GENETIC VARIABILITY OF THE RESISTANCE TO EPIZOOTIC RABBIT ENTEROPATHY (ERE) : NEW RESULTS

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INTRODUCTION

Disease resistance is a major challenge in livestock production with large research efforts worldwide. The outbreak of epizootic rabbit enteropathy (ERE) in 1997 has initiated many research programs concerning digestive disorders. In a recent study Rochambeau *et al*. (2005) have analysed the genetic variability for the resistance to three digestive stresses: inoculation of coccidia, fibre deficient diet, and experimental reproduction of epizootic rabbit enteropathy (ERE). There was a significant sire effect for mortality and morbidity in the two first trials but only for morbidity in the experimental reproduction of ERE trial. The aim of this paper is to provide some complementary results about the resistance to ERE by analysing a new trial involving an experimental reproduction of the disease with the INRA TEC3 inoculum.

MATERIAL AND METHODS

Animals. 22 bucks of the 1777 INRA lines produced 2 batches (B1 and B2) of young rabbits by inseminating 220 does two times with a 6 weeks gap. Young rabbits were identified and weighed at birth. A total cross-fostering was applied the following day in order to minimize maternal effects. Young rabbits were weaned at 31 days. Offspring of each buck were divided in two groups: 15 young rabbits were inoculated and 8 young rabbits were bred in an other place as a control group. Each batch consisted of 330 inoculated animals and of 176 control animals. The inoculated rabbits received 500µl of the inoculum INRA TEC3 (Licois *et al*, 2005) by oral administration. They were weighed and checked for clinical symptoms (bloated abdomen, diarrhoea) 5 days (D5), 12 days (D12), 19 days (D19), 26 days (D26) and 33 days (D33) after the inoculation. Individual mortality was recorded daily. The control animals were weighed at D12 and D33.

Traits analysed. Mortality, clinical symptoms and growth rate were used to assess individual response at each measured time point (D5, D12, D19, D26 and D33). The growth rate of period D0-D12 was declared abnormal for individual inoculated animals when it was inferior to the average growth of its control sibs minus two standard deviations. Four binary indexes were defined. Mortality was equal to 1 if the young rabbit was dead before D33 and equal to 0 otherwise. The diarrhoea index was equal to 1 when a rabbit presented at least one diarrhoea symptom during the testing period and was equal to 0 otherwise. The third index was abnormal growth at D12 (0, 1). The last index, resilience, dealt with survival and growth: A resilient rabbit was alive at D33 with a normal growth i.e. with an abnormal growth index equal to 0. A

good resistance is characterized by values of mortality, diarrhoea and abnormal growth indexes equal to 0 and by values of resilience index equal to 1.

Statistical analyses. The genetic variability of resistance was investigated using two methods:
The sire effect was estimated for the four binary indexes with a logistic regression using the "logistic" procedure of the SAS® (1999) software. The fixed effects batch (2 classes), sector of the shed (3 classes), birth weight (covariate) and presence of diarrhoea (except for the diarrhoea index) were also tested.
Genetic parameters were estimated with the REML methodology using the ASREML software (Gilmour *et al*., 2002). A threshold model (probit function) was applied to estimate the genetic variability of binary indexes, using a sire model. After a significance test, the fixed effect batch (2 classes) was fitted in the model for all traits. The linear covariate of birth weight was also included in the model for the abnormal growth index. The sire effect was included for all traits as a random effect.

RESULTS AND DISCUSSION

Description of mortality and morbidity. The evolution of cumulated mortality is given in figure 1. Mortality was higher in the batch 1 (76%) than in the batch 2 (27%). Nevertheless mortality occurred sooner in the batch 1 than in the batch 2. These results are explained by a colibacillus attack (E. coli 0103) which occurred in batch 1 and clearly increased mortality in this batch.

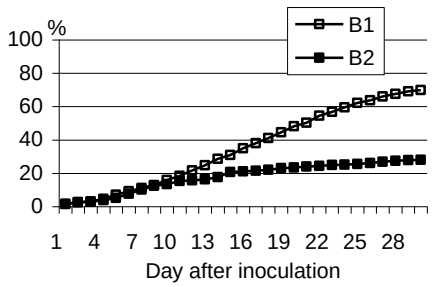

Figure 1 : Cumulative mortality in batch 1 (B1) and in batch 2 (B2)

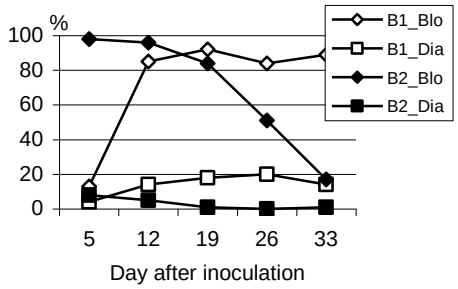

Figure 2 : Percentage of alive rabbits with bloated abdomen (Blo) and with diarrhoea (Dia) in batch 1 (B1) and in batch 2 (B2)

The evolution of disease symptoms is presented in figure 2. On average in the two batches, 83% of the rabbits showed at least one bloated abdomen and 21% suffered at least one time from diarrhoea. Bloated abdomen symptoms were more numerous in the batch 2 (94%) than in the batch 1 (72%) while the frequency of diarrhoea symptoms was higher in the batch 1 (30%) than in the batch 2 (13%). The morbidity profile was different between the two batches: The frequency of diarrhoea and bloated abdomen was maximum just after the inoculation in the batch 2, and then decreased steadily. In the batch 1, the frequency of disease symptoms was maximum in the middle of the testing period, i.e. between 2 and 4 weeks after the inoculation.

