

## **Genetic parameters of resistance to non-specific diseases in rabbits in selection and challenging environments**

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### **Summary**

Improving disease resistance is a key to improve animal welfare and reduce mortality. In our study, resistance to infectious diseases trait had a heritability of  $0.05 \pm 0.01$  in a selection environment and  $0.10 \pm 0.02$  in a challenging environment in rabbits. The genetic correlation between these two traits was  $0.70 \pm 0.13$ , indicating a genotype by environment interaction. The genetic correlations of the resistance to infectious diseases (in a challenging or selection environment) with the number of born alive and weaning weight were favourable. Recording disease resistance in challenging environment on sibs of candidates to selection increased the genetic gain on this trait by 30% compared to using records in the selection nucleus only.

*Keywords: disease resistance, genetic parameters, rabbit, heritability, genetic by environment interaction*

### **Introduction**

Improving disease resistance is a key to improve animal welfare. In rabbits, disease syndromes records can be used to improve resistance to respiratory (Eady et al., 2004), digestive (Garreau et al., 2008), and non-specific infectious (Gunia et al., 2015) diseases. However, the application of high biosecurity measures in nucleus breeding farms can make selection for disease resistance more difficult. To address this issue, the Hypharm breeding company implemented sib-testing in a challenging environment in addition to the nucleus farm testing.

The aim of this study was to assess: 1) the genetic parameters of various disease resistance traits to determine the trait to use in a breeding program, 2) the genetic correlations between the chosen disease trait and the production traits, 3) the genotype by environment interactions between nucleus and challenging farms for the disease traits, and 4) the consequences in term of genetic gain of using challenging environment records.

### **Material and methods**

#### **Animals**

The study was undertaken on data collected in a maternal rabbit line of the Hypharm breeding company. Records on 23,773 purebred rabbits from the AGP77 line were analysed.

Does were inseminated every 42 days and kits were weaned at 31 days of age. Rabbits were reared in two different environments: 1) the nucleus farm, a high bio-secure and controlled environment, where selection candidates were tested, referred to as selection (S) environment. 2) the sib-testing farms, constituted of 3 breeding farms with a less favourable environment referred to as challenging environment (Ch), where some full sibs and half sibs of the selection candidates were tested. This environment aims at increasing the occurrence of diseases. Fifty percent of the rabbits from every second weaning batch were reared in the challenging environment. In total, 6,061 rabbits had records in the Ch environment and 17,712 in S environment.

## Traits

The descriptive statistics of the disease and production traits are listed in Table 1 and 2. All animals in the dataset had disease records, recorded as 0 (absence) or 1 (disorder) at 70 or 80 days of age. Technicians monitored rabbits for infectious syndromes that occur naturally in farms. All clinical signs (even with a very low intensity) were recorded. The probable cause of death of rabbits that died before the end of the test was also recorded after autopsy. Disease traits were the following: 1) digestive syndromes (Dig = morbidity or mortality from diarrhea, bloated abdomen, and any form of digestive syndrome), 2) respiratory syndromes (Resp = morbidity or mortality from nasal discharge, lung lesion, eye infection, wry neck), 3) infectious syndromes (Infect), which combines digestive and respiratory syndromes and other infectious syndromes (morbidity or mortality). The disease traits were treated as separate traits depending on the environment (S or Ch), resulting in a total of 6 disease traits: Dig\_S, Resp\_S, Infect\_S, Dig\_Ch, Resp\_Ch, Infect\_Ch. The production traits were the number of kits born alive (NBA) and the weaning weight (WW).

*Table 1. Number of animals (N) and total prevalence of infectious (Infect), respiratory (Resp) and digestive (Dig) symptoms in selection (S) and challenging (Ch) environments*

	N	Prevalence		N	Prevalence
Infect_S	17712	26	Infect_Ch	6061	41
Resp_S	17712	14	Resp_Ch	6061	24
Dig_S	17712	11	Dig_Ch	6061	16

*Table 2. Number of animals (N), mean and standard deviation (Std) for number of kits born alive (NBA) and weaning weight (WW).*

	N	Mean	Std
NBA	4121	9.92	3.34
WW (g)	13090	664	102

## Genetic parameters analysis

All traits were analyzed using a restricted maximum likelihood method, with the ASReml 3.0 software (Gilmour et al., 2009). Genetic and phenotypic variances and covariances were estimated using multivariate linear animal models. The animal model included a random additive polygenic effect for all traits, a random common litter effect for the disease resistance traits and WW, a random maternal environmental effect and a random maternal genetic effect for WW, and a permanent environmental effect to take into account the repeated measurement of NBA on the does. 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). Fixed effects were first tested together, and then a stepwise selection of the significant ones was applied. Significant fixed effects ( $P < 0.05$ ) were maintained in the subsequent analyses. The fixed effects of the batch and sex were fitted for the disease resistance traits and WW. A farm effect was fitted for the disease traits in the Ch environment and for WW. A combined effect of the year and season of kitting and a combined effect of parity and physiological status (lactating or not at insemination) were fitted for NBA.

### Simulation of breeding schemes

We used the deterministic simulation program SelAction (Rutten et al., 2002) to compare the expected selection responses for two breeding schemes including or not disease records in the Ch environment. SelAction predicts selection response on pseudo-BLUP estimated breeding values. The program assumes random mating of the selected animals. In our study, we used the option of discrete generations and 1-stage selection. The selection intensity was 15% for males and 25% for females. Rabbits were selected at 70 days of age. The available information were the BLUP of the parents for all traits, the own performance and sib performances in the S environment for WW and Infect, sib performances in the Ch environment for Infect.

