



8th World Rabbit Congress – September 7-10, 2004 – Puebla, Mexico

PROCEEDINGS

Genetics – Short papers

ESTIMATION OF THE CORRELATION BETWEEN LONGEVITY AND LITTER SIZE

SÁNCHEZ J. P.¹, BASELGA M.¹, DUCROCQ V.²

¹ Departamento de Ciencia Animal. Universidad Politécnica de Valencia.
46022 Valencia. Spain.

² Station de Génétique Quantitative et Appliquée.
Institut National de la Recherche Agronomique, 78352 Jouy en Josas. France.

ESTIMATION OF THE CORRELATION BETWEEN LONGEVITY AND LITTER SIZE

SÁNCHEZ J. P.¹, BASELGA M.¹, DUCROCQ V.²

¹ Departamento de Ciencia Animal. Universidad Politécnica de Valencia. 46022 Valencia. Spain.

² Station de Génétique Quantitative et Appliquée. Institut National de la Recherche Agronomique.78352 Jouy en Josas. France.

ABSTRACT

An estimation of the genetic and the environmental correlations between prolificacy (BA and NW) and functional longevity in a population selected for litter size at weaning since 1992 is carried out. The method is only an approximation but suggests that genetically longevity and litter size are not antagonistic objectives in breeding programs, because the genetic correlations are around 0.

Key words: longevity, litter size, correlation.

INTRODUCTION

In rabbit breeding programs, selection mainly focuses on litter size at weaning or birth, in maternal lines; and feed conversion, indirectly evaluated through daily gain, in paternal lines (BASELGA and BLASCO, 1989).

Nowadays the culling rate in rabbit production is very high, yearly around 120% (RAMON and RAFEL, 2002), and the does are culled mainly because they die or get sick. Around 50% of the does are culled in the course of the first three kindlings (ROSELL, 2003). Despite the low price of the females the replacement is a negative factor in production because there is a period, between a doe get sick and culling; during this period a cage is occupied by a low productive animal. Most of the culled does are young and have not been profitable yet. When the replacement animals are bought outside, the high culling rate implies a very high proportion of animals coming into the farm periodically, increasing the risk of sanitarian problems. Thus, to improve the longevity of the does and to reduce the replacement rate could be very interesting.

In general, a breeding program has to take into account the genetic correlation between the selected traits. One way to improve the longevity in rabbits without increasing the generation interval could be to apply high intensities of selection (CIFRE *et al.*, 1998) to found a new strain. This strain could be used as a maternal strain in the current three ways cross scheme of production. Once this line has been founded with a high genetic level for longevity, it could be desirable to continue its selection for other economically important trait such as litter size. In this context, is important to know the consequences on longevity when selection for litter size is carried out and for this reason to estimate

the genetic correlation between longevity and litter size is the main objective of this paper.

MATERIAL AND METHODS

Animals

Data for this study were collected from the beginning of 1992 to the end of 2001 in a selection nucleus of rabbits, placed in Sant Carles de la Rápita (Tarragona), Spain. The animals belonged to the V strain (ESTANY *et al.*, 1989). These animals were selected for litter size at weaning and the genetic evaluation was carried out using a family index. In this nucleus, the management system is semi-intensive; the does are mated 11 days post-partum, the youngs are weaned at 35 days, and palpation is carried out 12 days post-mating. For a suitable genetic evaluation of animals in the nucleus, common culling criteria in commercial farms are not considered; i.e., does with low level of production or large intervals between parities, are not culled.

The data set involves 2417 records of longevity, defined as the time between the first positive palpation and the death or culling of the doe (1203 censored), 15235 kindlings (2320 does) and 14604 weanings (2219 does), and the pedigree file had 3031 records.

Statistical Methods

One way to study longevity taking into account censored data, the presence of time dependent covariates and the non normal distribution of the trait is to rely on the survival analysis methodology, which is based in the modelling of the hazard function. Litter size is studied through linear mixed models. There is no obvious way to perform a multiple trait analysis combining longevity and other linear traits when there are non zero residual correlations between traits (DUCROCQ, 1999). So, approximations must to be used (DUCROCQ, 2001).

