ESTIMATES OF GENETIC PARAMETERS FOR MILK FLOW KINETICS DURING MACHINE MILKING IN FRENCH LACAUNE DAIRY SHEEP

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INTRODUCTION

In France, since dairy sheep has been efficiently selected on milk traits, more attention is now given to face new goals relevant to reduce the production costs and increase the quality and safety of products. In that way, on-going research is focusing on genetic determinism of milkability which is an important functional trait with regard to udder health as well as to milking labour efficiency. Research regarding selection for mastitis resistance or udder morphology is on-going both on-farm and experimental flock (Barillet *et al.*, 2001 ; Marie-Etancelin *et al.,* 2001 ; Rupp *et al.,* 2002). Conversely in France, research on genetic determinism of milkability in sheep is in progress only in an INRA experimental flock (La Fage), since corresponding phenotypes have been recorded for several years only in this farm. Indeed unlike bovine, the individual milking time is not a relevant trait of the milkability of sheep, since it describes only the milking routine (Flamant, 1974). Therefore, in order to measure traits related to milkability, INRA conceived an electronic jars device for sheep and goats, enable to record milk flow kinetics (Ricard *et al.*, 1995).

The purpose of this paper is to present a first genetic analysis of milk flow kinetics of Lacaune ewes collected during 5 years in this experimental flock.

MATERIAL AND METHODS

Data. The data set included records from two first lactations Lacaune ewes collected from INRA experimental flock (La Fage) between 1997 and 2001. The edited file included respectively 751 and 615 first and second lactations of 751 ewes belonging to two divergent lines, denoted High and Low. These two lines have been selected for dry matter yield (fat and protein) since 1989. Each year, the 10-20 top-ranked and bottom-ranked rams were selected among 600 artificial insemination rams of the Lacaune breeding programme, to procreate 3-4 daughters per sire in the INRA experimental flock (Barillet *et al.,* 2001). Such a design corresponds to a pseudo-divergent selection of lines opened on the on-farm breeding scheme. Then if the genetic mean level of the 2 lines is increasing each year, the genetic difference for milk yield between the High and Low lines remains constant and limited to the difference in the EBV between the two groups of sires, about 60 liters, i.e. about 10 years of the estimated genetic trend in the Lacaune evaluation (Astruc *et al.*, 2002).

Definition of traits. Every 3 weeks, at morning milkings, were recorded milk yield and milk flow kinetics using INRA electronic jars (Ricard *et al*., 1995). The jars enable to store the

starting and total time of milking, the lag time between teat cup attachment and the arrival of 160 ml of milk in the jar needed to obtain a first measurement, and 12 intermediate measures of the milk volume in the jar during the milking at a fixed time interval chosen beforehand by the milker, i.e. every 10 seconds for the INRA flock.

In the present analysis, the following traits were considered :

- in a first step, 5 traits corresponding to morning test-days for the milk yield (MMY), the lag time (LT), the maximum milk flow (PEAK) and the moment of its occurrence (MOC) after the lag time, and the average milk flow (AMF) computed as the average of the 12 intermediate measures during milking. Because LT and MOC have highly skewed distributions, LLT and LMOC were defined respectively through the following logarithmic transformations: LLT = Log(TL+4) and LMOC = Log(MOC).

- in a second step, the arithmetic mean of each test-day trait described above were computed and considered as a lactation mean trait, i.e. (LMMY), (LLLT), (LPEAK), (LLMOC), (LAMF). On average, the arithmetic mean of each trait included 6.8 test-days since a total of 9288 morning milking kinetics were available for the two first lactations of the 751 ewes.

Estimation of genetic parameters. Variance components were estimated by REML applied to multivariate animal models, using the VCE package (Neumaier *et al.*, 1998).

In a first analysis, the 5 mean traits per lactation were considered as different traits in first and second lactation, and were analysed according to the following linear model :

$$Y_{ijklmn} = \text{Year}_i + \text{Line}_j + \text{Month}_k + \text{Age}_l + \text{Lambs}_m + a_{jn} + e_{ijklmn}$$

including the fixed effects year (5 levels), divergent lines (2 levels), month of lambing within parity (2 levels), age at lambing within parity (4 levels), number of suckled lambs (2 levels), and the random genetic effect of animal *n* within line *j*.

A second analysis was performed for the 5 mean traits in first lactation only with the same linear model, except that month and age at lambing were defined only in first parity.

Five generations of ancestors were traced for the relationship matrix and the total number of animals was 4726.

RESULTS AND DISCUSSION

Basic statistics. Basic statistics of the test-day traits in the two first lactations at morning milking are presented in table 1.

Table 1 . General statistics of the data set (9288 kinetics at morning milking in two first lactations)

Trait			Mean	S.D.	CV (%)
Test-days mean (1)					
Morning milk yield	(ml)	MMY	829	481	58
Lag time	(sec)	LT	29	22	76
Maximum milk flow	(ml/sec)	PEAK	12.9	6.2	48
Moment of its occurrence	(sec)	MOC	30	23	77
Average milk flow	(ml/sec)	AMF	5.4	3.7	69

(1) on average 6.8 test-days per mean trait

The average morning milk yield (MMY) was 829 ml. The lag time (LT) between teat attachment and the arrival of 160 ml of milk in the jar (due to the conception of the device) was 29 seconds. Then the maximum milk flow occurred 30 seconds later (MOC) and reached (PEAK) 12.9 ml/sec, i.e. 0.774 l/min. Finally the average milk flow (AMF) was 5.4 ml/sec or 0.324 l/min. On the other hand, the coefficients of variation of these 5 traits were high enough and ranged between 48 and 78 %.

