



HAL
open science

Genetic parameters for milk flow and relationships with bacterial infection, SCC and production traits in Lacaune dairy sheep

Charlotte Allain, Jean-Michel Astruc, David Portes, Christel Marie-Etancelin,
Gilles Foucras, Rachel Rupp

► **To cite this version:**

Charlotte Allain, Jean-Michel Astruc, David Portes, Christel Marie-Etancelin, Gilles Foucras, et al.. Genetic parameters for milk flow and relationships with bacterial infection, SCC and production traits in Lacaune dairy sheep. 11. World Congress on Genetics Applied to Livestock Production (WCGALP), Feb 2018, Auckland, New Zealand. Massey University, 1130 p., 2018, 11th World Congress on Genetics Applied to Livestock Production (WCGALP). <hal-02735637>

HAL Id: hal-02735637

<https://hal.inrae.fr/hal-02735637v1>

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



HAL Authorization

Genetic parameters for milk flow and relationships with bacterial infection, SCC and production traits in Lacaune dairy sheep

C. Allain¹, J.M. Astruc², D. Portes³, C. Marie-Etancelin¹, G. Foucras⁴ & R. Rupp¹

¹ GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet-Tolosan, France
charlotte.allain@inra.fr (Corresponding Author)

² Institut de l'Élevage, Castanet-Tolosan, France

³ INRA, Domaine de La Fage, Saint-Jean-et-Saint-Paul, France

⁴ IHAP, Université de Toulouse, INRA, INPT, ENVT, Toulouse, France

Summary

Improving milking ability is a major issue for consideration in dairy species. Milk flow is not yet recorded in dairy sheep flocks and so far recorded only in the INRA experimental sheep flock of La Fage. The objective of our study was thus to estimate heritability estimates for milk flow traits and genetic correlations with milk production and with udder health traits in dairy Lacaune sheep. Genetic parameters were estimated by multivariate REML with an animal model on first-lactation field data of 377,945 Lacaune ewes for milk production and somatic cell count traits, on additional experimental data of 1,641 ewes for milk flow and 518 ewes for intra-mammary bacterial infection. Heritability estimates were high for annual milk flow traits (ranging from 0.36 to 0.64) and moderate for subclinical intra-mammary infections (0.18). A low to moderate (from -0.13 to +0.53) genetic correlations were found between milk yield and milk flow traits and indicated that the current selection in Lacaune sheep based on yield is associated to an increase of both parameters, milk flow and milking time. Lactation somatic cell score was positively correlated with subclinical intra-mammary infections (+0.72) and unfavourably associated with milk yield (+0.12). These results reinforce the interest of including LSCS in the breeding objectives of dairy sheep in order to balance the negative effect of selecting for increased production on udder health. The genetic correlation of intra-mammary infections with latency time was unfavourable and moderate (-0.33). The hypothesis was that ewes with high milk flow rate may have a lower sphincter tone facilitating pathogen entry.

Keywords: milking speed, udder health, sheep, genetic parameters

Introduction

Improving milking ability is a major issue for consideration in breeding dairy species. Milking is the most time-consuming task in dairy farming and the constant increase of both average flock size and productivity has been contributing to the extent of milking time. In France, Lacaune ewes are selected on milk production traits, somatic cell count and udder morphology. On the one hand, selection on somatic cell count is carried out to reduce intra-mammary infections. On the other hand, selection on udder morphology aims to improve milking ability indirectly. Direct assessment of milk flow can be assessed with automatic milking jars (Marie-Etancelin *et al.*, 2006). It is not yet recorded routinely in dairy sheep

flocks, but such devices are becoming more common. This offers a new avenue for breeding programs but relationships with traits under selection and with udder health need to be estimated.

The purpose of this study was thus to estimate heritability estimates for milk flow traits and genetic correlations with milk production and with udder health traits characterised by milk bacteriological titer and somatic cell count in Lacaune dairy sheep.

