Selecting milk composition and mastitis resistance by using a part lactation sampling design in French Manech red faced dairy sheep breed

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Summary

To face the new challenge of selecting dairy sheep for udder functional traits, it is necessary to implement very simplified designs as part-lactation sampling promoted by ICAR in small dairy ruminants, to reduce dramatically recording costs. Such a design has been applied efficiently in Lacaune dairy sheep breed since 1985 for milk composition and also since 1999 for somatic cell count (SCC) after validation of its relevance for this udder health trait (SCC). Without any verification, such a part-lactation design has been implemented since 2002 in Manech red faced (MRF) breed. Records from 58 378 primiparous MRF dairy ewes were used to estimate genetic parameters for milk traits and SCC in this breed. The heritability estimate of SCC was 0.10 for the lactation mean trait. The genetic correlation between lactation SCC and milk yield was positive (0.21), i.e. antagonistic, as already found in Lacaune dairy sheep, in agreement with the well documented literature in dairy cattle. These results obtained for a medium milk yield level breed reinforce the idea that the genetic relationships between udder health (SCC) and milk yield are comparable between dairy cattle and dairy sheep. The results also confirm that the part-lactation sampling testing is a suitable design both for milk composition and SCC whatever the dairy sheep breed.

***Key words**: Dairy sheep, Recording design, Simplification, Milk yield, Fat and protein contents, Somatic cell count, Mastitis resistance, Breeding goals.*

Introduction

The emphasis for udder functional traits has resulted from the knowledge established during the last ten years that exclusive selection of dairy sheep on milk traits would lead in the long term to udders more difficult to milk by machine and also more susceptible to mastitis (Barillet, 2007). The French dairy sheep Lacaune

breed has the oldest and most efficient breeding scheme based on an extensive use of AI since the 1980s. It is therefore not surprising that the Lacaune breeders have chosen new breeding objectives in 2005 giving the same relative weights to milk production traits (milk yield and composition) and udder functional traits (udder scoring for milkability and somatic cell count (SCC) for mastitis resistance). The example of the Lacaune breed shows that a part-lactation sampling design allows efficient selection both on milk composition (fat and protein contents) and mastitis resistance (SCC), while reducing dramatically the number of test days involved in a qualitative recording compared to the A4 testing. Thus without no more verification this recording strategy has also been applied since 2002 for the second French dairy sheep breed, the Manech red faced (MRF) breed, to face its new breeding goals.

The objective of the present study is to analyse the MRF data to verify that such a design is suitable to MRF, i.e. to any breed, given that the MRF breed is a medium milk yield breed compared to the Lacaune dairy sheep belonging to the high milk yield level breeds. Regarding the MRF breed, the present study is the first step towards an evolution of its breeding goals.

Materials and methods

Data

The MRF breeding programme became fully efficient for milk yield in the 1990's exhibiting an annual genetic gain close to 4 litres, i.e. 2.2 % of the population mean (Astruc *et al.*, 2002). Therefore the recording of milk composition (fat and protein contents) became a priority at the beginning of the 2000's. To face the question and reduce dramatically the recording cost, a part-lactation sampling design in first lactation has been implemented as already practised in France in Lacaune breed, i.e. only two to four times during the first 4 test days of each ewe at the morning milking (Barillet, 1997). Moreover, it was assumed that such a part-lactation sampling

Table 1. Characteristics of the data.

Characteristics	
Breed	Manech red faced
Study period	2002-2007
Animals in data (first lactation for milk traits and SCC)	58 378
Animals in pedigree	118 313
Number of flocks (flock x year)	258 (1221)
Mean ± standard deviation of the traits	
Lactation number	First lactation
Length of milking period d (after a 30-d suckling period)	132d±42
Milk yield, litre (lactation basis[1])	149.2l±63.1
Equivalent mature milk yield corrected for length of milking period, litre... (lactation basis[1])	217.2l±65.8
Fat yield, g (part lactation sampling[2])	1 3096g±3 820
Protein yield, g (part lactation sampling[2])	1 0333g±3 073
Fat content, $g.l^{-1}$ (part lactation sampling[2])	61.1g/l±8.8
Protein content, $g.l^{-1}$ (part lactation sampling[2])	47.8g/l±3.9
Lactation SCS (LSCS) arithmetic mean of SCS (2)	3.36±1.38

