Genetic Evaluation of Mastitis in Dairy Cattle in France

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Abstract

Genetic parameters of clinical mastitis were estimated for the three main French dairy breeds: Holstein, Montbéliarde and Normande. Records were clinical mastitis events reported by farmers to milk recording technicians and the analyzed trait was the binary variable describing the occurrence of a mastitis case within the first 150 days of a lactation. Low heritability estimates were found: between 2 and 4 % depending on the breed but the trait has significant genetic variance despite its low heritability: efficient genetic improvement is possible.

Genetic correlations with other traits were estimated, showing large correlations (often >0.50, in absolute value) between clinical mastitis and somatic cell score (SCS), longevity and some udder traits. Correlation with milk yield was moderately large and unfavorable (ρ=0.26 to 0.30). High milking speed was genetically associated with less mastitis in Montbéliarde (ρ = -0.14) but with more mastitis in Holstein (ρ=0.18). Interbull genetic correlations are very high with Nordic countries, where much stricter recording systems exist (ρ =0.94). They were lower (around 0.80) with countries supplying SCS as a proxy for the international evaluation on clinical mastitis.

Clinical mastitis has been included since 2010 in routine evaluations using a multiple trait animal model. Mastitis estimated breeding values (EBV) are combined with somatic cell scores EBV into an udder health index which receives a weight of 14.5% to 18.5% in the new French Total Merit Index (ISU) of the three breeds.

Keywords: clinical mastitis, somatic cell,, genetic parameters, genetic evaluation, total merit index

1. Introduction

For the past two decades, there has been an increasing focus to control udder health in dairy cattle. Mastitis is a complex disease defined as an inflammation of the mammary gland. The consequences of clinical mastitis are higher veterinary costs, a decrease of milk production and higher rate of involuntary culling. The increase of Somatic Cell Scores (SCS, an indicator of subclinical and clinical mastitis) also has a strong incidence on milk price.

If management is an effective way to avoid mammary infection, selection for mastitis resistance is also a solution to be considered. Since 1997 in France, genetic evaluation of SCS has been an indirect way to evaluate resistance to mastitis (Rupp and Boichard, 1999). SCS records are available on a large scale at a moderate cost whereas clinical mastitis events are not compulsorily recorded. Although the genetic correlation between SCS and clinical mastitis is high, these traits cannot be considered as the same trait (Heringstad *et al.*, 2006). Furthermore, clinical mastitis is also unfavorably correlated with milk production. So on the long term, consequences of clinical mastitis for breeders are increasingly detrimental. To have a direct selection on this trait becomes a real need.

This paper describes the different steps which led to the implementation of a routine genetic evaluation on occurrence of clinical mastitis.

2. Material and Methods

2.1 Data and trait definition

Collection of data on occurrences of clinical mastitis started in France in 1995 on a small scale and was generalized to the whole country in 2008. Farmers are supposed to report any

event of clinical mastitis to the milk recording technician during his/her monthly visit. In practice, some herds do not report any case; others may not report all mastitis cases. As a consequence, a careful edit of the data has to be performed to exclude herds with suspected underreporting.

The analyzed trait for parameters estimation and genetic evaluation was defined as a binary (0/1) variable equal to 1 if at least one clinical mastitis event was reported within the first 150 days of lactation. To increase the probability that a 0 record (no mastitis occurrence) really corresponds to a healthy cow and not to an unreported event, records were selected only from farms (and regions) which seemed to correctly declare mastitis events, based on various criteria such as a minimum of 5% of lactations with a reported case of mastitis per herd and per year.

Only the first three lactations were considered, for the three main dairy cattle breeds in France: Holstein (HO), Normande (NO) and Montbéliarde (MO).

2.2 Genetic parameter estimation

Altogether, 206,661 MO, 187,668 NO and 296,758 HO lactations of cows were used for genetic parameters estimation. Records from lactations 2 and 3 were included only if records from previous lactation(s) were known.

Variance components were estimated either using a threshold sire model (with an in-house software called "catkit") or a sire or an animal linear model using restricted maximum likelihood as implemented in the WOMBAT software (Meyer, 2007).

A multiple trait mixed linear model treating each lactation record as a distinct trait was also tested. Genetic correlations between lactations were very high (results not shown). Therefore, only results based on threshold and linear models with permanent environment effects are presented here.

