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Genetic analysis models and selection in small populations of meat rabbits

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SUMMARY - An univariate mixed model approach, concerning genetic analysis, genetic merit prediction and estimation of response to selection, is shown. Models are proposed to analyse litter size and growth traits in meat rabbit populations. A model to analyse genetically lung lobe injuries is also given. Results of the application of the anterior methodology to four strains of meat rabbits are pointed out, referring the largest size of the analysis completed.

Key words: Rabbit mixed models, genetic value prediction, variance components, growth and reproduction traits.

RESUME - "Modèles d'analyse génétique et de sélection dans des populations d'effectif limité de lapins pour la production de viande". On présente un modèle mixte univariable concernant l'analyse génétique, la prédiction de la valeur génétique et l'estimation de la réponse à la sélection. Les modèles sont utilisés pour analyser la taille de portée et les caractères de croissance dans des populations de lapins à viande. Un modèle pour l'analyse des lésions pulmonaires à incidence génétique est aussi donné. Les résultats de l'application de la méthodologie à 4 lignées de lapines du Département de Sciences Animales à Valencia sont donnés ainsi que l'indication de la plus grande taille de l'analyse permise par la procédure établie et le matériel informatique utilisé (programmes APL, ordinateurs PC ou PS avec 640 K de mémoire centrale et disque dur). Dans le but de simplifier les calculs dans la méthode de prédiction de la valeur génétique on fait une comparaison entre valeurs d'index classique et BLUP.

***Mots-clés:** lapin, modèle mixte, prédiction de la valeur génétique, composantes de la variance, reproduction, croissance.*

Introduction

Important traits in meat rabbit production are those related to growth, reproduction and rusticity, including resistance to digestive and respiratory diseases. Genetic work is closely concerned with these traits. When the size of the populations is small, items such as inbreeding and genetic drift control, or use of the relevant information which originates in the population, becomes important.

It is possible to classify the genetic work into three different classes: genetic analysis of the traits, selection methods and evaluation of the genetic response.

In this paper we discuss the approach used by the Departamento de Ciencia Animal de la E.T.S.I.A. in the analysis, selection and control of four different rabbit strains. Their size ranged between 80-120 females and 20-25 males by generation. Two strains were selected by weaning litter size and the others by growth rate between weaning at 28 days and slaughter at 70-77 days.

The principal part of our approach includes a mixed model methodology and allows the treatment of analysis, selection and control problems, as a unity. Our approach needs to compute the numerator relationship matrix for all individuals that belong to or have belonged to each strain from its foundation. This point is an important one if we want to take account of all information produced and if we want to use genetic analysis methods unbiased with selection.

The models and methods that will be shown later are not perfect or comprehensive solutions to the problems faced by a center or organisation involved in the genetic improvement of meat rabbit strains. We think that the solutions are reasonable. For the time being APL programmes have been written and they run on PC or PS computers with 640 K of central memory and hard disc.

1. Computing the A and A^{-1} matrices

We name A the numerator relationship matrix between the individuals involved in the analysis or evaluation. Matrices related with A, are:

$$A^{-1}, L \text{ and } L^{-1}$$

A^{-1} and L^{-1} are, respectively, the inverses of A and L. L is an inferior triangular matrix, Cholesky factorization of A. We follow HENDERSON (1976) and QUASS (1976) to compute the matrices before. Our interest in one or more of them depends on the actual problem in which we are involved.

Computing the matrices before is easier if no inbreeding is assumed in the populations. In this case, the computations are of order n (number of individuals).

The order is n^2 when the inbreeding is considered. When the inbreeding in the populations is small the first approach is good enough. We have not observed differences in the predictions of genetic values when we computed A^{-1} by one or another method (ESTANY et al., 1988a).

The matrix A^{-1} is necessary for the BLUP method of predicting genetic merit and for the ML, REML or approximate methods of estimating variance-covariance components. The latters could also need A, L or L^{-1}.

Our longest problem which required the computation of A^{-1}, A and L, involved data of more than 20500 individuals, 1133 of them being parents. The model used was an animal model including maternal effects.

2. Genetic analysis of lung injury

A model was developed with the intention of analysing the nature of variation in lung injury. The lung lobes were inspected just after slaughtering at 70 days, and each of the four lobes was scored from 0 to 5 to determine the extension of its lesions. A lobe scored with 0 has no lesion, and 5 means maximun extension of lesions. The model proposed was,

$$Y_{oesdip} = L_o + S_e + B_s + B_d + M_d + C_i + e_{oesdip}$$

Y- score of the p-th (O to 5) lobe of the i-th rabbit.

L- fixed effect of the parity (first, second, third and following).

S- fixed effect of e-th year-season (1 to 5).

B_d (B_s)- breeding value of the dam (sire) of i-th rabbit (random).