[1]Monthly recording design at the morning milking (AC method) with 4.4 test days on average per first lactation.
[2]Part lactation sampling with 2.8 test days on average at the morning milking within the first 4 test days for milk yield of each ewe.

design was also relevant in MRF breed for SCC as previously demonstrated in Lacaune breed (Barillet *et al.,* 2001; Rupp *et al*., 2003). The years 2002-2007 were needed to generate enough data on milk composition and SCC in the MRF nucleus flocks, and were simultaneously made profitable to intensify the PrP selection: from 2001 to 2005, the ARR allelic frequencies at the PrP gene in the MRF nucleus flocks increased from 0.19 to 0.50, while it reached 0.74 for the AI rams born in 2004 (Barillet, 2007). Under these conditions, after data editing, 58,378 MRF ewes, recorded in first lactation for milk composition and SCC between 2002 and 2007, were included in the analysis (Table 1).

These primiparous MRF ewes were recorded on average with 4.4 test days for milk yield per first lactation and, due to the part lactation sampling design, with 2.8 test days on average for milk composition (fat and protein contents) and SCC, at the morning milking only, since all these recordings were carried out in the framework of the AC method as described in ICAR rules for dairy sheep (Table 1).

Estimation of genetic parameters

A cell count lactation mean (LSCS) was computed as the arithmetic mean of test-day somatic cell score (SCS) as proposed by Wiggans and Shook (1987), SCS being defined in a classical way through a logarithmic transformation

$$SCS = \log_2(SCC/100\,000)+3$$

to account for the highly skewed distribution of SCC. Genetic parameters for milk production traits and LSCS were estimated using a REML method applied to an animal model on the 58,378 MRF ewes with data in first lactation and 118 313 animals in pedigree traced up to 4 generations of ancestors for the ewes with records (Table 1). The fixed effects corresponded to those applied in the calculation of the official EBV for each trait (Astruc *et al*., 2002): for milk traits considered on a lactation basis, the model included the fixed effects of flock x year x parity, age and month at lambing within parity and year, for milk yield the lambing-first test-day interval within year and parity, for fat and protein yields or contents the effect of qualitative recorded category defined with the number of test-days x average lactation stage at recording.

Results and discussion

Genetic parameters are presented in table 2. They follow the well known patterns for milk traits (Barillet, 1997 and 2007), given the part-sampling design for fat and protein contents. Indeed, fat (FC) and protein (PC) contents determined from a part lactation sampling (2.8 test days at the morning milking versus 4.4 on average for milk yield – Table 1) are, as expected, less heritable (0.28 and 0.51 respectively for FC and PC) than the homologous genetic parameters when using the A4 method (heritabilities in the range of 0.60 for FC and 0.55 for PC). We can notice that the decrease of heritability is really limited for part lactation sampling PC, in agreement with previous Lacaune results. Nevertheless heritabilities of FC and PC with such a part-lactation sampling design remain high enough, and at least comparable to those of fat or protein yields (0.28 to 0.30), which is suitable for selection purposes, since the breeding scheme is designed for milk, fat or protein yields. Moreover heritabilities of yields based on such a part lactation sampling are quite identical to the heritabilities of yields when recorded on a A4 basis. Furthermore the genetic antagonism between milk yield (MY) and FC or PC (-0.39 and -0.44 respectively) is the same whatever the design (A4 or part lactation sampling) in MRF breed as already shown in Lacaune breed (Barillet, 1997 and 2007).

Table 2. Genetic parameters: heritabilities[1] on diagonal, genetic correlations[2] above and environmental correlations under the diagonal.

