

Improving dairy ewes resistance to gastro-intestinal parasites in natural conditions by selecting rams in artificial infections

S. Aguerre¹, P. Jacquiet², H. Brodier², J.P. Bournazel², C. Grisez², F. Prévot², L. Michot³, F. Fidelle³, J.M. Astruc⁴ & C.R. Moreno¹

¹ *GenPhySE, Université de Toulouse, INRA, INPT, ENVT, 31320, Castanet-Tolosan, France*
sophie.aguerre@inra.fr (Corresponding Author)

² *INRA-ENVT UMR1225, 31076, Toulouse, France*

³ *CDEO, Quartier Ahetzia, 64130, Ordiarp, France*

⁴ *Institut de l'Élevage, 31321, Castanet-Tolosan, France*

Introduction

Gastro-intestinal nematodes (GIN) are a major constraint in sheep breeding and cause substantial economic losses (Mavrot *et al.*, 2015). Genetic selection for resistance to GIN as a complementary control strategy to anthelmintic treatments is of interest as resistance of nematodes to these molecules is now widespread (Geurden *et al.*, 2014).

In several countries, selection for parasite resistance is based on fecal egg counts measured in natural infections on pasture (Bisset *et al.*, 2001). In France, parasite infectious pressure on pasture is variable because of variations of climatic conditions. Consequently, an experimental design has been developed to evaluate the resistance of the young rams involved in the breeding programs. The efficiency of this design to select resistance of ewes in pasture was assumed based on previous knowledge showing a high correlation between resistance to experimental and natural challenges and resistance to different parasites (Gruner *et al.*, 2004a; 2004b) and high genetic correlations between adult sheep and lambs (Bouix *et al.*, 1998). But no previous study allowed direct evaluation of the genetic correlation between young rams resistance in experimental conditions and the resistance of ewes at different physiological stages in natural conditions.

The aim of this paper is to explore this genetic correlation in the Blond-faced Manech dairy breed, reared in the South West of France, before implementing experimental parasite infections to select rams to improve dairy ewes resistance in farms.

Material and methods

Rams dataset

Between 2008 and 2016, fecal egg counts (FEC) and losses in packed cell volume (PCV) of 603 rams of the breeding organization of Blond-faced Manech were recorded following two successive experimental infections with *Haemonchus contortus* of the “Humeau” strain. The rams were naïve at the beginning of the experiment and kept indoors. They were 2 or 3 years old when inoculated with infective doses of 3,000 to 7,500 larvae in first and second infections. FEC and PCV loss were measured 30 days after each infection then the rams were given an oral drench of ivermectine (0.2 mg/kg of body weight, Oramec[®] Merial) to eliminate the infections. The two infections were separated by 15 days recovery time.

Female offspring dataset

Four hundred Blond-faced Manech ewes, female offspring of 103 of 603 rams, were selected in 7 flocks to be measured for FEC and PCV in natural conditions. On average, 57 ewes per flock were measured (from 51 to 66 ewes). The average number of offspring per ram was 3.9. The ewes were 2 to 4 years old. They were exposed to natural GIN infections i.e. mainly *Haemonchus contortus*, *Teladorsagia circumcincta*, *Trichostrongylus axei* and *T.colubriformis*, *Cooperia curticei* and *Oesophagostomum venulosum* (Jacquet *et al.*, 2004). The phenotypes were recorded three times a year (spring, summer and autumn) in 2015 and 2016. The ewes were phenotyped three times on average (1 to 6 sampling dates for each ewe). For each trait, a total of 1,312 measures were available.

Sample analysis

FEC were determined using a modified MacMaster technique (Raynaud, 1970) with a sensitivity of 15 eggs per gram. PCV was measured from each blood sample collected in EDTA coated tubes after centrifugation in microhematocrit tubes at 10,000 rpm for 10 minutes.

Data analysis

A fourth root transformation was applied to correct FEC data for over dispersion.