M- maternal effect of d-th dam on its progeny scoring (random).

C- effect of the i-th rabbit on its four lobes after considering the above effects (random).

e- error component.

The aim was to estimate σ_A^2 (additive variance) = $4\sigma_B^2$, σ_M^2, (maternal variance), σ_c^2 (individual variance), and σ_e^2 (error variance). The methodology used was a ML one (SEARLE, 1979), the relationships between parents were considered and a direct method was used to solve the equation system and the inverse needed. The method is based on the Reverse CUTHILL-MCKEE algorithm, the CHOLESKY factorization and partitioned matrices (GEORGE and LIU, 1981). It is useful for large, sparse, positive-definite and symmetric matrices. Our aim was to save computing time and memory with the method, mainly memory. However, we now think that with the previous model and considering the relationship matrix it would have been better to have applied an indirect method.

The results (BASELGA et al., 1988) shown in the Table 1, give scope for achieving progress when selecting for resistance to respiratory diseases.

Table 1.

ESTIMATES OF THE HERITABILITIES OF LOBE SCORE (h^2) AND AVERAGE SCORE (h^2_4), AND REPEATABILITY OF LOBE SCORE (r) IN STRAINS R, B, A AND V. S.E. STANDARD ERROR

Strain	h^2 ± SE	h^2_4 ± SE	R ± SE
R	0.18 ± 0.09	0.28 ± 0.16	0.53 ± 0.04
B	0.17 ± 0.10	0.28 ± 0.14	0.55 ± 0.04
A	0.13 ± 0.05	0.22 ± 0.09	0.45 ± 0.02
V	0.07 ± 0.03	0.12 ± 0.05	0.50 ± 0.02

3. Genetic analysis and genetic response prediction in growth traits.

3.1 PREDICTION OF THE RESPONSE

The genetic change was analysed in four strains of rabbits, two selected for growth rate and two for litter size at weaning. The genetic change was estimated for the growth rate between 28 and 77 days, and for the individual weights at those dates. The model developed for the analysis was one of parents (ESTANY et al., 1988b.) This model was,

$$Y_{ijklm} = L_i + E_j + B_k + B_l + P_l + e_{ijklm}$$

where,

L is the parity effect (fixed)

E is the year season effect (fixed)

B is the sire additive effect (random)

B is the dam additive effect (random)

P is the permanent non additive effect of the doe (random)

e is the residual (random)

The results of its application are shown in the Tables 2 and 3 (ESTANY et al., 1988b) and we can say that the model fits well to the data, monitoring the changes by generation in the three traits.

A sire and dam model is a less adequate approach than an animal model to a prediction problem but it needs less computing time and for this reason it was used initially.

The largest analysis made with this model referred to 8 generations of selection of a strain involving 754 dams and 145 sires.

Table 2

AVERAGES OF PREDICTIONS OF ADDITIVE VALUES OF GROWTH RATE (GR), SLAUGHTER WEIGHT (SW) AND WEANING WEIGHT (WW) OF A LINE SELECTED FOR GROWTH RATE (LINE B) (GRAMS).

Generation	DAMS			SIRES		
	WW	SW	GR	WW	SW	GR
1	3.3	12.7	10.0	11.7	44.3	34.9
2	9.6	50.5	47.3	17.9	88.5	79.0
3	15.7	92.4	88.9	22.8	137.9	136.4
4	24.4	129.6	121.7	35.5	164.6	145.4
5	33.2	166.1	151.3	31.4	164.4	152.3
6	31.9	183.9	174.3	29.0	176.7	171.5

Table 3

AVERAGES OF PREDICTION OF ADDITIVE VALUES OF GROWTH RATE OF TWO LINES SELECTED ON NUMBER OF WEANED RABBITS (GRAMS).

Generation	LINE A		LINE V	
	DAMS	SIRES	DAMS	SIRES
0	-	-	11.2	44.5
1	8.9	44.9	29.7	62.9
2	42.8	29.0	65.7	81.4
3	31.8	45.3	69.0	68.1
4	47.1	62.5	69.8	60.7
5	62.1	72.7	-	-
6	86.1	91.5	-	-
7	84.7	81.0	-	-

3.2 GENETIC ANALYSIS

ML, REML and others are iterative methods designed to estimate variance-covariance components. They need to solve a mixed model including the genetic value of sires, dams or individuals and, consequently, it is possible to evaluate the genetic change through generations. These methods are more complex and require more computing time than those used only for the prediction of the genetic value. However, we are now using an animal model with maternal effects. The model is,

$$Y_{ijml} = L_i + E_j + A_m + P_l + E_{ijml}$$

where,

L and P have been defined in 3.1

A is the individual additive effect (random)

e is the residual (error)

In this model it is assumed that the individual additive effects are related through the matrix A, and that there is no correlation between the different P_l and between these and the additive effects.

