

***PASTEURELLA MULTOCIDA* EXPERIMENTAL INFECTION 3): RELATIONSHIP BETWEEN RESISTANCE TO DISEASES AND PRODUCTION TRAITS IN RABBITS RAISED IN COMMERCIAL FARMS**

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ABSTRACT

Pasteurellosis is the first cause of female mortality in rabbit farms. The RELAPA project aims at studying the genetic determinism of resistance to pasteurellosis. 955 rabbits produced by 65 sires from 6 commercial lines were inoculated at 6 weeks of age with a pyogenic strain of *Pasteurella multocida* (*Pm*) and were monitored during 14 days. These rabbits were scored for resistance to pasteurellosis from 0 to 4 by taking into account post-mortem examinations. Fifty five sires having at least 10 inoculated offspring produced also 9943 rabbits tested for health and growth and 1468 females with 6676 litters tested for reproduction in commercial farm conditions. Weaning and final growing weights were significantly higher in offspring of resistant sires than in offspring of susceptible sires (+7 g, $P=0.04$ and +14 g, $P=0.02$ respectively). On the contrary, total number born and number born alive were significantly lower in daughters of resistant sires than in daughters of susceptible sires (-0.27, $P=0.02$ and -0.41 $P=0.003$). Prevalence of digestive diseases and infectious diseases were significantly lower in the resistant growing rabbits than in the susceptible ones (-1.9 point, $P=0.006$ and -3.2 points, $P < 0.001$ respectively). This result suggest that resistance to pasteurellosis assessed by an experimental infection using a single strain of *Pasteurella multocida* is favorably correlated to resistance to other infectious diseases.

Key words: pasteurellosis, resistance, rabbit.

INTRODUCTION

Pasteurellosis is one of the most common bacterial infection in commercial rabbit farms (Lopez *et al.*, 2005). Genetic selection for resistance to pasteurellosis is therefore an important issue. Following the collection and characterization of *Pasteurella multocida* strains (Helloin *et al.*, 2013), the RELAPA project (Genomics for the Genetic Resistance of Rabbits to Pasteurellosis) aims at identifying genomic regions associated with the resistance to pasteurellosis.

To establish a successful commercial breeding program to improve resistance to pasteurellosis, we need to evaluate the relationship between this trait and resistance to other diseases and production traits. This study aims at comparing production and health traits of growing rabbits and breeding does raised in commercial farms and produced from the resistant and susceptible sires having offspring tested through experimental inoculation with *Pasteurella* in the RELAPA project.

MATERIALS AND METHODS

Sires evaluation

In the RELAPA program, 955 crossbred rabbits were inoculated at 6 weeks of age with a pyogenic strain of *Pasteurella multocida* and the response to inoculation was assessed during the following 14 days, the animals being sacrificed after 14 days (Gunia *et al.*, 2017, Helloin *et al.*, 2015). These crossbreeds are progenies from six sire lines (two lines each from breeding companies Eurolap, Hycote, and Hypharm) and one dam line (INRA 1777). The rabbits were scored for resistance to pasteurellosis from 0 to 4, by taking into account scores for extent of abscesses (0 to 4), scores of *P. multocida* presence (0 to 4), and status of the rabbits (dead/alive) at the end of the experiment. (Gunia *et al.*, 2017). Among the sires used for RELAPA, 55 having produced at least 10 inoculated animals were classified as resistant (28 sires) or susceptible (27 sires) according to the mean resistance value of their inoculated offspring (Table 1).

Table 1: Means and standard deviation of the resistance score of resistant and susceptible sires calculated from their inoculated offspring score

Group of sire	Number	Mean resistance score	Standard deviation of resistance score
Resistant	28	1.57	0.16
Susceptible	27	2.03	0.26

Animals and measured traits

The 28 resistant sires produced 4991 growing rabbits (RG) and 884 breeding does (RD) while the 27 susceptible sires produced 4952 growing rabbits (SG) and 712 breeding does (SD). Growing rabbits and does were raised in six commercial farms belonging to the three breeding companies partners of the RELAPA project. The does were raised in conventional housing, inseminated for the first time at 19 weeks of age and then every 42 days. Females produced 6676 litters, or 4.2 litters per female on average. For each insemination, fertility was scored one (AI followed by a kindling) or zero (AI not followed by a kindling). For each litter, the number born alive and dead has been recorded. The total number born is the sum of number born alive and dead. The litter balance after adoption was obtained by adding the number of adoptees to number born alive and subtracting the number of kits removed. Stillbirth is calculated as the difference between the total number born and the number born alive divided by total number born. Nest mortality was calculated as the difference between the litter balance after adoption and the number of weaned rabbits divided by the litter balance.

The rabbits were weighed at weaning and at the end of the test. The weaning age ranged from 28 to 35 days, while the age of the end of fattening ranged from 66 to 70 days depending on the rearing farm. Mortality and clinical signs of diseases occurring in growing rabbits were recorded at the end of the test. The most likely cause of death of rabbits that died before the end of the test was also recorded. Disease traits were coded as 0 (absence) or 1 (disorder= morbidity or mortality). They were the following: 1) digestive disease, which includes diarrhea, bloated abdomen, and any form of digestive symptoms, 2) respiratory diseases which includes nasal discharge, pneumonia, 3) all infectious diseases, which combines digestive and respiratory diseases, abnormal low weights and other clinical signs of infectious origin. The basic statistics of growth and reproduction traits are given in Table 2.