For the ram dataset, a linear mixed model using age and infectious group as fixed effects was used to analyze FEC and PCV loss data. For the female offspring dataset, a random regression model was used to take into account the repeated measures of FEC and PCV. The tested fixed effects for the female offspring were the age, the flock, a combination of the year and season and a combination of the treatment (eprinomectin, ivermectin, oxfendazole, doramectin or moxidectin) and the number of days between the date of treatment and the sampling date (less than 70 days, between 70 and 100 days, more than 100 days).

Genetic, permanent environment and residual variances were estimated by average information restricted maximum likelihood using AIREMLF90 (Misztal, 1999) in multitrait analyses to compute heritabilities, genetic and phenotypic correlations. The pedigree files contained respectively 2,907 animals for the ram dataset and 2,054 animals for the female offspring dataset.

Results and discussion

With the ram dataset, the heritability of FEC estimated was low in first infection but FEC were moderately heritable in second infection (0.14 and 0.35 respectively) as reported by previous studies (Assenza *et al.*, 2014) (Table1). These two traits were highly correlated with a genetic correlation of 0.92. With the female offspring dataset, the heritability of FEC in natural conditions was lower (0.18) consistent with other studies on dairy ewes in natural conditions (Sechi *et al.*, 2009; Gutiérrez-Gil *et al.*, 2009) (Table 2).

With the ram dataset, the genetic correlation between FEC and PCV loss was high in first infection (0.86) but lower in second infection (0.16) (Table 1). With the female offspring dataset, the estimated genetic correlation between FEC and PCV measured in natural condition of infection was not significantly different from 0 (Table 2).

Table 1. Genetic and phenotypic parameters estimated from rams in experimental infections.

	root_FEC_inf1	root_FEC_inf2	PCV_loss_inf1	PCV_loss_inf2
root_FEC_inf1	0.14 ± 0.04	0.92 ± 0.08	0.86 ± 0.09	0.11 ± 0.34
root_FEC_inf2	0.34 ± 0.04	0.35 ± 0.08	0.66 ± 0.20	0.16 ± 0.35
PCV_loss_inf1	0.25 ± 0.04	0.22 ± 0.04	0.24 ± 0.05	0.07 ± 0.32
PCV_loss_inf2	0.03 ± 0.04	0.27 ± 0.04	0.01 ± 0.04	0.18 ± 0.06

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

Table 2. Genetic and phenotypic parameters estimated from ewes in natural infections.

	root_FEC	PCV
root_FEC	0.18 ± 0.04	-0.12 ± 0.54
PCV	-0.09 ± 0.03	0.12 ± 0.08

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

An original result in our study was the genetic correlations of 0.71 and 0.56 between FEC measures of the ram dataset in experimental infections and FEC of the female offspring dataset in natural infections (Table 3). The correlation between sires genetic values based on their own FEC measured after second infection and sires genetic values based on the FEC of their offspring was also estimated and was 0.87 (Figure 1).

Table 3. Genetic parameters for the FEC measured in the 603 experimentally infected rams and the FEC measured in the 400 naturally infected ewes.

	root_FEC_inf1	root_FEC_inf2	root_FEC
root_FEC_inf1	0.12 ± 0.004	0.93 ± 0.002	0.71 ± 0.008
root_FEC_inf2		0.37 ± 0.008	0.56 ± 0.01
root_FEC			0.19 ± 0.006

Heritabilities in bold and genetic correlations above the diagonal.

¹ root_FEC_inf1 and root_FEC_inf2 are the fourth-root transformed values for FEC measured in the 603 experimentally rams in first and second infection respectively

² root_FEC: FEC values after fourth-root transformation measured in the 400 naturally infected ewes

Figure 1. Correlation between the sires genetic values based on their own FEC following the second experimental infection and the sires genetic values based on their female offspring FEC measured in natural infections.

¹ root_FEC: FEC values after fourth-root transformation measured on the 400 naturally infected dairy ewes

² root_FEC_inf2: fourth-root transformed FEC values measured on the 603 experimentally infected rams

Conclusion

Our findings indicate that selecting rams for resistance in experimental infections is an efficient way to increase resistance to GIN in naturally infected ewes in pastures. However, before routinely implementing selection for parasitism resistance in breeding schemes, further studies are needed to check the absence of unfavourable genetic correlation between milk production traits, reproduction traits and longevity and parasite resistance traits.

