**PROCEEDINGS OF THE 11th WORLD RABBIT CONGRESS**
Qingdao (China) - June 15-18, 2016
**ISSN 2308-1910**

Session
# Breeding and Genetics

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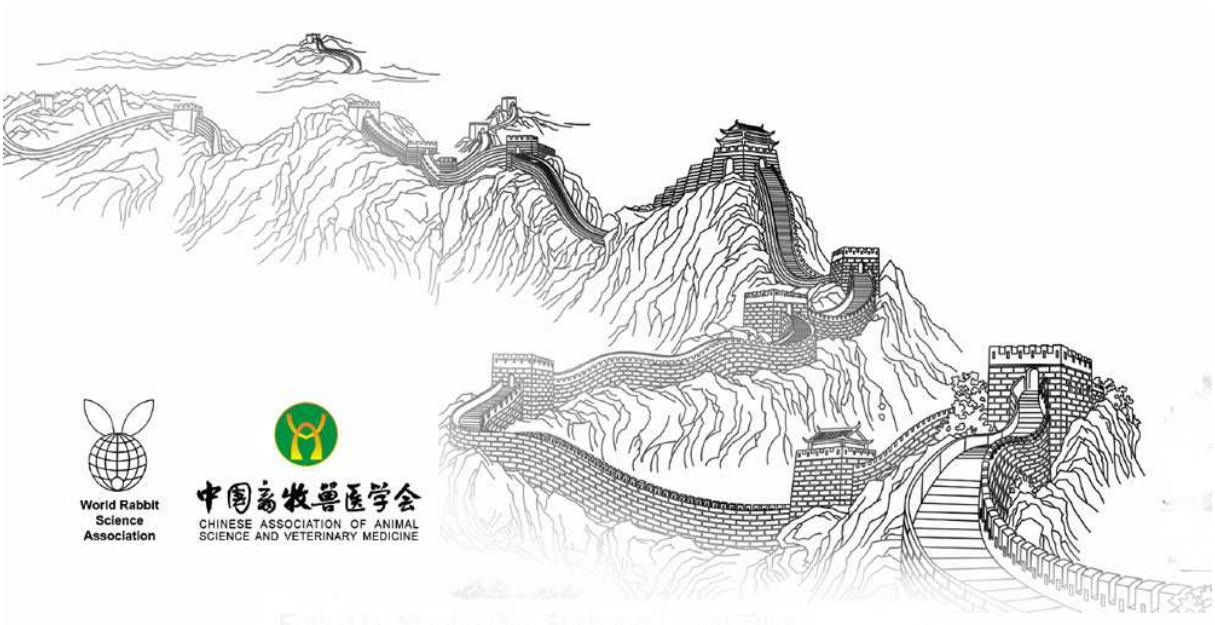
**Full text of the communication**

*How to cite this paper :*
*Gunia M., David I., Hurtaud J., Maupin M., Gilbert H., Garreau H., 2016* - Genetic parameters for resistance to infectious diseases in two French paternal meat rabbit lines. *Proceedings 11th World Rabbit Congress - June 15-18, 2016 - Qingdao - China, 51-54.*



# GENETIC PARAMETERS FOR RESISTANCE TO INFECTIOUS DISEASES IN TWO FRENCH PATERNAL MEAT RABBIT LINES

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## ABSTRACT

Selecting animals for their resistance to diseases is a way to improve their health and welfare and reduces the need for veterinary treatment. The objectives of this study were to estimate: i) the genetic parameters for simple visually assessed disease syndromes, and for a composite trait of resistance to infectious disease including all disease syndromes, ii) their genetic correlations with production traits. Clinical signs were recorded during weighing at 63 or 70 days of age on above 150,000 rabbits of two commercial paternal rabbit lines (HYPLUS) of the French breeding company Hypharm. Disease traits were: digestive syndromes, respiratory syndromes, infectious syndromes (a composite trait including digestive and respiratory syndromes), and infectious mortality. The production traits were body weight and carcass yield at 63 or 70 days of age. The heritabilities were low for disease traits (0.01 to 0.08 ± 0.01), and moderate for production traits. The genetic correlations between digestive and respiratory syndromes were slightly negative (-0.18 ± 0.07). The genetic correlations between the composite infectious disease trait and digestive or respiratory syndromes were moderate (0.65 ± 0.04 and 0.61 ± 0.04, respectively). Genetic correlations between disease and production traits were either null or favorable. Our results indicate that it is possible to select rabbits using visually assessed disease syndromes without the need for a trade-off between health and production traits. Using a composite criterion that includes all infectious syndromes is a promising way to improve the general disease resistance in rabbits.

**Key words**: disease, disease resistance, heritability, genetics

## INTRODUCTION

Improving the health of breeding rabbits is becoming a crucial issue with the decreasing antibiotic use in farm animals. Selecting rabbits for disease resistance is one of the method that can be used. Some selection programs that include disease resistance have been successfully implemented in rabbits (Garreau et al., 2012). Previous studies showed that it is possible to select rabbits for their resistance to bacterial infectious diseases (Eady et al., 2007) as well as their resistance to digestive disorders by using simple records of disease syndromes (Garreau et al., 2008). However, little is known about the genetic correlations among various disease traits and between disease and production traits. The possibility to select livestock for general resistance or general immunity has been widely discussed (Bishop, 2014), but until now, no study on this topic has been conducted in rabbits. The objectives of this study were to estimate: i) the genetic parameters for simple visually assessed disease syndromes, and for a composite trait of resistance to infectious disease including all disease syndromes, ii) their genetic correlations with production traits.