Material and methods

Data: animals and phenotypes

Data originated, on the one hand, from 473 official milk recording flocks, and on the other hand, from the INRA experimental sheep flock of La Fage (Saint-Jean-et-Saint-Paul, France). The on-farm data set included 377,945 first-lactation Lacaune ewes evaluated in the official milk recording system from 2006 to 2016. Milk production and somatic cell count traits were those considered for official genetic evaluation: 150-d lactation for milk yield (MY), fat and protein contents (FC and PC) and lactation somatic cell score (LSCS) as described in Rupp *et al.* (2003). These 377,945 first lactations included 1,641 first lactations from the experimental INRA flock recorded over the same period.

The INRA experimental flock provided additional data on milk flow and udder health. First, milk flow patterns were measured by an automatic milk-recording device, conceived by the INRA-SAGA (European patent No. 94916284.6). This machine consists of a set of 24 jars operating simultaneously during the collective milking as described by Marie-Etancelin *et al.* (2006). Briefly, each jar, with a capacity of 2.9 L, has a central bar composed of switches and which slides a float thereby actuating this switches according to the milk volume. Jars store the starting and total time of milking, the latency time between the teat cup attachment and the recording of 51 mL of milk in the jar (needed to obtain a first measurement), and 50 intermediate measures of the milk volume in the jar every 5 seconds. From 2006 to 2016, milk flows measurements were collected at each official milk recording and the latency time (LT), the real milking time (RMT), the maximum milk flow (MMF) and the average milk flow (AMF) were estimated for each milking. Then these 4 traits obtained at morning milking were averaged per ewe over the entire lactation period. The arithmetic mean of each trait included 6.5 test-days since a total of 10,728 morning milk flow patterns of 1,641 primiparous ewes were available.

Second, milk samples were collected between 2008 and 2014 at INRA La Fage experimental farm on a subset of 518 primiparous ewes to analyze udder health status and intra mammary infections (IMI). Milk samples of each half of the udder were aseptically collected after lambing and at three dates during lactation. Milk staphylococci were quantified by a molecular technique developed at IHAP (ENV Toulouse, France). Briefly, the method combines an original extraction technique (pre-centrifugation of milk in 96-well format and semi-automated DNA extraction) and semi-high throughput qPCR in 384-well format. The result was a bacterial titer expressed as a quantity of bacterial genomes in 10 μ L of milk, expressed on a logarithmic scale. To study genetic parameters, we used lactation average bacterial titer (BACT).

Genetic parameter estimation

Heritability estimates and genetic correlations among the nine lactation traits described previously were estimated by multivariate REML, using WOMBAT software (Meyer, 2007). The animal model included the following fixed effects: flock by year combination (4,154 levels), age at lambing (6 levels), month of lambing (6 levels), time between lambing and the first test-day (5 levels), combination of test-day records (6 levels), number of suckled lambs (2 levels), the random genetic effect of animal and the residual. Five generations of ancestors were traced for the relationship matrix (578,521 animals). Genetic parameters were estimated from a series of tri-variate analyses. The LSCS trait was always included because half of the 1,641 ewes of the experimental farm were divergently selected for that trait.

Results and discussion

Summary statistics are presented in Table 1. The mean LSCS was close to that observed by Rupp *et al.* (2003). The average value of BACT was 0.69 and ranged from -1.25 to 5, which corresponds to 400 staphylococci per mL of milk (range from 0 to 1 000 000). LT and MMF were 26 s and 14.4 mL/s, respectively and were in the range of values observed previously by Marie-Etancelin *et al.* (2006), in the same breed. However, AMF was 8.6 mL/s and notably higher than the mean reported by Marie-Etancelin *et al.* (2006), i.e. 5.4 mL/s. This difference could be partly due to the calculation of AMF, which was done using 5 s intervals in the present study whereas Marie-Etancelin *et al.* (2006) used 10 s intervals. RMT, a new trait considered in our study, was 122 s on average in Lacaune ewes.