Trait	MY	FY	PY	FC	PC	LSCS	Trait	σp[3]	σg[4]
Milk yield (MY)	**0.33**	0.87	0.92	-0.39	-0.44	0.21	MY	51 l	30 l
Fat yield (FY)	0.84	**0.28**	0.91	0.10	-0.16	0.25	FY	3161 g	1662 g
Protein yield (PY)	0.96	0.82	**0.30**	-0.16	-0.06	0.25	PY	2352 g	1277 g
Fat content (FC)	-0.17	0.34	-0.16	**0.28**	0.60	0.07	FC	7.8 $g.l^{-1}$	4.1 $g.l^{-1}$
Protein content (PC)	-0.34	-0.20	-0.04	0.16	**0.51**	0.07	PC	3.6 $g.l^{-1}$	2.6 $g.l^{-1}$
LSCS (LSCS)	-0.26	-0.16	-0.17	0.16	0.38	**0.10**	LSCS	1.31	0.42

[1]Standards errors between 0.01 and 0.02
[2]Standards errors between 0.01 and 0.03.
[3]Phenotypic standard deviation.
[4]Genetic standard deviation.

On the other hand, the present results (Table 2) regarding the cell count mean (LSCS) confirm, in MRF breed as in Lacaune breed (Barillet *et al.,* 2001), that the genetic parameters are quite similar for part-lactation or total lactation sampling of SCC: a moderate heritability (0.10) of LSCS whatever the sampling design and a genetic antagonism between LSCS and milk yield (0.21) or fat (0.25) or protein yields (0.25). Thus the balance between cost and genetic efficiency is clearly in favour of the part lactation design both for milk composition (FC and PC) and SCC (LSCS). Such SCC results for MRF breed are in agreement with all the homologous results obtained in Lacaune dairy sheep breed between 2001 and 2007 (Table 3) and with the abundant literature in dairy cattle. As reported in dairy cattle reviews (Mrode and Swanson, 1996; Detilleux, 2002; Rupp and Boichard, 2003), heritability estimates of single SCC range from 0.05 to 0.14 for monthly test-day and increase on average up to 0.15 for lactation mean (LSCS) with a range 0.10-0.20. Moreover, in dairy cattle, the genetic antagonism between SCC and milk production traits is well documented (Mrode and Swanson, 1996; Rupp and Boichard, 2003): genetic correlation between SCC and milk yield is equal on average to 0.14, with a range 0.10-0.20 in cattle.

In dairy sheep, contrary to cattle, the lactation incidence of clinical mastitis (CM) is low and around 5 %, while the prevalence of subclinical mastitis (resulting mainly from bacterial infections whose reservoir is generally in the udder or teats) ranges from 10 to 50 % or more (Bergonnier *et al*., 2003; Berthelot *et al*., 2006). Thus, in dairy sheep, considering SCC only appears as a sound approach for selecting mastitis resistance. Assessment of the suitability of SCC for udder health in dairy sheep is under way in an experiment based on SCC divergently selected Lacaune dairy sheep lines in an INRA experimental flock (La Fage): first results show a clear decrease of CM and udder infections caused by mammary pathogens (measured by repeated bacteriological tests during the lactation) for the low SCC line (Rupp *et al.*, 2006). Since SCC is a suitable tool for selecting resistant dairy sheep, it is therefore important to overcome the present inconsistency regarding SCC genetic parameters in this species. In dairy sheep, heritability estimates of single SCC range between 0.04 and 0.14 for monthly test-day and between 0.10 and 0.18 for lactation measures (Table 3), which is in agreement with homologous dairy cattle results. But genetic relationships of udder health (SCC) with milk yield (or fat or protein yields) are quite inconsistent in dairy sheep, ranging from antagonistic (Mavrogenis *et al*., 1999; Barillet *et al*., 2001; Rupp *et al*., 2003; Barillet, 2007; Riggio *et al*., 2007) to favourable (El-Saied *et al*., 1998; Othmane *et al*., 2001; Serrano *et al*., 2003; Hamann *et al*., 2004; Legarra and Ugarte, 2005). When looking at these results (Table 3), we

Table 3. Estimates of genetic parameters for milk yield (MY) and somatic cell score (SCS) in dairy sheep.