## MATERIALS AND METHODS

### Animals

The study was undertaken on data collected in the selection nucleus of two meat rabbit lines (AGP39 and AGP59) belonging to the HYPHARM breeding company. Both lines are paternal lines, reared in two

different rooms in the same building, and selected on live weight at 63 or 70 days of age, carcass yield, and resistance to digestive syndromes. Records on 85,502 rabbits from line AGP39 and on 67,898 rabbits from line AGP59 were analyzed. All rabbits were born between 1998 and 2014. Does were inseminated every 42 days and had an average of 3.8 parities. Kits were weaned at 31 days and tested in line AGP39 until 63 days of age and in line AGP59, until 70 days of age.

**Traits**

The descriptive statistics are listed in Table 1. The production traits were live weight, recorded at the end of the test on 137,860 animals and carcass yield (cold carcass weight/ live weight just before slaughter) recorded on 13,765 animals. All the animals (153,400) in the data set had disease records, recorded as 0 (absence) or 1 (disorder). The technicians recorded the health status of each individual rabbit at the end of the test, at 63 or 70 days of age. They monitored rabbits for infectious syndromes that occur naturally at the breeding farm. The probable cause of death of rabbits that died before the end of the test was also recorded. If a rabbit had more than 1 disease syndrome, only the predominant one was recorded. Disease traits were the following: 1) digestive syndromes (morbidity or mortality from diarrhea, bloated abdomen, and any form of digestive syndrome), 2) respiratory syndromes (morbidity or mortality from nasal discharge, lung lesion, eye infection, and wry neck), 3) infectious syndromes, which combines digestive and respiratory syndromes and other infectious syndromes (morbidity or mortality), 4) infectious mortality: mortality from infectious syndromes.

**Table 1**: Disease traits with their prevalence from 1998 to 2014, production traits with their mean and standard-deviation (in parentheses)

| Disease trait | | Production trait | |
|---|---|---|---|
| Trait | Prevalence (%) | Trait | Mean (standard-deviation) |
| Digestive syndromes | 7.1 | Carcass yield (%) | 57.692 (1.915) |
| Respiratory syndromes | 4.0 | Live weight (kg) | 2.878 (0.385) |
| Infectious syndromes | 12.1 | | |
| Infectious mortality | 4.7 | | |

**Statistical Analysis**

All traits were analyzed using a restricted maximum likelihood method, with ASReml 3.0 (Gilmour et al., 2009). Genetic and phenotypic variances or covariances were estimated using a pairwise bivariate animal model. The animal model included a random additive polygenic effect and a random common litter effect for all traits and a maternal genetic effect for live weight. Both rabbit lines were analyzed together, simultaneously considering the 2 pedigrees. For the binary disease traits, a threshold model was also used by running univariate analyses. Genetic correlations could not be estimated with the threshold model with ASReml software.

The significance of the fixed effects was determined for each trait using the Wald *F* statistic, which is similar to an ANOVA (Gilmour et al., 2009). All fixed factors were first tested together, and then a stepwise selection of the significant ones was applied. Significant fixed factors ($P < 0.05$) were maintained in the subsequent analyses. The fixed effects of the line, the contemporary group within the line, sex, and cage were fitted for all traits. The cage effect covered both rabbits in collective cages with restricted feeding and rabbits fed ad libitum in individual cages. Other fixed effects were the parity of the dam and litter size recorded 21 days after delivery. The age at weighing was fitted for live weight. Interactions between the sex, parity of the dam, litter size, cage effects, and the line effects were fitted when significant.

## RESULTS AND DISCUSSION

### Heritability

Heritability estimates are presented in Table 2. Heritabilities were low for disease traits, ranging from 0.030 ± 0.003 for infectious syndromes to 0.043 ± 0.004 for infectious mortality with the linear model. Heritabilities of live weight and carvass yield were moderate. The threshold model did not give much higher heritability estimates for the binary diseases traits than the linear model. Heritabilities varied from 0.014 ± 0.010 for infectious mortality to 0.079 ± 0.010 for respiratory syndromes with the threshold model. The composite trait "infectious syndromes" grouping all disease syndromes was heritable, which means that rabbits could be selected on general disease resistance. Our results are in accordance with those of previous studies in commercial meat rabbits. A heritability of 0.08 ± 0.02 was previously found for digestive syndromes in the AGP39 rabbit line with a threshold model (Garreau et al., 2008). Heritability of bacterial infectious syndromes at 9 or 10 week of age estimated with a linear model was 0.04 ± 0.01 in French meat rabbit populations (Eady et al., 2004) and 0.06 ± 0.02 in Australian meat rabbit populations (Eady et al., 2007). The efficiency of selection for digestive syndromes has already been demonstrated by an experimental inoculation with *Escherichia coli* O 103 (Garreau et al., 2012).