Table 2: Number of animals, mean and standard deviation (Std) for growth and reproduction traits.

Trait	Number of animals	Mean	Standard deviation
Weaning weight (g)	8025	866	232
Final weight (g)	7477	2292	258
Fertility (0/1)	6676	0.87	-
Total number born / litter	5798	10.80	3.10
Number born alive / litter	5798	10.09	3.57
Stillbirth (%)	5137	7.35	-
Nest mortality (%)	5069	9.81	-

The total prevalence of digestive, respiratory, infectious diseases and mortality recorded during the growing period are given in Table 3.

Table 3: Mean prevalence (in %) of digestive, respiratory, all infectious diseases and mortality (%) recorded during the growth period.

Trait	Mean
Digestive diseases	8.7
Respiratory diseases	7.1
All infectious diseases	21.3
Mortality	5.3

Statistical analysis

The growth performances were analyzed with the GLM procedure of the SAS software (2008). The significant fixed effects ($P < 0.05$) retained in the model were: the sire's resistance group ($n = 2$), the combined effect batch * genotype ($n = 30$), the litter size at birth ($n = 12$), the litter size at weaning ($n = 10$), the parity of the birth litter ($n = 4$). The effect of weaning age was added to the weaning weight model while the end of fattening age effect was added to the final weight model. Health traits were analysed with the same procedure and the same fixed effects but without the litter size and the parity of the birth litter, which were not significant for this model.

The reproduction performances were analyzed with the PROC MIXED procedure of the SAS software (2008). The fixed effects retained in the model were: the sire's resistance group ($n = 2$), the combined effect year * season * farm ($n = 26$), the combined effect parity * physiological stage (lactating or not) ($n = 9$). The random effect of the female was added to the model to take into account the repetition of female performances.

RESULTS AND DISCUSSION

Differences in least squares means of traits are presented in table 4. Weaning and final weight were significantly higher in RG than in SG (+7 g, $P=0.04$ and +14 g, $P=0.02$ respectively). This favorable relationship is in agreement with the positive and favorable genetic correlation estimated by Shrestha *et al.* (2018) between resistance to pasteurellosis and average daily gain from birth to weaning recorded in inoculated animals of the same experiment. A moderate and favorable correlation between natural resistance to infectious diseases and weaning weight was also observed in another study carried in a commercial population (-0.34 ± 0.12) (Gunia *et al.*, 2018). This suggest that breeding for pasteurellosis resistance is not detrimental to breeding for growth traits. On the contrary, total number born and born alive were significantly lower in litters of RD than in litters of SD (-0.27 , $P=0.02$ and -0.41 $P=0.003$). Birth mortality was also higher in litters of RD than in litters of SD. These results suggest that breeding for resistance to pasteurellosis could decrease the prolificacy of does.

Table 4: Differences in least squares means between offspring of resistant and susceptible sires for growth, diseases and reproduction traits and P value of the sire group effect.

Trait	Difference resistant-susceptible	P value
Weaning weight (g)	7	*
Final weight (g)	14	*
Digestive diseases (%)	-1.910	**
Respiratory diseases (%)	-0.790	ns
Infectious diseases (%)	-3.200	***
Mortality (%)	-1.210	*
Fertility (0/1)	-0.019	ns
Total number born / litter	-0.270	*
Number born alive / litter	-0.410	**
Stillbirth (%)	1.580	***
Nest mortality (%)	0.49	ns

ns = non significant ; * : $P < 0.05$; ** : $P < 0.01$; *** : $P < 0.001$.

Prevalence of digestive diseases and infectious diseases were significantly lower in RG than in SG (-1.9 point, $P=0.006$ and -3.2 points, $P < 0.001$ respectively). This interesting result suggest that resistance to pasteurellosis assessed by an experimental infection using a single strain of *Pasteurella multocida* is favorably correlated to resistance to other infectious diseases. Gunia *et al.*, (2015) demonstrated that a composite trait grouping all disease syndromes was heritable in rabbit. However, there was almost no genetic correlation between digestive and respiratory disease traits. This result can be partly explained by the fact only one syndrome was recorded per animal. The difference in prevalence of respiratory disease between RG and SG is not significant (-0.79 point, $P=0.17$). This could be explained by a lack of homogeneity in the recording of the trait between the different farms: some breeders considered only true respiratory symptoms (nasal discharges, pneumonia) while some others included some other symptoms related to pasteurellosis (abscesses, wryneck, eye infections).

CONCLUSIONS

This part of the RELAPA project shows significantly different health and production performances between offspring of resistant and susceptible RELAPA sires. Resistant grower rabbits have a higher weight at weaning and at the end of fattening. They also have a lower prevalence of digestive and general infectious diseases compared to susceptible rabbits. This suggest that, if the RELAPA experimental infection is used in a breeding scheme to improve resistance to pasteurellosis, it may also improve resistance to digestive disorders and to other infectious diseases. The main issue of this project is to breed for resistance to pasteurellosis without degrading the prolificacy. Given the lower prolificacy of resistant does, there may be trade-off between resistance to pasteurellosis and reproductive performances of does.

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