Given the binary nature of clinical mastitis, a threshold model is supposed to be more adequate. It assumes that the trait depends on the value of an unobserved underlying variable, which is normally distributed. Given the position of this value with respect to a threshold, the observed record is either 0 or 1. The model used was:

$$\mathbf{y} = \mathbf{X\ß} + \mathbf{Za} + \mathbf{Zp} + \mathbf{e} \qquad (1)$$

where **y** is the clinical mastitis indicator (or the underlying variable for the threshold model), **ß** is the vector of fixed effects consisting of a herd * year effect, a month of calving * region * year effect, and an age of calving * parity * year effect, **a** is the vector of normally distributed additive genetic effects $N(\mathbf{0}, \mathbf{A}\sigma_g^2)$ where **A** is the relationship matrix), **p** is the vector of random permanent environment effects $N(\mathbf{0}, \mathbf{I}\sigma_p^2)$ and **e** is a vector of random residual $(\mathbf{0}, \mathbf{I}\sigma_e^2)$. **X** and **Z** are incidence matrices and σ_g^2, σ_p^2 , σ_e^2 are the genetic, permanent environment and residual variances.

The year classes were defined from September 1st to August 31st the next year. Age at calving was defined as 3-month classes for first parity, and 4-month classes for second and third parity. Records from cows with calving below 21 months of age were removed from the analysis.

2.3 National genetic evaluation

A genetic evaluation for clinical mastitis was implemented. It has been running three times a year since June 2010 for the three main dairy breeds MO, NO and HO and was extended to five minor breeds (Brown Swiss, French Simmental, Tarentaise, Abondance and Red) in June 2011.

The genetic evaluation consisted of two steps: first, a univariate evaluation of clinical mastitis was performed, based on the same original database and the same trait definition and statistical model (1) as for the genetic parameters estimation. The only difference was that an heterogeneity of residual variances per region * year and per parity * year combination was included to account for the effect of the fluctuating mean incidence of mastitis on the variability of the binary trait. At the end of this evaluation, a pre-adjusted record was computed for each recorded cow using the methodology developed by Ducrocq (2001) and validated by

Lassen *et al.* (2007): original records were corrected by subtracting solutions for fixed effects, permanent environment effect and half the dam's genetic effect of the univariate evaluation. These corrected records were averaged over lactations 1 to 3 of each cow and a weight was associated to each of them. A special treatment was necessary for functional longevity records (see Ducrocq, 2001). Then, these pre-adjusted records together with similar records for other traits of interest and predictor traits computed in other evaluations (for production, type, functional traits, etc) were combined and analyzed with a multiple trait BLUP animal model. This multiple trait evaluation resulted in new breeding values for all traits and all animals which optimally combined direct performances and indirect information from correlated (indicator) traits. These combined breeding values are the ones which are officially published. They are also the ones included in the French Total Merit Index (called ISU).

2.4 Genetic correlations with other traits

To select the most relevant predictors for mastitis occurrence and to estimate the genetic correlations required for the multiple trait evaluation, a subset of the complete data file of each breed was prepared. Genetic correlations were then estimated by REML assuming known genetic and residual variances. The dataset consisted of records of daughters born between 1994 and 2008 from sires with a minimum of 10 daughters for MO and NO, and 30 for HO. In total, 1,113,331 (MO), 995,759 (NO) and 1,737,308 (HO) records of daughters of respectively 2,666, 2,101 and 2,429 sires were included in the analysis. After a trait selection step based on 2 by 2 correlations and discarding type traits non informative for any functional trait, genetic correlations between 16 (for MO and NO) or 17 (for HO) traits were estimated altogether with the following model:

$$\mathbf{y^*} = \mathbf{year} + \mathbf{Z\,a} + \mathbf{e^*} \qquad (2)$$

where **y*** is the pre-adjusted performance, **year** is the year of birth of the sire (to account for possibly biased genetic trend in the initial univariate analysis), **a** is the additive genetic effect and **e*** is a vector of random residuals with a specific variance for each pre-adjusted record accounting for the amount of information (weight).'

2. Results and Discussion

3.1 Genetic parameters

Results with the threshold model for the Montbéliarde breed gave a heritability of 6% on the underlying scale which corresponds to 3% on the observed scale. This value is slightly higher than the value of 2.3% obtained with the linear model. These results are consistent with a previous study by Bonaiti *et al.* (2005) reported heritability estimates using a threshold model also equal to 6%. The advantage of the threshold model is relatively small here because the mean incidence of the trait is not too extreme. For computation simplicity and consistency with the evaluation of other traits, the (animal) linear model was retained.

Heritability estimates for occurrence of clinical mastitis within the first 150 days of lactation are reported in table 1 for the three breeds.

Table 1. Genetic parameters for clinical mastitis, when using a repeatability animal model.