**Table 2**: Estimates of direct heritability ($h^2$), common litter effect ($c^2$), maternal heritability ($m^2$), phenotypic variance (Vp) and standard-error of estimates (in parentheses) for disease and production traits with a linear model and a threshold model

| | Threshold model (underlying scale) | | Linear model (observed scale) | | | |
|---|---|---|---|---|---|---|
| Trait | $h^2$ | $c^2$ | Vp | $h^2$ | $c^2$ | $m^2$ |
| Digestive syndromes | 0.037 (0.007) | 0.133 (0.008) | 0.051 (0.000) | 0.034 (0.003) | 0.090 (0.002) | |
| Respiratory syndromes | 0.079 (0.010) | 0.121 (0.009) | 0.037 (0.000) | 0.041 (0.004) | 0.057 (0.002) | |
| Infectious syndromes | 0.032 (0.005) | 0.114 (0.005) | 0.093 (0.000) | 0.030 (0.003) | 0.076 (0.002) | |
| Infectious mortality | 0.014 (0.010) | 0.157 (0.013) | 0.028 (0.000) | 0.043 (0.004) | 0.127 (0.003) | |
| Carcass yield | - | - | 2.602 (0.038) | 0.243 (0.026) | 0.098 (0.012) | |
| Live weight | - | - | 0.080 (0.001) | 0.130 (0.009) | 0.137 (0.003) | 0.136 (0.008) |

### Genetic and phenotypic correlations

The genetic and phenotypic correlations are presented in Table 3. The genetic and phenotypic correlations between infectious syndromes on the one hand and digestive and respiratory syndromes on the other are moderate. The composite infectious syndromes trait could, therefore, be a good indicator trait to improve general disease resistance and to reduce the sensitivity of rabbits to digestive or respiratory infections. The genetic and phenotypic correlations between respiratory and digestive syndromes are negative. This result can be partly explained by the fact that only 1 syndrome was recorded per animal but also by the independent genetic susceptibility to digestive and respiratory diseases. Similar genetic independence has been observed in pigs (Henryon et al., 2001). The genetic and phenotypic correlations between infectious mortality and digestive syndromes are high, because diarrhea is the main cause of infectious death. The genetic and phenotypic correlations between disease traits and carcass yield are moderate and negative. Healthy animals have a better carcass yield. Most of the genetic correlations between disease traits and live weight were not significantly different from 0.

Genetic correlations between resistance and production traits can be favorable or unfavorable. They depend on both the consequences of being infected as well as the costs of mounting or being able to mount appropriate immune responses (Bishop and Stear, 2003). The duration, the prevalence of the disease, the method and time of measurement affect the direction and the magnitude of the correlation between resistance and production traits.

**Table 3**: Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlations, and their standard-error of estimates (in parentheses) between disease and production traits.

| | Digestive syndromes | Respiratory syndromes | Infectious syndromes | Infectious mortality | Carcass yield | Live weight (direct) | Live weight (maternal) |
|---|---|---|---|---|---|---|---|
| Digestive syndromes | | -0.18 (0.07) | 0.65 (0.04) | 0.92 (0.02) | -0.40 (0.07) | 0.11 (0.07) | -0.11 (0.06) |
| Respiratory syndromes | -0.03 (0.00) | | 0.61 (0.04) | -0.27 (0.06) | -0.10 (0.08) | 0.01 (0.06) | -0.06 (0.06) |
| Infectious syndromes | 0.71 (0.00) | 0.60 (0.00) | | 0.52 (0.05) | -0.35 (0.08) | 0.06 (0.07) | -0.25 (0.06) |
| Infectious mortality | 0.70 (0.00) | 0.02 (0.00) | 0.54 (0.00) | | -0.18 (0.08) | 0.00 (0.07) | 0.14 (0.06) |
| Carcass yield | -0.20 (0.01) | -0.02 (0.01) | -0.05 (0.01) | -0.08 (0.01) | | -0.21 (0.06) | 0.23 (0.06) |
| Live weight (direct) | -0.34 (0.00) | -0.04 (0.00) | -0.31 (0.00) | -0.13 (0.00 | 0.15 (0.01) | | -0.10 (0.06) |
| Live weight (maternal) | | | | | | | |

## CONCLUSIONS

The results suggest that it is possible to select rabbits for disease resistance by using simple health records without causing negative effects on production, at least in environments with moderate infectious challenge. It also seems possible to select rabbits for general disease resistance based on syndromes of any infectious diseases. Breeding for general disease resistance based on the simple visual assessment of the presence of infectious diseases is very promising. Phenotyping costs are low, so the number of records can be high. In a context of reduction of antibiotic treatments, the potential outcome of more resistant animals is of major importance for breeders. The present study paves the way for actual breeding for resistance to infectious diseases in rabbits.

## ACKNOWLEDGEMENTS

M. Gunia acknowledges the financial support of “IDEX Nouveaux-Entrants” from “Université de Toulouse”.

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