Table 1. Summary statistics for nine traits pertaining to milk production, udder health and milking speed measured in 473 Lacaune sheep flocks.

	N	Mean	SD	Min	Max
Milk Yield (MY) (L)	377,945	333.9	70.9	25.8	836.5
Fat Content (FC) (g/L)	377,917	67.9	8.5	25.0	115.0
Protein Content (PC) (g/L)	377,917	53.9	4.3	35.0	75.0
LSCS	377,945	2.87	1.4	-1.44	9.91
Milk bacterial titer (BACT)	518	0.695	0.913	-1.254	5.000
Latency Time (LT) (s)	1,641	26.4	8.7	10.2	86.7
Real Milking Time (RMT) (s)	1,641	122.7	20.5	30	213.3
Maximum Milk Flow (MMF) (mL/s)	1,641	14.4	4.1	2.8	33.0
Average Milk Flow (AMF) (mL/s)	1,641	8.6	2.0	2.2	27.7

Genetic parameters are provided in Table 2. The heritability estimates of lactation milk production traits (ranging from 0.46 to 0.62) were higher than those found by Barillet (2007), using a sire model. Heritability estimates for annual milk flow traits were high (ranging from 0.36 to 0.64), and were similar to those described previously by Marie-Etancelin *et al.* (2006). The heritability of the annual average RMT was 0.47. The estimates of genetic correlations among milk flow traits were high. The genetic correlation between TL and MMF was consistent with the estimate reported by Marie-Etancelin *et al.* (2006). The genetic correlations between TL and AMF (-0.83) and between MMF and AMF (+0.89) were higher and more precise than those of Marie-Etancelin *et al.* (2006). The genetic correlations between RMT and other milk flow traits were also high (from -0.72 with MMF to +0.81 with

TL). These high genetic relationships showed that those variables were partly expressions of the same trait.

Table 2. Heritability estimates (standard errors) [on diagonal] and genetic correlations (standard errors) [above the diagonal] between milk production (MY, FC, PC), udder health (LSCS and BACT) and milking speed traits (log(LT), RMT, MMF, AMF) in Lacaune dairy sheep.

	MY	FC	PC	LSCS	BACT	Log(LT)	RMT	MMF	AMF
MY	0.46 (0.004)	-0.27 (0.005)	-0.55 (0.006)	+0.12 (0.01)	+0.31 (0.17)	-0.13 (0.07)	+0.28 (0.08)	+0.32 (0.07)	+0.53 (0.07)
FC		0.60 (0.004)	0.63 (0.004)	+0.10 (0.01)	+0.17 (0.18)	+0.13 (0.07)	+0.07 (0.08)	-0.12 (0.07)	-0.25 (0.08)
PC			0.62 (0.004)	+0.06 (0.01)	+0.12 (0.17)	+0.01 (0.07)	-0.12 (0.07)	-0.08 (0.07)	-0.24 (0.08)
LSCS				0.22 (0.004)	+0.72 (0.15)	-0.24 (0.07)	-0.10 (0.08)	+0.27 (0.08)	+0.26 (0.09)
BACT					0.18 (0.07)	-0.33 (0.17)	-0.04 (0.19)	+0.28 (0.18)	+0.30 (0.20)
Log(LT)						0.64 (0.05)	+0.81 (0.04)	-0.93 (0.02)	-0.83 (0.04)
RMT							0.47 (0.05)	-0.72 (0.06)	-0.59 (0.08)
MMF								0.54 (0.05)	+0.89 (0.03)
AMF									0.36 (0.05)

The genetic correlations of milk flow traits with milk production traits were low to moderate, and were largest for MY, particularly between MY and AMF (+0.53). The latency time was less milk yield dependent (from -0.13 with MY to +0.13 with FC). The result indicated that the current selection based on yield in Lacaune sheep is associated with increased milk flow as reported by Marie Etancelin *et al.* (2006) and, to a lesser extent, to increased milking time (+0.28 with MY).