Genetic variability. Table 1 presents the results of the logistic regression. Sire effect was not significant for mortality index which reflected a low variability between sires of the average mortality of their offspring (μ_{sire}=52%, standard error between sires=8%). The low genetic variability of mortality was also confirmed by the heritability estimate of this trait (0.05) given in the table 2. Licois *et al*. (2005) have also demonstrated that the mortality response is not correlated with the inoculum's dose: Mortality can be stronger with a low dose than with a high dose. These results suggest that mortality is not a valuable criterion to measure the intensity of the pathology of this disease.

Table 1. Significance of the fixed effects for mortality, diarrhoea, abnormal growth and resilience indexes

Response index	Frequency	Significance of tested effects				
		Sire	Batch	Sector	Birth weight	Presence of diarrhoea
Mortality	52%	NS	***	NS	NS	*
Diarrhoea	21%	*	***	NS	NS	-
Abnormal growth at D12	69%	**	***	NS	*	***
Resilience	27%	**	***	NS	NS	***

Table 2. Estimates of heritability (± standard error) for mortality, diarrhoea, abnormal growth and resilience indexes

	Mortality index	Diarrhoea index	Abnormal growth index	Resilience index
Heritability	0.05 ± 0.05	0.21 ± 0.16	0.38 ± 0.21	0.08 ± 0.07

There was a significant sire effect for the diarrhoea index ($p < 0.05$), for the abnormal growth index ($p < 0.01$) and for the resilience index ($p < 0.01$). The risk of diarrhoea was 6.5 times lower for the best sire than for the worst sire. The risk of abnormal growth was 9 times lower for the best sire than for the worst sire. Finally the chance to have resilient offspring was 9.5 higher for the best sire than for the worst. Even if heritability estimate of resilience was low (0.08), it was a better criterion than mortality to discriminate sires for resistance to ERE, because this criterion involved the abnormal growth index which was more heritable (0.38). The batch effect was significant for all binary indexes, reflecting the difference of response between the two batches. The presence of diarrhoea was associated with a higher risk of mortality (relative risk=1.3), a higher risk of abnormal growth (relative risk=1.3) and a lower frequency of resilient rabbits (relative risk=9.1).

It was finally possible to find some sires with several favourable responses of their offspring: few abnormal growths, few diarrhoea symptoms and a good resilience like sires 4 and 6 presented in the figure 3 which give the rank of sires according to the results of the logistic regression. On the contrary, some other sires cumulated several unfavourable characteristics, like sire 14, 19 and 20.

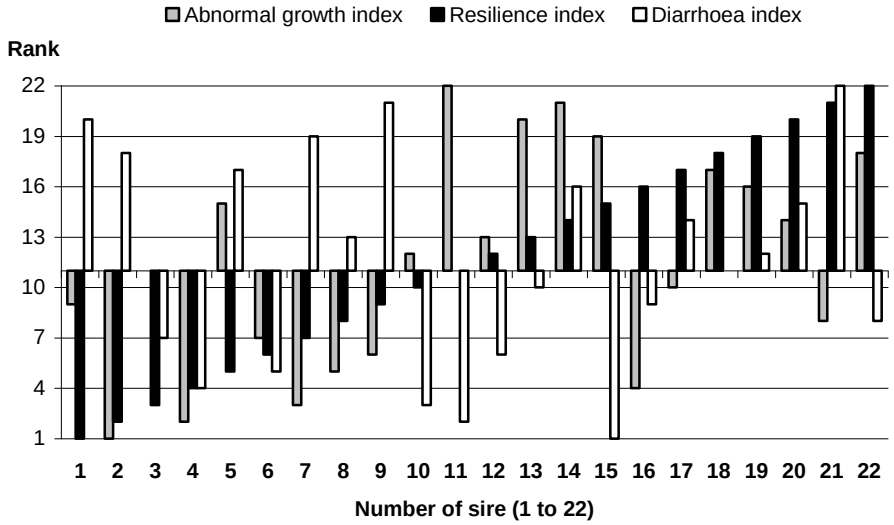

Figure 3. Rank of the 22 sires for abnormal growth, diarrhoea and resilience indexes based on the results of the logistic regression

CONCLUSION. In this new experiment aiming to estimate the genetic variability of resistance to ERE, the response to inoculation was very different between the 2 batches, especially for mortality. The high mortality of batch 1, partly caused by a coli bacillus attack, may have affected results of the analysis of that criterion for which no significant effect of the sire was found. Abnormal growth, diarrhoea and resilience indexes allowed a better discrimination of sires and presented higher estimates of heritability. Further analyses are required to estimate the genetic correlation between resistance traits and productivity traits in order to define selection criterion that could be used in commercial breeding programs

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