Genetic parameters. Heritability estimates for the five mean traits defined as 5 different traits in first and second lactations were very similar (table 2) : on the first hand, they ranged between 0.35 and 0.43 for milk yield (LMMY), and increased from about 0.35 for LAMF, 0.50 for LPEAK to about 0.60 for LLLT which appeared as the more heritable kinetic trait. On the other hand, the high genetic correlations between parities, 0.90 to 0.98 according to the trait, showed that each studied milk yield or kinetic trait was the same trait genetically between first and second lactation.

The heritability estimates of milk yield trait (LMMY), 0.35 to 0.43, are a little bit high compared to literature. Indeed for the usual lactation trait computed with Fleischman method, Barillet (1997) reviewed an heritability equal on average to 0.32. It is probably due either to the fact that the morning milking yield needed to be adjusted for days in milk or that data should have been weighted according to the number of test-day records to account for the milking length of each animal when computing LMMY. However, the heritability of LMMY is consistent enough to show that heritabilities of LLLT and LPEAK are higher (respectively about 0.60 and 0.50) in general agreement with dairy cattle literature. In cattle, heritability of LPEAK ranged from 0.21 (Santus *et al.,* 1998) to 0.48 (Duda, 1996; Dodenhoff *et al*., 2000). LLLT, not usually recorded in cattle since meters and not jars are used for the recording, shows the higher heritability estimate in our data set, and consequently appears as the more relevant trait to describe the milk flow kinetics in sheep.

Table 2. Genetic parameters of milk yield and kinetics traits defined as different traits in first and second lactation

Traits	Heritabilities *(s.e.)* in 1st lactation	Heritabilities *(s.e.)* in 2nd lactation	Genetic correlation *(s.e.)* between 1st & 2nd lactation traits
LMMY	0.43 *(0.047)*	0.35 *(0.051)*	0.96 *(0.033)*
LLLT	0.57 *(0.047)*	0.62 *(0.049)*	0.90 *(0.019)*
LPEAK	0.50 *(0.042)*	0.50 *(0.049)*	0.98 *(0.011)*
LLMOC	0.46 *(0.039)*	0.47 *(0.049)*	0.98 *(0.010)*
LAMF	0.36 *(0.046)*	0.34 *(0.050)*	0.98 *(0.027)*

The genetic correlations between the 5 mean traits in first lactation are presented in the table 3. Genetic correlations between LMMY and LAMF (0.99) showed that they were the same trait genetically, as between LLLT and LPEAK (-0.92). Genetic correlations between LLLT and LLMOC (0.74) or between LPEAK and LLMOC (-0.64) were higher than between LPEAK and LAMF (0.51), but were all very coherent. Finally the genetic correlations respectively between LMMY and LLLT (-0.23) or LPEAK (0.46) or LLMOC (0.32) indicated that, when selecting on milk yield, an indirect favourable genetic response on milkability by machine is

expected : the lag time is decreasing, the milk flow peak is higher and occurs earlier, and globally the average milk flow is increasing. This indirect response is in agreement with the existence of an efficient breeding program on milk yield, managed by breeders who have simplified and standardized the machine milking routine which provides suitable environmental conditions for such an indirect response (Marie et al., 1999). Furthermore, the same favourable trend between milk yield and maximum milk flow was estimated in dairy cattle : genetic correlations ranging from 0.46 to 0.50 among cattle breeds (Duda, 1996; Santus *et al.,* 1998).

Table 3. Genetic correlations (*standard errors*) between milk yield and kinetic traits in first lactation

	LLLT	LPEAK	LLMOC	LAMF
LMMY	- 0.23 *(0.048)*	0.46 *(0.044)*	0.32 *(0.047)*	0.99 *(0.005)*
LLLT		- 0.92 *(0.022)*	0.74 *(0.048)*	- 0.27 *(0.058)*
LPEAK			- 0.64 *(0.053)*	0.51 *(0.047)*
LLMOC				0.25 *(0.058)*

CONCLUSION

This first genetic analysis showed that basic parameters of kinetics as lag time or maximum milk flow were relevant criteria for milkability classification in sheep, since they presented high heritabilities and favourable genetic correlations with milk yield ability. Further research will focus now on a more appropriate modelling of these time dependant data. Then research is needed to investigate the genetic relationships between milkability traits, udder scores, somatic cell scores, and milk production traits. Indeed the general objective corresponds to the definition of a global udder index allowing to improve both udder health and milkability with an acceptable loss of genetic gain on milk traits. Moreover, on-going QTL detection programs (Carta *et al.,* 2002 ; Schibler *et al*., 2002) may provide complementary results.

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