Heritability for BACT was moderate (0.18). It was the first estimate for subclinical IMI in dairy sheep, and one of the very few available in dairy ruminants (Weller *et al.*, 1992; review in Rupp *et al.*, 2011). It was close to the heritability of LSCS (0.22), which was slightly higher than the previous estimate in this breed with a sire model (0.13) (Rupp *et al.*, 2003) and in other sheep and cattle populations (heritability around 0.15 in the review by Rupp *et al.*, 2011). The genetic correlation between LSCS and BACT was high with a value of +0.72, while it was also estimated at close to unity in a study based on 9,800 cows (Weller *et al.*, 1992). These reasonably high values suggest common mechanisms that lead to either continuously low SCC or better resistance to persistent IMI.

The genetic relationship between LSCS and milk yield was moderate and unfavourable (+0.12) in first lactation, as also reported by Rupp *et al.* (2003). The genetic correlation between BACT and milk yield was also unfavourable and higher (+0.31). These results reinforce the interest of including LSCS in the breeding objectives of dairy sheep in order to balance the negative effect of selecting for increased production on udder health.

The genetic relationships of LSCS with milk flow traits and of BACT with milk flow traits were very similar. For both traits, the genetic correlations with RMT were close to zero, ranging from -0.24 to -0.33 with LT and ranging from +0.26 to +0.30 with AMF and MMF. These results are consistent with the hypothesis that ewes with high milk flow are more likely to allow the mastitis pathogens entering the udder due to a higher relaxing ability of the teat muscle (Dhorne-Pollet *et al.*, 2012). It may also reflect an indirect association due to the unfavorable genetic correlation of BACT/LSCS traits with milk production traits.

Conclusion

Genetic parameters for bacterial titers in milk and real milking time were estimated for the first time. In dairy ewes, genetic selection for milk yield reduced latency time and increased milk flow. This indirect genetic selection on milk flow may have led to reduction of sphincter tone, facilitating pathogen entry. The genetic selection on SCC has probably reduced this adverse effect, and contributed to an improved udder health. Large scale recording for milk flow should soon be possible with the LactoCorder®, a new automatic milk-recording device conceived for official milk recording and recently agreed upon by ICAR for sheep.

List of References

- Barillet, F., 2007. Genetic improvement for dairy production in sheep and goats. *Small Rumin. Res.* 70: 60-75.
- Dhorne-Pollet, S., C. Robert-Granié, M.-R. Aurel & C. Marie-Etancelin, 2012. A functional genomic approach to the study of the milking ability in dairy sheep. *Anim. Genet.* 43 (2) : 199–209.
- Marie-Etancelin, C., E. Manfredi, M.R. Aurel, F. Pailler, J. Arhainx, E. Ricard, G. Lagriffoul, P. Guillouet, B. Bibé & F. Barillet, 2006. Genetic analysis of milking ability in Lacaune dairy ewes. *Genet. Sel. Evol.* 38(2): 183-200.
- Meyer, K., 2007. WOMBAT: A tool for mixed model analyses in quantitative genetics by REML. *J. Zhejiang Univ. Sci. B* 8: 815–821.
- Rupp, R., G. Lagriffoul, J.M. Astruc, M. Jacquin & F. Barillet, 2003. Genetic parameters for milk somatic cell scores and relationships with production traits in French Lacaune dairy sheep. *J. Dairy Sci.* 86: 1476-1481.
- Rupp, R. & G. Foucras, 2011. In: *Breeding for disease resistance in farm animals*. Chapter 9. *Genetics of Mastitis in Dairy Ruminants*. 3rd ed. Wallingford: CABI publishing; 2011.
- Weller, J., A. Saran & Y. Zeliger, 1992. Genetic and environmental relationships among somatic cell count, bacterial infection, and clinical mastitis. *J. Dairy Sci.* 75(9): 2532–2540.