## Results and discussion

### Genetic parameters for disease resistance and production traits

The genetic parameters for disease resistance are presented in Table 3. The heritability estimates were similar for all traits within each environment. They were higher in Ch (0.08 to 0.10) than S (0.04 to 0.05). The genetic and phenotypic correlations between infectious syndromes on the one hand and digestive and respiratory syndromes on the other hand were moderate to high, ranging from 0.52 to 0.73, and they were similar in both environments. The composite infectious syndromes trait can, therefore, be a good indicator trait to improve general disease resistance and to reduce the sensitivity of rabbits to digestive and respiratory infections.

*Table 3. Estimates of heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for infectious disease (Infect), respiratory symptoms (Resp), and digestive symptoms (Dig) in selection (S) and challenging (Ch) environments ( $\pm$ standard errors).*

	Infect_S	Resp_S	Dig_S		Infect_Ch	Resp_Ch	Dig_Ch
Infect_S	0.05 $\pm$ 0.01	0.69 $\pm$ 0.08	0.66 $\pm$ 0.09	Infect_Ch	0.10 $\pm$ 0.02	0.74 $\pm$ 0.08	0.52 $\pm$ 0.13
Resp_S	0.67 $\pm$ 0.00	0.04 $\pm$ 0.01	-0.06 $\pm$ 0.16	Resp_Ch	0.66 $\pm$ 0.01	0.10 $\pm$ 0.02	-0.19 $\pm$ 0.17
Dig_S	0.60 $\pm$ 0.01	-0.12 $\pm$ 0.01	0.04 $\pm$ 0.01	Dig_Ch	0.54 $\pm$ 0.01	-0.25 $\pm$ 0.01	0.08 $\pm$ 0.02

The genetic correlation between Infect\_S and Infect\_Ch was below unity (0.70 $\pm$ 0.13), which shows a significant interaction between the genotype and the environment (Table 4). The main difference between appeared with WW\_direct with a higher negative genetic correlation for Infect\_S. Heavier kits at weaning in the S environment could therefore be more resistant to diseases during the testing period. The other genetic correlations were not significantly different from zero.

Table 4. Estimates of heritabilities (diagonal), genetic correlations (above diagonal), and phenotypic correlations (below diagonal) for infectious disease (Infect) in selection (S) or challenging (Ch) environment, Number of born alive (NBA), and the direct and maternal effects of weaning weight (WW) ( $\pm$ standard errors).

	Infect_S	Infect_Ch	NBA	WW_direct	WW_maternal
Infect_S	0.05 $\pm$ 0.01	0.70 $\pm$ 0.13	-0.08 $\pm$ 0.14	-0.34 $\pm$ 0.12	-0.06 $\pm$ 0.20
Infect_Ch	-	0.10 $\pm$ 0.02	-0.06 $\pm$ 0.16	-0.05 $\pm$ 0.14	-0.04 $\pm$ 0.22
NBA	-0.38 $\pm$ 0.03	-0.37 $\pm$ 0.02	0.16 $\pm$ 0.03	-0.22 $\pm$ 0.11	0.51 $\pm$ 0.16
WW_direct	-0.13 $\pm$ 0.01	-0.11 $\pm$ 0.02	0.03 $\pm$ 0.03	0.29 $\pm$ 0.04	-0.71 $\pm$ 0.12
WW_maternal					0.05 $\pm$ 0.02

### Genetic progress with or without disease records in the challenging environment

We considered a fictive breeding objective with a weight of 10% on NBA, 15% on WW\_direct and 15% on WW\_maternal, and 60% on Infect\_Ch. The aim of this breeding goal was to improve disease resistance in less favourable environments while increasing weaning weight and stabilising NBA. In the first scenario, Infect\_Ch was recorded on sibs of the selection candidates while in the second scenario this trait was not recorded. Infect\_S records were taken into account in both scenarios, even if this trait was not included in the breeding objective. The aim of the simulation (Table 5) was to determine whether the records in the challenging environment brought additional genetic progress or not.

Table 5. Genetic progress with or without disease records in the challenging environment (in trait units) per generation

	NBA	WW_direct	WW_maternal	Infect_Ch	Infect_S
Infect_Ch recorded	0.007	16.240	-2.159	-0.057	-0.046
Infect_Ch not recorded	0.003	18.656	-2.284	-0.043	-0.047

Recording Infect\_Ch increased the genetic progress of this trait by 33%, while reducing genetic gain on WW\_direct by 13% and on Infect\_S by 2%. The decrease in NBA was reduced by 33%.

In a 5-years-term (6 generations) for the same exposure to pathogens, we could expect a reduction of prevalence for Infect\_Ch from 41% to 30% with this breeding objective and records on Infect\_Ch.

### Conclusion

The resistance to infectious disease (in S or Ch) is a trait with low heritability and favourable correlation with the other disease and production traits. A genotype by environment interaction exists for this trait between the selection and challenging conditions. If the goal of the selection is to improve health in less favourable farms conditions, the recording of infectious disease in challenging environment brings higher genetic gains than using only records of nucleus breeding farms.

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