The method used to estimate σ_A^2 and σ_P^2 is close to REML. It is the pseudo-expectation approach derived by SCHAEFFER (1986), that does not need to compute the inverse matrix required by REML. The procedure is iterative, and each iteration, a mixed model is solved taking advantage of the reduced animal model (QUASS, 1984) and the Gauss-Seidel method. The largest problem treated with this model referred to 20517 individuals, 1033 of them being parents.

4. Breeding value prediction and genetic analysis of reproductive traits.

4.1 Breeding value prediction

Two strains are being selected by litter size at weaning (28 days) in the Departamento de Ciencia Animal de la E.T.S.I.A., as we said before.

The procedure is to evaluate sires and dams by generation with the aim of selecting the progeny from the best matings. A different method of evaluation is used for each strain. One (BASELGA et al., 1984) is a usual selection index that computes breeding value considering the own data (if we are evaluating a dam), and the data from its mother, full and half sisters according to the classical model (ROUVIER, 1977). The method accounts for the structure and amount of the available information that is variable between individuals, it does not consider environmental effects and is very easy to compute.

The other method of evaluation is a BLUP with the following model,

$$Y_{ijkl} = L_i + E_j + A_k + P_k + e_{ijkl}$$

L_i is the parity-lactation state of the does (fixed). There are three levels, nulliparous N (i=1), lactating doe L (i=2), non nulliparous and non lactating doe NL (i=3) at the moment of mating.

E is the year-season in which the parity occurred (fixed). There is a maximun of 22 levels.

A is the additive value of the doe or the buck.

P is the permanent non genetic effect on the doe (random).

e is the temporary environmental effect on the doe.

Y is the 1th size of the litter parity of the kth doe, made in the jth year-season when the parity-lactation state of the doe was i.

The relations between variables A_k and P_k, are the same as pointed out in 3.2 for the analogous variables.

An improvement of 0'05-0'16 rabbits in weaning litter size by generation has been estimated with the previous model (ESTANY et al, 1987), applied to the totality of generations in every strain.

In order to simplify, as much as possible, the evaluation methods in progeny selection from the best matings, the results (Table 4) of ESTANY et al. (1988a) are relevant. These show that the loss of efficiency is negligible when the matrix A is computed assuming no inbreeding; data of two generations are only considered and index or BLUP are used. The evaluations between both methods are highly correlated. This might be expected if it is accepted that the main difference between both is concerned with the fixed effects. These are well considered by BLUP but not by index, but this is not important when the data arise in a sole selection nucleous in a relatively short period of time.

4.2 Genetic analysis of reproductive traits.

Models have been proposed to analyse litter size at birth, weaning and slaughtering (77 days) for the first, second or third parturition. The model for the 2-nd or 3-rd parturition is,

$$Y_{ijk} = L_i + E_j + A_k + e_{ijk}$$

L_i- the parity-lactation state of the does (i=1, lactating doe; i=2, non lactating doe at the moment of the mating. fixed).

E the year-season effect (fixed).

A the individual additive effect (random).

e the residual (random).

The model for the first parturition is the same, omitting L_i- The methodology used to estimate σ is the same as the one described in 3.2

The h^2 estimated with this model are close to 0'10 for the litter size at first parturition, near zero at third and intermediate at second. The improvement in litter size

Table 4

CORRELATIONS BETWEEN PREDICTED ADDITIVE VALUES OF BLUP, INCLUDING A DIFFERENT AMOUNT OF INFORMATION AND FAMILIAR INDEX. CORRELATION BETWEEN RANKING NUMBER OF THE EVALUATED ANIMAL IN THE SAME CASE. B1, B2, B3 AND B4: BLUP INCLUDING INFORMATION OF 4, 3, 2 AND 1 GENERATION RESPECTIVELY. IX FAMILIAR INDEX. BO: BLUP INCLUDING INFORMATION OF 5 GENERATIONS AND USING INBREEDING COEFFICIENT. SIRE AND DAMS INFORMATION ARE CONSIDERED. LINE V IS USED.

Method	BLUP (BO)		INDEX (IX)	
	Predictions	Rankings	Predictions	Rankings
B1	1.00	1.00	0.85	0.86
B2	0.99	0.99	0.85	0.86
B3	0.96	0.96	0.88	0.89
B4	0.77	0.74	0.69	0.73
IX	0.85	0.86	–	–

referred in 4.1. agrees with the one estimated for lst parturition with these models but not for the other parturitions. The explanation could be the underestimation of h^2, which is more important as the order of parturition increases, due to the association between year season and genetic value. If this is true, it would be necessary to analyse the litter sizes of the successive parturitions at the same time, considering them as either different traits or repeated measures of the same trait. At this moment our work is concerned with this task and with the extension of the methodology in order to consider the growth and reproductive traits together.

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