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Genetic Selection of resistance to *Haemonchus contortus* : integration of a phenotyping protocol in the selection scheme of two dairy sheep breeds in France

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Gastrointestinal nematode (GIN) infection is one of the main health issue for grazing dairy sheep due to growth retardation, milk production losses and sometimes anemia and mortality. Their control requires the use of anthelmintic drugs, which are becoming less effective with the increasing (multi)resistance of GIN (Arsenopoulos *et al.* 2021). In the Pyrénées-Atlantiques region (South-West of France), dairy sheep farming is facing emerging multi-resistant *Haemonchus contortus* populations (Bordes *et al.* 2019). With the purpose to limit the use of treatments and to improve the resistance of the host, two local dairy sheep breeds, the Blond-Faced Manech (BFM) and the Basco-Bearnaise (BB), have started a selection for resistance to GIN for several years.

This selection is made every year on the elite rams of both breeds, intended for the diffusion of genetic progress by artificial insemination. These rams are raised indoors in the breeding center and have never been naturally infected by GIN.

The protocol of phenotyping consists in an experimental infection design where rams are challenged by two infections with *H. contortus* L3 larvae for a 28 days period and separated by a recovery period of 15 days (Figure 1). At the beginning and end of each infection, Fecal Egg Count (FEC) (Reynaud *et al.* 1970) and Packed Cell Volume (PCV) of each ram were measured. Currently, 1,113 BFM and 254 BB rams have been phenotyped. Data were analysed using a linear mixed model including the contemporary group and age as fixed effects (Aguerre, 2018).

The estimations of heritabilities, genetic and phenotypic correlations are presented in Table 1.

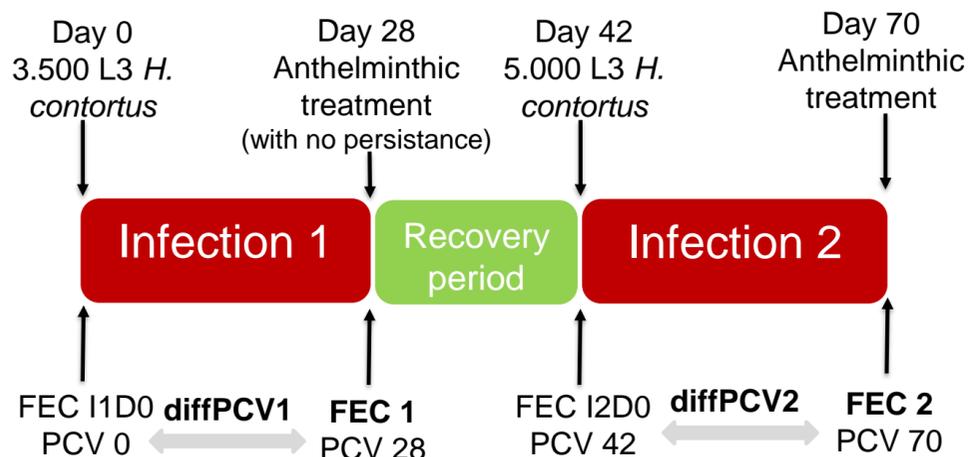


Figure 1 : Experimental infection protocol for the phenotyping of rams. FEC : Fecal Egg Count ; PCV : Packed Cell Volume ; diffPCV : difference between PCV at the beginning and at the end of the infection.

The heritabilities were weak for the differences between PCV in both breeds and for FEC1 in BFM and moderate for FEC1 in BB (0,37) and for FEC2 (0,34 and 0,3 in BFM and BB respectively). The estimated phenotypic correlations between the different traits were positive and grossly similar across both breeds. The estimated genetic correlations between FEC1 and FEC2, FEC1 and DiffPCV1, FEC2 and DiffPCV1, FEC2 and DiffPCV2 were strong in both breeds. However, conflicting estimated genetic correlation were observed between FEC1 and DiffPCV2 (+0,46 in BFM and -0,19 in BB).

	BFM BB	FEC1	FEC2	DiffPCV1	DiffPCV2
FEC1	0.16 0.37	+0,86 +0,60	+0,79 +0,79	+0,46 -0,19	
FEC2	+0,35 +0,32	0.34 0.30	+0,67 +0,48	+0,49 +0,37	
DiffPCV1	+0,29 +0,25	+0,17 +0,23	0.11 0.17	+0,09 +0,02	
DiffPCV2	+0,13 -0,03	+0,40 +0,45	+0,03 +0,10	0.08 0.18	

Table 1 : Genetic and phenotypic parameters estimated for **BFM** (red) and **BB** (blue) rams.

Heritabilities are written in bold on the diagonal, genetic correlations are above the diagonal and phenotypic correlations are below the diagonal.

In conclusion, by using the same phenotyping protocol, both breeds showed similar heritabilities and genetic correlations for most of the considered traits. These data show that it is possible to select dairy sheep for an enhanced resistance to GIN using controlled infections with *H. contortus*. Currently, the estimation of genetic parameters in BB is based on a smaller number of phenotyped rams, compared to those of the BFM. New phenotypes collected in the next years on new batches of rams will permit to confirm the trends observed in this breed and estimate the genetic correlations with the dairy traits. According to this dataset, it is possible to assign each ram an individual estimated breeding value on GIN resistance. As a result, since 2017, rams considered as the most susceptible to GINs are discarded from the selection scheme.

In order to develop this genetic selection and to extend it to other dairy or meat sheep/goats breeds, a phenotyping platform is under construction in the South-West of France.

Sources :

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Bordes *et al.*, *Parasitology International*, 2019
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