterior densities of the curve parameters for both models, with and without genetic effects. Parameters for males have been estimated with a higher accuracy, since they have more individual data. Although the estimated means generally agree, standard deviations were considerably higher for the model including genetic effects. The model with genetic effects has the advantage of considering the relationships between individuals, which influences the standard deviation of the posterior distributions. However, it is a model that depends on the estimates of the genetic parameters, necessarily inaccurate given the reduced amount of data common in this type of experiments.

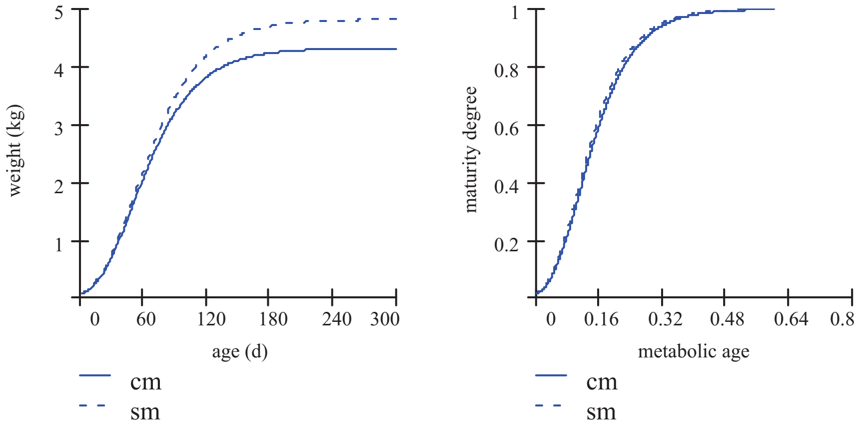
Table 1. Means and standard deviations (sd) of the posterior densities of the curve parameters. Model without genetic effects (A) and with genetic effects (B)

		a			b			k		
		Mean	sd	Pr>0	Mean	sd	Pr>0	Mean	sd	Pr>0
A	CM	4320	113		4.49	0.07		0.0300	0.0008	
	CF	4520	108		4.54	0.07		0.0295	0.0008	
	SM	4820	108		4.40	0.07		0.0287	0.0008	
	SF	4650	92		4.69	0.09		0.0321	0.0008	
	SM-CM	503	135	1	-0.09	0.09	0.14	-0.0013	0.0010	0.11
	SF-CF	126	155	0.83	0.15	0.08	0.98	0.0025	0.0009	1
	S-C	315	103	1	0.03	0.06	0.70	0.0007	0.0007	0.84
B	CM	4420	233		4.46	0.11		0.0299	0.0014	
	CF	4610	233		4.53	0.11		0.0294	0.0014	
	SM	4820	161		4.42	0.09		0.0288	0.0010	
	SF	4640	154		4.70	0.10		0.0322	0.0010	
	SM-CM	398	282	0.92	-0.04	0.14	0.39	-0.0011	0.0017	0.26
	SF-CF	26	275	0.55	0.16	0.13	0.90	0.0028	0.0016	0.96
	S-C	212	262	0.80	0.06	0.12	0.70	0.0009	0.0015	0.73

CM: Males of group C; CF: Females of group C; SM: Males of group S; SF: Females of group S; Pr>0: Probability of the difference being higher than 0

Selection on growth rate was successful. The practical consequence of this progress is a reduction of the age of slaughter, because slaughter weight is fixed by the market. An undesirable consequence, however, is the increment of the adult weight because it augments the costs of maintaining a parent population. BLASCO et al. (1990) also found an increment in adult weight in a line selected for growth rate, but they did not have any control population, thus the validity of their results was limited. Adult weight (*a*-parameter of the Gompertz curve) increased with selection, whereas the parameters related to the slope of the curve did not practically change (figure 2). This result is clearer when comparing males of group S and C than when comparing females, probably due to the limited amount of records in the females side. When curves are represented in the Taylor's metabolic scale all the effect of selection disappears (figure 2). This was predicted by TAYLOR (1985), who stressed that all weights are correlated and a selection for growth rate can easily lead to an increase in adult weight with no changes in the curve slope. McCARTHY and BAKER (1979) produced changes in the curve slope (1979) in mice, but the selection process is very inefficient, since the remaining genetic variation after restricting adult weight is very small due to the genetic correlations between all weights along the growth curve. In these circumstances, it can be predicted that male lines will become giant lines and the management of reproduction will be more difficult, unless artificial insemination is used.

Figure 2. Fitted growth curves of control and selected groups for males in the original scale and in Taylor's metabolic scale. cm: Control males. sm: Selected males



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REFERENCES

Blasco, A., P. Gou, M.A. Santacreu, 1990. The effect of selection on changes in body composition of two lines of rabbit. *4th World Congress on Genetics Applied to Livestock Production*. Madrid. XVI : 362-365.

Blasco, A., E. Gomez, 1993. A note of growth curves of rabbit lines selected on growth rate or litter size. *Animal Production*. 57: 332-334.

Blasco A, Piles M, Rodriguez E, Pla M. 1996. The effect of selection for growth rate on the live weight growth curve in rabbits. *VI World Congress on Cuniculture.*Toulouse 2: 245-248.

Gelfand, A., Dey, D.K., Chang, h., 1992. Model determination using predictive distributions with implementation via sampling-based methods (with discussion). In: *Bayesian statistics 4*, ed. J.M. Bernardo, J.O. Berger, A.P. Dawid, and A.F. Smith, 147-167. New York. Oxford Univ. Press.

McCarthy, J., Bakker, H. 1979. The effect of selection for different combinations of weights at two ages on the growth curve of mice. Theoret. Appl. Genet. 55 : 57-64.

Piles M. 2000. Ph D. Thesis. Universidad Politécnica de Valencia. Valencia. Spain.

Sorensen, D., C. S. Wang, J. Jensen, D. Gianola, 1994 Bayesian analysis of genetic change due to selection using Gibbs sampling. Genet. Sel. Evol. 26**:** 333-360.

Taylor St. C. S. 1985. Use of genetic size-scaling in evaluation of animal growth. *Journal of Animal Science*. 61 Suppl. 2: 118-143.

Varona, L.; Moreno, C.; Garcia Cortes, L.A.; Altarriba, J. 1997. Multiple Trait genetic analysis of underlying biological variables of production functions. *Lives. Prod. Sci.* 47:201-209.