The proposed approach aims at summarising the data in such a way that the simplest linear animal model can be used for each trait. This implies the calculation of a “pseudo-record” $y_{t,i}^*$ for each animal i and each trait t . The “pseudo-record” combines individual records pre-adjusted for fixed effects and random effects other than the additive effect. The resultant “pseudo-records” with their weights ($\omega_{t,i}$) can be analysed with the following animal model:

$$y_{t,i}^* = \mu_t + a_{t,i} + e_{t,i}; \text{Var}(a) = A \times \sigma_{a,t}^2; \text{Var}(e_t) = \text{diag}\{1/\omega_{t,i}\} \times \sigma_{e,t}^2 \quad [1]$$

In order to estimate the genetic correlation between the risk of being culled (a trait opposite to longevity) and the number weaned or born alive, an equivalent model to [1] can be used to avoid the heterogeneous residual variance:

$$(\omega_{t,i})^{1/2} \times y_{t,i}^* = (\omega_{t,i})^{1/2} \times \mu_t + (\omega_{t,i})^{1/2} \times a_{t,i} + (\omega_{t,i})^{1/2} \times e_{t,i} \quad [2]$$

With $\text{Var}(\mathbf{a}_t) = \mathbf{A} \times \sigma_{a,t}^2$; $\text{Var}((\omega_t)^{1/2} \times \mathbf{e}_t) = \mathbf{I} \times \sigma_{e,t}^2$

$\text{Cov}(\mathbf{a}_{t1}, \mathbf{a}_{t2}) = \mathbf{A} \times \text{cov}(\mathbf{a}_{t1}, \mathbf{a}_{t2})$; $\text{Cov}([(\omega_{t1})^{1/2} \times \mathbf{e}_{t1}], [(\omega_{t2})^{1/2} \times \mathbf{e}_{t2}]) = \mathbf{I} \times \text{cov}(\mathbf{e}_{t1}, \mathbf{e}_{t2})$

The random regression model [2] is solved keeping constant the variances ratio estimated with the correct models and the original data, in order to just estimate the genetic correlation between the risk of being culled and the others two traits.

Calculation of “pseudo-records” and their associated weight

For born alive (BA) and number at weaning (NW), a two-trait repeatability animal model was used in order to estimate the variance components, and the fixed effects and permanent environment effect estimates to pre-correct the data. The models for both traits included a year-season effect (ys), a physiological state effect (ps) (nulliparous, primiparous suckling, primiparous weaned, multiparous suckling and multiparous weaned), a random permanent environment effect (p) and a random additive genetic effect (a). The REML variance components estimation was carried out using VCE software (GROENEVELD, 1998) and the effects estimation was carried out using the PEST software (GROENEVELD, 1990).

The “pseudo-records” and their weights were calculated as:

$$y_{BA,i}^* = \frac{\sum_{z=1}^{n_{BA,i}} [BA_{ikjz} - (\hat{p}_{BA,i} + y\hat{s}_{BA,k} + p\hat{s}_{BA,j})]}{n_{BA,i}} \quad \omega_{BA,i} = n_{BA,i}$$

$$y_{NW,i}^* = \frac{\sum_{z=1}^{n_{NW,i}} [NW_{ikjz} - (\hat{p}_{NW,i} + y\hat{s}_{NW,k} + p\hat{s}_{NW,j})]}{n_{NW,i}} \quad \omega_{NW,i} = n_{NW,i}$$

where $n_{i,i}$ is the number of kindlings or weanings of doe i and $\hat{p}, \hat{y}s, \hat{p}s$ are estimates of the permanent environment effect and the fixed effects in the model.

For the hazard of being culled for the doe (H), a Cox sire-maternal grandsire frailty model was used to estimate the sire variance of the trait, and once this variance was estimated and transformed into the additive genetic variance, a Cox animal frailty model was fitted in order to estimate the fixed effects and the additive effects. The fixed effects included in both models were: a year-season effect (ys) (time dependent, changing every 3 months), an interaction between cycle order (co) (time dependent with 3 levels; first, second and third and more) and physiological status (ps) (time dependent with 4 levels; pregnant (with positive palpation), suckling, non-pregnant, and pregnant and suckling). These analyses were carried out using the Survival Kit 3.0 program (DUCROCQ and SÖLKNER, 1998).

For this trait, the “pseudo-records” and their weights were calculated following the same approach as in DUCROCQ (2001) for Weibull models. These values were:

$$y_{H,i}^* = \frac{\delta_i}{\omega_i} - e^{\hat{a}_i} + \hat{a}_i \quad \omega_{H,i} = \sum_{T_f=1}^{f_i} \left[d_f \cdot \frac{e^{\bar{x}'_i(T_f) \cdot \hat{\beta}}}{\sum_{j \in R(T_f)} e^{\bar{x}'_j(T_f) \cdot \hat{\beta} + \hat{a}_j}} \right]$$

where δ_i is the variable which shows if the data of the animal i is censored or not, \hat{a}_i is the EBV of the animal i , T_f are the distinct failure times in the whole population, f_i is the time when the animal i dies or is censored, d_f is the number of does culled at time T_f (to correct for ties), $R(T_f)$ is the group at risk at time T_f and $\bar{x}'_i(T_f) \cdot \hat{\beta}$ is the estimate of the vector of all fixed effects affecting animal i at time T_f .

For the analysis of the multiple trait random regression model [2], the program REMLF90 (MISZTAL, 2002), modified in order to keep constant the variance ratios, was used.

