Genetic evaluation of mastitis in France

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Abstract - A genetic evaluation for clinical mastitis was developed for the Brown Swiss breed in 2011. 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 lactation. Low heritability estimates were found (around 2%) 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 (0.40 to 0.66 in absolute value) between clinical mastitis and somatic cell score (SCS), longevity and some udder traits. Correlation with milk yield was moderate and unfavorable (ρ=0.20).
Clinical mastitis has been included since 2011 in routine evaluations using a multiple trait animal model, which accounts for selection correlated traits. Mastitis estimated breeding values (EBV) are combined with somatic cell scores EBV into an udder health index.

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

L'évaluation génétique des mammites cliniques en France

Résumé *-Une évaluation génétique sur la résistance aux mammites cliniques a été mise au point pour la race Brune en 2011. Les données d'entrée sont les déclarations des cas de mammites par les éleveurs auprès des techniciens dans le cadre du contrôle laitier. Le caractère analysé est une variable binaire (0/1) indiquant l'existence ou non d'au moins un cas de mammites durant les 150 premiers jours de la lactation. Ce caractère présente une faible héritabilité (environ 2%), mais la variabilité génétique est suffisante pour envisager une sélection génétique.*
L'estimation des corrélations génétiques avec d'autres caractères montre des valeurs relativement élevées (de 0.40 à 0.66 en valeur absolue) entre résistance aux mammites et comptages cellulaires, longévité et certains caractères de morphologie. La corrélation génétique avec la production laitière est modérée et défavorable (ρ=0.20).
La résistance aux mammites cliniques est évaluée avec un modèle multi-caractère depuis juin 2011, qui fournit des index mammites cliniques combinés, prenant en compte la sélection effectuée sur les autres caractères (lait, cellules, fertilité, morphologie). Un index Santé Mamelle combinant les index mammites et les index cellules officiels est également publié.

Mots clés*: mammites cliniques, comptages cellulaires, paramètres génétiques, évaluation génétique, index synthétique.*

1. Introduction

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 a higher rate of involuntary culling.
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). Although the genetic correlation between SCS and clinical mastitis is high, these traits cannot be considered as the same trait (Heringstad et al. 2006). 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 in France for the Brown Swiss breed.

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. Only the first three lactations were considered. 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 3% of lactations with a reported case of mastitis per herd and per year.

2.2 Genetic parameter estimation

We used the same genetic parameters as the Holstein breed. They were estimated from 296,758 lactations of cows (three first lactations).Variance components were estimated either using a model describe as:

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

where **y** is the clinical mastitis indicator, **ß** is the vector of fixed effects (herd * year, month of calving * region * year, and age of calving * parity * year), **a** is the vector of additive genetic effects, **p** is the vector of random permanent environment effects and **e** is a vector of random residual. **X** and **Z** are incidence matrices.

2.3 National genetic evaluation

A genetic evaluation for clinical mastitis was developed in 2011 for the Brown Swiss breed. It 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 differences were that region was ignored in the month of calving * region * year effect and a heterogeneity of residual variances 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.
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. For this purpose, we used genetic correlations estimated for the Holstein breed by REML assuming known genetic and residual variances..
This multiple trait evaluation resulted in EBVs for 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).

3. Results and Discussion

3.1 Genetic parameters and genetic correlations

Heritability estimates for occurrence of clinical mastitis within the first 150 days of lactation was 1.8%. Mean incidence (8.7%) during this period was low and probably underestimated. The repeatability estimate was 5.5% and the genetic standard deviation was equal to 0.0412. Theses results are consistent with a previous study by Bonaiti et al. (2005). 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).
Genetic correlations between mastitis occurrence and other traits are reported in Table 1.

Table 1: genetic correlations with clinical mastitis

	Occurrence of clinical Mastitis
Milk yield	0.20 *
Somatic cell score	0.66
Functional longevity	-0.38 *

Conception rate	-0.17
Fore udder attachnment	-0.12
Udder depth	-0.02

*negative values are favorable (e.g., lower milk yield or good (shallow) udder depth or body condition are genetically associated with fewer mastitis occurrences)

As expected, an unfavorable positive correlation with production was observed. The large genetic correlation between somatic cell score (SCS) and mastitis 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 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.

3.2 Genetic evaluation

Table 2 shows the number of lactations included in the June 2012 univariate genetic evaluation for the Brown Swiss. The large decrease of number of lactations is explained by the strong selection of the data with different criteria, which assure the quality of breeding values. Around 750 bulls born after 1990 are concerned by this evaluation, and 66 have reliability over 0.50. The correlation between SCS EBV and mastitis EBV for these 66 bulls is 0.45.

Table 2: Number of lactations included in the June 2012 (univariate evaluation)

	Number of lactations
Before edits	228 726
After edits	84 265
Mastitis occurrence (%)	8.74
Number of bulls	1 403

Combined breeding values obtained with the multiple trait approach are the officially published EBV. Breeding values are expressed in genetic standard deviations. Figure 1 shows the genetic trend for SCC and mastitis, per year of birth of the bulls.

Figure 1: genetic trends (bulls with reliability > 0.30)

The genetic trends show that the implementation of an official somatic cell count evaluation in 1997 and its inclusion in the total merit index (ISU) in 2001 had a positive effect on mastitis occurrence.

Conclusion

Combined EBV on clinical mastitis have been published in France three times per year since June 2011. 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. Indeed, these combined EBV are now used to define an Udder Health (UH) composite, introduced in France in February 2012.

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