	MO	NO	HO
Mean incidence (%)	10	13	14
Genetic variance	0.0019	0.0022	0.0017
Heritability (%)	2.3	2.1	1.8
Repeatability (%)	5.5	6.2	5.5

Differences in heritability observed between breeds seemed to be at least partly related to the mean incidence of the trait and the quality of the data. A comparison of estimates obtained from different regional subsets showed that underreporting of mastitis cases (reflected by incidences lower than expected) led to lower heritability estimates. In Nordic countries. Heringstad *et al.* (1999) found a heritability of 3% with the same model as here. Only the definition of the trait differed (mastitis with a veterinarian treatment).

Table 2 shows the number of the lactations included in the June 2012 univariate genetic evaluation for MO, NO and HO.

Table 2. Number of lactations included in the June 2012 genetic evaluation.

	MO	NO	HO
Before edits	5,589,618	3,898,868	20,967,680
After edits	1,157,289	1,079,640	6,767,747
Mastitis occurrence (%)	8.8 [(a)]	12.4[(a)]	14.1[(a)]
Number of bulls	20,036	8,906	70,413

(a) At least one mastitis between 0 and 150 days in milk

3.2 Genetic correlations

Genetic correlations between mastitis occurrence and production traits are reported in Table 3. Standard errors were small (e.g., 0.028 to 0.04 for the Normande breed). As expected, an unfavorable positive correlation (0.26 to 0.30) with production was observed for all breeds. The large genetic correlations between somatic cell score (SCS) and mastitis (0.59 to 0.70) were consistent with the vast majority of published studies (e.g., Carlén *et al.*, 2004; Heringstad *et al.*, 2006), illustrating also that the two traits are far from being identical. The correlations with functional longevity (FL) were very similar across breed (-0.47 to -0.56) and of the same magnitude as the correlations between SCS and FL: for a cow, clinical and subclinical mastitis strongly increase the risk of being culled. Interestingly, the relationship between milking speed and mastitis occurrence varied from slightly favorable in MO (-0.14) to slightly unfavorable in HO (0.18). This may be the consequence of the strong selection to improve milking speed in HO, resulting in leakage for some cows, which is recognized as favoring mastitis. Udder depth was systematically the best morphological predictor of resistance to mastitis, especially in Montbéliarde (-0.54). Good conception rate and body condition score (available only in HO) were also favorably correlated with mastitis resistance.

Table 3. Genetic correlations with clinical mastitis in the three breeds HO, NO and MO.

	Occurrence of clinical Mastitis		
Trait	MO	NO	HO
Milk yield	0.30*	0.26*	0.26*
Somatic cell score	0.68	0.59	0.70
Functional Longevity	-0.56*	-0.48*	-0.47*
Milking speed	-0.14*	0.12*	0.18*
Udder depth	-0.54.*	-0.34*	-0.30*
Udder balance	-0.18*	-0.15*	-
Fore udder	-	-	-0.13*
Conception Rate	-0.29*	-0.31*	-0.25*
Body condition score	-	-	-0.32*

*negative values are favorable (e.g., it would be desirable to have high milk yield or good udder depth or body condition score genetically associated with fewer mastitis occurrence)

3.3 Genetic evaluation

These correlations were used in the multiple trait evaluation of which clinical mastitis is only one trait among many others. The importance of indirect predictors is illustrated by the increase in reliability when moving from the univariate evaluation to the multivariate one (Figure 1). On average, mastitis reliability was below 0.50 for progeny tested bulls whatever their birth year, i.e., below the reliability threshold for official EBV publication in France. For old proven bulls, this is related to the fact that most of their progeny had their first lactations before mastitis recording became a common practice in all French regions. For younger bulls, the low reliability simply reflects the low heritability of the trait. With the addition of other functional traits (SCS and FL essentially), reliability increased by about 0.20 whatever the age of the bulls. Udder traits added an extra 0.01 for old bulls and 0.03 for younger bulls. As a result, nearly all bulls – including the youngest ones- passed the 0.5 reliability threshold for official publication.

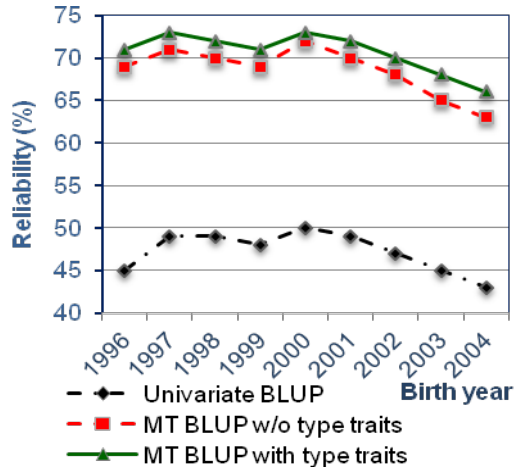

Figure 1. Mean reliability of mastitis EBV for bulls evaluated with different uni/multi-variate models (Holstein).