RESULTS AND DISCUSSION

Validation

The validity of the “pseudo-records” for longevity was checked by computing the correlation between the EBVs from the Cox animal model and those based on model [1] using the “pseudo-records”, their weight, the additive variance estimated with the Cox sire-maternal grandsire model and a residual variance of 1.0. This correlation should be close to 1.0. In our case this correlation was 0.9988.

For BA and NW the correlation between EBVs from univariate analysis, with the correct models and data, and the estimated ones using model [1] with the “pseudo-records”, their weight and the variance components estimated in the univariate REML analysis, was 0.9999.

Correlation estimation

Table 1 shows the variance components used in the analyses to estimate the correlations between BA and H, and NW and H, in two separate bivariate analyses. The ratios between variance components were kept constant. These values were estimated by single trait analyses for H (Survival Analysis) and by a bivariate analysis for BA and NW (REML)

Table 1.- Variance components used to estimate the correlations

	BA	NW	H
σ_e^2	8.937	5.524	1.0
σ_a^2	1.766	0.546	0.105

The genetic and residual correlations estimated with model [2] between BA and H were -0.012 and -0.23 respectively. The same values estimated between NW and H were -0.014 and -0.061.

The genetic correlations are very low but in the expected direction: a negative correlation implies that when BA or NW are increased, the probability of culling an animal becomes lower and its longevity increases.

Only the environmental correlation between BA and H shows a value clearly different from 0, showing that some environmental factors influencing the hazard of being culled act in the same direction on BA.

These results are in agreement with previous estimations of the effect of the factor “born alive” on the hazard (GARREAU *et al.*, 2001; SÁNCHEZ *et al.*, 2003). In both works, an increase in BA leads to a lower risk of being culled.

These results show that both longevity and litter size are not antagonistic objectives in breeding programs, because the selection in one of them practically does not influence the other.

ACKNOWLEDGEMENTS

This work has been supported by the Spanish Research Project AGL2000-0595-C03 (CYCIT).

REFERENCES

- BASELGA, M., BLASCO, A. 1989. Mejora genética del conejo de producción de carne. Edit. Agroguias mundi-prensa. Madrid, Spain.
- CIFRE, J., BASELGA, M., GARCÍA-XIMÉNEZ, F., VICENTE, J.S. 1998. Performance of a hyperprolific rabbit line. I. Litter size traits. *J. Anim. Breed. Genet.* **115**, 131-138.
- DUCROCQ, V., SÖLKNER, J. 1998. The survival kit V3.0, a package for large analyses of survival data. 6th World Congress on Genetics Applied to Livestock Production, Vol. 27, Armindale, Australia, pp. 447- 450.
- DUCROCQ, V. 1999. Topics that may deserve further attention in survival analysis applied to dairy cattle breeding – some suggestions. In: Proceeding of International Workshop on Genetics Improvement of Functional Traits in Cattle (GIFT); Longevity. Jouy-en-Josas, France. Bulletin No 21, pp. 181 – 189.
- DUCROCQ, V. 2001. A two step procedure to get animal model solutions in Weibull survival models used for genetic evaluations on length of productive life. In:

- Proceedings of the 2001 interbull meeting. Budapest, Hungary. Bulletin No 27, pp. 147-152.
- ESTANY, J., BASELGA, M., BLASCO, A., CAMACHO, J. 1989. Mixed model methodology for the estimation of genetic response to selection in litter size of rabbits. *Livest. Prod. Sci.* **21**: 7-75.
- GARREAU, H., LARZUL, C., DUCROCQ, V. 2001. Analyse de longévité de la souche de lapins INRA 1077. 9^{èmes} Journ. Rech. Cunicole, Paris, France, pp. 217 - 220.
- GROENEVELD, E. 1990. Pest user's manual. Institute of Animal Husbandry and Animal Behavior, FAL. Germany.
- GROENEVELD, E. 1998. VCE4 user's guide and reference manual, version 1.3. Institute of Animal Husbandry and Animal Behavior, FAL. Germany.
- MISZTAL, I. 2002. REMLf90 Manual.
<http://nce.ads.uga.edu/~ignacy/numpub/blupf90/docs/remlf90.pdf>
- RAMÓN, J., RAFEL, O. 2002. 1991-2000. Diez años de gestión global en España. In: Expoaviga 2002, X jornada cunícola, Barcelona, pp.113–117.
- ROSELL, J.M. 2003. Health status of commercial rabbitries in the Iberian peninsula. A practitioners study. *World Rabbit Sci.* **11**, 157-169.
- SÁNCHEZ, J.P., PEIRÓ, R., SILVESTRE, M.A., BASELGA, M. 2003. Análisis de los factores que influyen en la supervivencia del conejo de carne. In: Proceeding of X Jornadas sobre Producción Animal, Zaragoza, España, Vol. Extra, N° 24 – Tomo II, pp.459-461.