

GENETIC ANALYSIS ON LUNG INJURY IN FOUR STRAINS OF MEAT RABBIT

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INTRODUCTION

Respiratory troubles is one of the most important diseases associated with rabbit production. Their significance is due to their high frequency, to the economic loses that they cause and to the difficulty of control.

The organisms responsible are Pasteurella multocida and Bordetella bronchiseptica, the frequency of the first being higher (RENAULT, 1984). This organism seems to be ubiquitous in all rabbit farms. It is transmitted by air and through direct contact between animals or with infected material, such as the watering nipples (PATTON et al., 1984).

The symptoms vary with the severity of the disease and can include rhinitis, broncho-pneumonias, genital infections, torticollis, abscesses and death (GODARD, 1980). All these symptoms have important economic consequences, thus it would be interesting its control. Elimination of sick animals, hygienic environment, vaccination, medicamentous treatments and others have revealed themselves as insufficient to an effective control of this disease.

It could also be beneficial to develop strains selected on their genetic resistance to the respiratory diseases.

The authors only know the announcement of the OSU Rabbit Research Center (1981, 1982) about the development of a pasteurella resistant strain. Unfortunately, the methodology used to develop this strain has not been reported. Also, natural resistance to pasteurella infections has been pointed out in rabbits (LELKES et al., 1985).

There are several mechanism involved in the resistance of animals to bacterial infections. In most of them genetic variation (EDFORS-LILJA, 1986) has been detected. The above information should encourage some research specifically devoted to the improvement of our knowledge of the genetic bases for resistance to respiratory diseases.

The lung is one of the main targets of these diseases. Our aim is to analyse the nature of the variation in lung injury, the lung lobes being inspected just after slaughtering.

MATERIAL AND METHODS

Four strains of rabbits selected to improve their litter size at weaning (A, V) or their post-weaning growth rate (R, B) were used. The strain A is a New Zealand White, the B is Californian and R and V are synthetics. Rabbits are mated at first when they are 4 months old. They are mated again nine days after kindling. Weaning is made at 28 days and the growing period finished at 70 days. At this time the rabbits are slaughtered and their lungs are immediately inspected. Each of the four lobes is scored from 0 to 5 to determine the extension of its lesions. A lobe scored with 0 has not lesion, and 5 means maximum extension of lesions.

The study began in march-1985. It spent 15 months and was divided into 5 seasons of three months duration. The sire, dam, parity number and season associated with every progeny scored were recorded, as well as the pedigree of the sires and dams.

The number of sire, dams, litters and progeny by strain are shown in Table 1.

Table 1. Number of sires, dams, litters and progeny scored for lung lesions in strains R, B, A and V.

Strain	Sires	Dams	Litters	Progeny
R	29	103	228	748
B	32	104	174	528
A	49	194	352	1230
V	45	218	563	2267

The model proposed for the analysis was:

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

being,

Y - score of the p-th (1 to 4) lobe of the i-th rabbit

L - fixed effect of the o-th 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 analysis was conducted in two steps. The first step takes advantage of the balanced condition of data at level of rabbit to estimate σ_e^2 separately. The second step analyses, by mixed model methodology and a maximum likelihood approach (SEARLE, 1979), the rabbit average score Y_{oesdi} .

To solve the mixed model associated to Y, the relationships between parents were considered and a direct method was used. 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.

RESULTS AND DISCUSSION

Maximum likelihood requires an iterative algorithm. After five iterations convergency was reached in the total output of the analysis, only with the exception of $\hat{\sigma}_M^2$ which continued going down. Computing cost forced us to stop the process after the fifth iteration, however $\hat{\sigma}_M^2$'s were enough low to consider the results reliable.

Table 2 shows the estimation of the parity effects on the lung score expressed as differences between them and the first parity.

The effect of parity is quite low. The maximum difference within strain being 0.27 in strain R. It is also remarkable that the effect increases when the litter number increases only in strain V. This result can be expected by accepting that the dam is an important factor for transmitting the disease and the risk of transmission increases with the age of the dam (PATTON et al., 1984). A doe shows symptoms of respiratory troubles when is culled after weaning its litter. The strain V has been the less culled, and the strain B the most; this culling could account for the opposite order of the effects in both strains.

The meaning of table 3 is the same of table 2, but referred to year-season effects. The importance of these effects is higher than the importance of the parity ones. The maximum difference is 0.83 points corresponding to the difference between the best year-season for the strain B (5) and the worst (3). With the only exception of strain B, the worst year-season effect on lung injury is the year-season number 4.

Table 2. Number of rabbits scored (N) and estimates (X) of the parity effects expressed as differences between them and the first litter in strains R, B, A and V.

Strain		Parity			
		1	2	3	4 or +
R	N	215	173	121	239
	X	0	-0.10	0.14	-0.13
B	N	251	139	74	64
	X	0	-0.02	-0.09	-0.15
A	N	517	393	147	173
	X	0	0.02	-0.16	0.05
V	N	654	549	378	686
	X	0	0.02	0.15	0.21

The reason could be that it include data from december 1985 to february 1986, the coldest season of the five studied.

Table 4, shows the estimates of variance components corresponding to breeding values ($\hat{\sigma}_B^2$), maternal effects ($\hat{\sigma}_M^2$), individual effects ($\hat{\sigma}_C^2$) and intra-individual effects ($\hat{\sigma}_e^2$). The phenotypic variances corresponding to the values of Table 4 are 2.28, 2.17, 2.76 and 2.15 for strains R, B, A and V, $\hat{\sigma}_C^2$ has significantly higher values than $\hat{\sigma}_M^2$, $\hat{\sigma}_M^2$ has values like $\hat{\sigma}_B^2$ (0.25 $\hat{\sigma}_A^2$, $\hat{\sigma}_A^2$ being the additive variance) and $\hat{\sigma}_C^2$ and $\hat{\sigma}_e^2$ also have similar values.