Breed (authors and year)	Data	Heritabilities MY	Heritabilities SCS	Genetic correlation MY- SCS
Chios (Mavrogenis *et al.,* 1999)	1 457 ewes/1 457 lactations first lactation (test day model)	0.26	0.18	0.20
Churra (El-Saied *et al.,* 1998)	2 379 ewes/3 231 lactations all lactations (lactation model)	0.24	0.12	- 0.15
Lacaune (Barillet *et al*., 2001)	5 272 ewes/5 272 lactations first lactation (lactation model)	0.34	0.15	0.11
	first lactation (test day model)	0.24	0.08	0.04
Churra (Othmane *et al*., 2001)	1 111 ewes/1 962 lactations all lactations (lactation model)	0.26	0.11	- 0.17
Lacaune (Rupp *et al*., 2003)	94 474 ewes/139 973 lactations lactations 1 and 2 (if 1 known) (lactation model)	0.28	0.13	0.18
Manchega (Serrano *et al*., 2003)	28 694 ewes/36 873 lactations 3 lactations (lactation model)	0.27	0.12	- 0.12
East-Friesian (Hamann *et al*., 2004)	1 108 ewes/1 746 lactations all lactations (test day model)	0.15	0.16	- 0.08
Latxa (Legarra and Ugarte, 2005)	6 165 ewes/9 805 lactations all lactations (lactation model)	0.21	0.13	-0.29
Lacaune (Barillet, 2007)	121 283 ewes /121283 lactations first lactation (lactation model)	0.32	0.15	0.15
Valle del Belice (Riggio *et al*., 2007)	2 277 ewes/13 066 test-days first lactation (test day model)	0.14	0.14	0.16

can notice that authors studying only first lactations or two first lactations only if the first one was also available in the data (Rupp *et al.,* 2003) found antagonistic relationships between SCC and milk yield (Table 3) as in dairy cattle. On the contrary all the analysis estimating favourable relationships between SCC and milk yield were based on data including all lactations (Table 3). Moreover these studies were usually based on a few years of experimental recording with more records in multiparous lactations than in first lactations. Thus data editing did not exclude a later parity if the previous one was unknown in the data. Therefore culling on milk yield or udder health over lactations not taken into account in these studies could explain favourable and thus probably biased association found in these analysis. The contradictory results in Latxa breed (Legarra and Ugarte, 2005) and Manech red faced breed (this paper), these 2 breeds belonging to the same medium milk yield Pyrenean population, reinforce the present interpretation: the genetic correlation between SCS and milk yield was estimated as favourable in Latxa breed (- 0.29 with 9805 multiparous lactations) and as antagonistic in Manech red faced breed (+0.21 with 58 378 first lactations in the present results). Under these conditions, we incline to consider unfortunately as more likely that in dairy sheep as in dairy cattle the genetic relationship between udder health (SCC) and milk production traits is antagonistic, and that udder health will be deteriorated when selecting only production traits.

Conclusion

Genetic improvement of udder functional traits has become a new challenge in dairy sheep, since there is now evidence that selection on milk traits only will lead in the long term to udders more difficult to milk by machine and more susceptible to mastitis. The present results obtained in MRF breed, first confirm the genetic trends described above specially for mastitis susceptibility, second validate the part-lactation sampling design as a suitable tool both for milk composition (FC and PC) and udder health (SCC) whatever the breed. Thus including udder scoring and SCC in the breeding goals, at the moment on a quantitative genetic basis, is a new challenge applied in France for the Lacaune breed since 2005 and in progress for other breeds such as MRF breed. Moreover windows opened by molecular genetics will be profitable for udder functional traits as it is already the case for the PrP gene for scrapie resistance (Barillet, 2007).

Finally the promotion of the part-lactation sampling design by the ICAR dairy sheep group appears as a sound strategy to reduce dramatically the recording cost in small dairy ruminants while facing new objectives related to udder functional traits. On the other hand this strategy of reducing the qualitative tests to decrease the recording costs in small ruminants needs to maintain a high accuracy of each individual test day as presently defined in ICAR requirements regarding manual or electronic milk recording devices and analytical quality analysis of sheep milk in laboratories.

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