List of references

- Assenza, F., J.M. Elsen, A. Legarra, C. Carré, G. Sallé, C. Robert-Granié & C.R. Moreno, 2014. Genetic parameters for growth and faecal worm egg count following *Haemonchus contortus* experimental infestations using pedigree and molecular information. *Genet. Sel. Evol.* 46: 1-13.
- Bisset, S.A., C.A. Morris, J.C. McEwan & A. Vlassof, 2001. Breeding sheep in New Zealand that are less reliant on anthelmintics to maintain health and productivity. *NZ Vet J.* 49: 236-246.
- Bouix, J., J. Krupinski, R. Rzepecki, B. Nowosad, I. Skrzyzala, M. Roborzynski, W. Fudalewicz-Niemczyk, M. Skalska, A. Malczewski & L. Gruner, 1998. Genetic resistance to gastrointestinal nematode parasites in Polish long-wool sheep. *Int. J. Parasitol.* 28: 1797-1804.
- Geurden, T., H. Hoste, P. Jacquiet, D. Traversa, S. Sotiraki, A. Frangipane di Regalbono, N. Tzanidakis, D. Kostopoulou, C. Gaillac, S. Privat, A. Giangaspero, C. Zanardello, L. Noé, B. Vanimisetti & D. Bartram, 2014. Anthelmintic resistance and multidrug resistance in sheep gastro-intestinal nematodes in France, Greece and Italy. *Vet. Parasitol.* 201: 59-66.
- Gruner, L., J. Bouix & J.C. Brunel, 2004a. High genetic correlation between resistance to *Haemonchus contortus* and to *Trichostrongylus colubriformis* in INRA 401 sheep. *Vet. Parasitol.* 119: 51-58.
- Gruner, L., J. Bouix, J. Vu Tien Khang, N. Mandonnet, F. Eychenne, J. Cortet, C. Sauvé & C. Limouzin, 2004b. A short-term divergent selection for resistance to *Teladorsagia circumcincta* in Romanov sheep using natural or artificial challenge. *Genet. Sel. Evol.* 36: 217-242.
- Gutiérrez-Gil, B., J. Pérez, L.F. de la Fuente, A. Meana, M. Martínez-Valladares, F. San Primitivo, F.A. Rojo-Vazquez & J.J. Arranz, 2009. Genetic parameters for resistance to trichostrongylid infection in dairy sheep. *Animal.* 4: 505-512.
- Jacquiet, P., J.P. Alzieu, J. Cabaret, C. Vial-Novella, C. Garrain, S. Minery, J.M. Arranz, F. Prévot, J.P. Bergeaud, C. Grisez, J. Cortet, C. Sauvé, P. Dorchies, & L. Gruner, 2004. Epidémiologie comparée en Ariège et dans les Pyrénées-Atlantiques des brebis à l'herbe par les helminthes et par *Oestrus ovis*. *Bulletin des GTV, Hors-série*: 91-97.
- Mavrot, F., H. Hertzberg & P. Torgerson, 2015. Effect of gastro-intestinal nematode infection on sheep performance: a systematic review and meta-analysis. *Parasites & Vectors.* 8: 557.
- Misztal, I., 1999. Complex Models, More Data: Simpler Programming?
http://nce.ads.uga.edu/wiki/lib/exe/fetch.php?media=bul20_5.pdf
- Raynaud J.P., 1970. Etude de l'efficacité d'une technique de coproscopie quantitative pour le diagnostic de routine et le contrôle des infestations parasitaires des bovins, ovins, équins et porcins. *Ann. Parasitol.* 45: 321-342.
- Sechi, S., S. Salaris, A. Scala, R. Rupp, C.R. Moreno, S.C. Bishop & S. Casu, 2009. Estimation of (co)variance components of nematode parasites resistance and somatic cell count in dairy sheep. *Ital. J. Anim. Sci.* 8: 156-158.