The estimates of heritabilities and repeatabilities are in Table 5. The repeatability ranges between 0.45 and 0.55. These high values indicate the similarity of the injury of the four lung lobes of a rabbit.

Table 3. Number of rabbits scored (n), and estimates (x) of year-season effects (x) expressed as differences between them and the first year-season in strains R, B, A and V.

Strain		Year-season				
		1	2	3	4	5
R	N	153	176	82	168	169
	X	0	-0.08	-0.26	0.03	-0.42
B	N	98	136	108	109	77
	X	0	0.67	0.75	0.01	-0.08
A	N	188	567	195	177	173
	X	0	0.28	0.21	0.32	0.04
V	N	409	971	334	289	264
	X	0	0.02	-0.12	0.22	-0.03

Table 4. Estimates and standard errors (SE) of the variances of breeding values ($\hat{\sigma}_B^2$), maternal effects ($\hat{\sigma}_M^2$) individual effects ($\hat{\sigma}_C^2$) and error effects ($\hat{\sigma}_e^2$) in strains R, B, A and V.

Strain	$\hat{\sigma}_B^2 \pm SE$	$\hat{\sigma}_M^2 \pm SE$	$\hat{\sigma}_C^2 \pm SE$	$\hat{\sigma}_e^2 \pm SE$
R	0.10 \pm 0.05	0.06 \pm 0.06	1.03 \pm 0.08	0.99 \pm 0.03
B	0.09 \pm 0.05	0.13 \pm 0.08	0.83 \pm 0.09	1.03 \pm 0.04
A	0.09 \pm 0.03	0.02 \pm 0.04	1.15 \pm 0.08	1.41 \pm 0.03
V	0.04 \pm 0.02	0.04 \pm 0.02	0.97 \pm 0.05	1.06 \pm 0.02

Table 5. Estimates of the heritabilities of lobe score (h^2) and rabbit average score (h^2_4), and repeatability of lobe score (r) in strain R, B, A and V. S.E. Standard error

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

The estimates of the heritability range between 0.07 and 0.18 for the lobe score, and between 0.12 and 0.28 for the rabbit average score.

There is a respiratory disease in swine called atrophic rhinitis caused by Bordetella bronchiseptica as principal agent. EDFORS-LILJA (1986) reviews heritability estimates of resistance to this disease finding out that these estimates range from 0.12 (KENNEDY and MOXLEY, 1980) to 0.60 and that most of the estimates are below 0.25. These results mean that there is a genetic bases of resistance to atrophic rhinitis in swine.

Our results have the same meaning and show that there is some scope to improve the genetic resistance to respiratory diseases in rabbit population. Apparently it was done by the OSU Rabbit Research Center (1981) but unfortunately the pasteurilla-resistant strain seems to be lost.

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Rabbits from four strains, slaughtered at 70 days, were scored just after for lung lesions. Every lobe was scored between zero and 5 (0, meaning no lesions; 5, meaning maximum injury). The number of rabbits scored were 748 in the strain R, 528 in strain B, and 1230 and 2267 respectively for the strains A and V. The scoring of every lobe was analysed under a model which included: the litter number and the year-season as fixed effects, the breeding value of the sire and the dam, the maternal effect and the individual effect on the four lobes, as random effects.

The estimation of the variance components, related to the random effects was made by the maximum likelihood method. The equations of the model were solved by using a direct method, developed for symmetric, definite positive sparse matrices (the reverse Culthill-McKee algorithm and Cholesky factorization).

The score heritability estimates of each lobe ranged between 0.07 ± 0.03 and 0.18 ± 0.09 . The repeatability estimates ranges between 0.45 ± 0.02 and 0.55 ± 0.04 . These results show that the genetic basis for resistance to the lung lesions is substantial.

The estimates of the litter number and year-season effects were not significant or consistent between strains.

ANALISIS GENETICO DE LAS LESIONES PULMONARES EN CUATRO LINEAS
DE CONEJO DE CARNE

Tras el sacrificio, a los 70 días de edad, se puntuaron los lóbulos pulmonares de conejos pertenecientes a cuatro líneas, respecto a la extensión de las lesiones que presentaban. Una puntuación de 0 significaba que no habían lesiones y una puntuación de 5 indicaba que la extensión de las lesiones era máxima. Se puntuaron 748, 528, 1230 y 2267 conejos en las líneas R, B, A y V respectivamente. El carácter fue analizado a través de un modelo mixto que incluía el número de camada y el año-estación como efectos fijos, y el valor de mejora del padre, de la madre, los efectos maternos y los individuales sobre los cuatro lóbulos como efectos aleatorios.

Las componentes de varianza se estimaron por máxima verosimilitud. Las ecuaciones del modelo se resolvieron a través de un método directo desarrollado para matrices simétricas, definidas positivas y vacías (algoritmo de Cuthill-McKee invertido y factorización de Cholesky).

Las estimas de la heredabilidad de la puntuación de cada lóbulo oscilaban entre 0.07 ± 0.03 y 0.18 ± 0.09 y las de la repetibilidad entre 0.45 ± 0.02 y 0.55 ± 0.04 indicando que la base para la resistencia genética a las lesiones pulmonares es apreciable. Las estimas de los efectos del número de camada y del año-estación no mostraron significación, ni consistencia entre estirpes.