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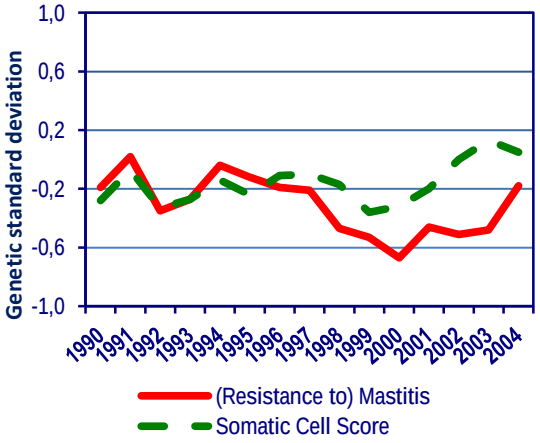

Figure 2. Genetic trend in Holstein (bulls with reliability >0.50).

Genetic trends (Figure 2 for HO) show that mastitis resistance declined even deeper than its predictor trait (SCS) in the nineties, as a result of the strong selection on production. The implementation of an official somatic cell count evaluation in 1997 and its inclusion in the total merit index (ISU) in 2001 reversed this trend for SCS for the past decade. This had a positive effect on mastitis but the genetic correlation between the two traits being far from unity, the genetic trend for mastitis is still lagging. Hopefully, this new evaluation will lead to a faster increase.

For the Montbéliarde breed, the trend was much flatter and it was more erratic (due to the influence of few sires of sons?) for the Normande breed.

EBV for mastitis from the univariate evaluation were sent to Interbull for the September 2011 test run. Interbull clinical mastitis (CM) evaluations are based on SCS proofs for most countries except for the Nordic countries (DFS) which are supplying CM evaluation based on an efficient and strict mastitis recording system. Replacing SCS by the French direct (i.e., not combined) CM EBV led to a very high genetic correlation between France and DFS (0.94), quite similar to the genetic correlations (0.90 to 0.97) between countries supplying the same trait (SCS) to the SCS international evaluation. In contrast, the genetic correlations between France or DFS and the countries supplying SCS EBV as proxy for the CM international evaluation were lower (around 0.80). This illustrates the added value of actually collecting direct information on clinical mastitis occurrence. It also shows that the less accurate recording system used in France based on voluntary reporting of health events give results equivalent to stricter recording protocols.

Table 4. Genetic correlations between countries used in Interbull MACE for somatic cell score and mastitis occurrence.

Interbull evaluation	Somatic cell score (SCS)		Clinical Mastitis (CM)		
Country	FRA	DFS	Trait used	FRA	DFS
DFS	0.97	-	CM	0.94	-
NLD	0.94	0.95	"SCS"	0.83	0.84
DEU	0.94	0.95	SCS	0.78	0.81
CAN	0.93	0.92	SCS	0.81	0.80
USA	0.90	0.88	SCS	0.82	0.83

Source: http://www-interbull.slu.se/udder/framesida-udder.htm

Conclusion and implication

Combined EBV as well as genomically enhanced EBV on clinical mastitis have been published in France three times per year since June 2010. Despite a not particularly strict data collection system and a low heritability, these EBV are a valuable tool together with the EBV for SCS to counterbalance the decline in mastitis resistance due to selection on production traits.

The inclusion of clinical mastitis in the approximate multivariate BLUP animal model evaluation leads to EBV optimally combining all sources of information regarding udder health and to higher reliabilities. Indeed, these combined EBV are now used to define an Udder Health (UH) composite which is included in the new French Total Merit Index (ISU) introduced in February 2012. This new ISU confers a larger part to Udder Health (see table 5) than before (12.5%) for all breeds. More sustainable genetic trends should follow.

Table 5. Relative weight (%) of Somatic cell score (SCS) and Clinical Mastitis (CM) in the Udder Health (UH) composite and of the various composite indices in the Total Merit Index (ISU).

Breed	MO	NO	HO
SCS in UH	60	50	60
CM in UH	40	50	40
Udder Health	14.5	18.5	18
Production	45	40	35
Type composite	12.5	18	15
Fertility composite	18	15.5	22
Funct. longevity	5	5	5
Milking speed	5	3	5

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