Development of a Breeding Value for Mastitis Based on SCS-Results

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Abstract

Aim of this study was to develop a trait for the breeding value estimation of direct mastitis based on results of the national routine evaluation for SCS. Two traits were chosen based on their impact on direct mastitis. Standard deviation of residual SCS-scores (STD) and number of excessive SCS-values during a lactation (N_SCS). STD was analysed having largest influence on mastitis. Heritabilities for the two traits were estimated with .09 (STD) and .04 (N_SCS) with a genetic correlation of 0.76 between both traits. Although validation data with direct mastitis was quite small the two traits derived from SCS routine estimation showed promising results to become indicator traits for a routine evaluation for mastitis in Germany. Advantage of the new traits is the availability for all bulls and cows in the actual routine evaluation. Genomic breeding values can easily be derived because all bulls in the actual reference population will get proofs for the new traits immediately without new performance recording.

Key words: Mastitis, breeding value estimation, SCS, udder health

Introduction

Udder health is an economic important trait in dairy production e.g. involuntary culling due to mastitis belongs to the most important culling reasons. Because in most countries data on direct mastitis is not available or only for a smaller proportion of milk recorded cows, cell count is used as indicator trait. In Germany cell count is available from milk recording for all cows on a monthly base. In genetic evaluation cell count is used on a logarithmic scale as SCS (Somatic Cell Score) and the published breeding values are representing SCS differences in the first 3 lactations. The relevance of this trait in practical breeding schemes is obvious and a typical example is a weight of 7% in the German total merit index RZG, where SCS is a part of since 1997. Additional to this, SCS is an important part in the complex of functional longevity. The relevance of udder health in total merit index is then higher than its direct weight implements.

Actual projects estimated genetic correlations of mastitis to SCC moderate to high between .5 and .8. Because heritabilities for mastitis as a direct health trait are with 4% to 8% (Heringstadt, 2000 and 2008; Madsen *et al.*, 2008; Miglior *et al.*, 2012; Govignon-Gion *et al.*, 2012) lower compared to SCS (20-30%) using the indicator trait in selection for lower mastitis incidence is possible.

Nevertheless having estimates on the desired trait mastitis directly would be better. But direct mastitis causes additional (health data) recording. Except for Scandinavia direct mastitis is not available for all cows. Recording has started in many countries including Germany in recent years but not in the entire population. But several countries introduced genetic evaluation for mastitis. The published breeding values (EBV) for bulls are mainly indices of direct mastitis and predictor trait including SCS. Because of the relative few data on direct mastitis compared to data e.g. for SCS, the contribution is low and the published mastitis indices at least for younger bulls with limited number of daughters are more some kind of indicator trait rather than direct mastitis.

EBV for SCS average in the entire lactation (305-days) has the disadvantage that high peaks in cases of clinical mastitis are ‘diluted’ in average lactation SCS. So alternative trait definitions based on raw test-day SCS data were investigated in order to predict clinical and subclinical mastitis. E.g. test-day results from milk-recording for SCC were defined in excessive values (>500.000 cells/mL) and the

standard deviation of SCC was used as indicator. Genetic correlations of alternative traits were higher (.62 - .82) than direct measurement of SCS (Madsen *et al.,* 2008; Miglior *et al.,* 2012). Excessive phenotypic values have the disadvantage that they are only true indicators of mastitis if the threshold is very high. So they indicate mastitis only in a smaller proportion of all mastistis cases when the test-day was by chance relatively close to the mastitis incidence and no treatment was given between mastitis and test-day. In case the threshold is set lower, it is no clear indication of mastitis any more. E.g. according to lactation stadium herd*year*season medium cell count measures can either indicate mastitis or be 'normal' for two different cows in different situations.

In routine genetic evaluation for SCS for German Holsteins with a Random-Regression-Test-Day-Model (RRTDM) the above mentioned effects are corrected. The aim of this study is to evaluate if data from the RRTDM can be used in a new way to derive information on direct mastitis.

Material and Methods

The routine RRTDM for Holsteins in Germany is based on monthly tests of cell count for all cows in milk recording. Actual amount of data comprises nearly 19 million cows with records from 340.000 sires. The statistical model is

$$y_{ijklo} = h_{il} + \sum_{m=1}^{3} \beta_{jlm} f_{jlm} + \sum_{m=1}^{3} b_{klm} a_{klm} + \sum_{m=1}^{3} b_{klm} p_{klm} + e_{ijklo}$$

with

y_{ijklo} SCS on Testday *o* in lactation *l* of cow *k*

h_{il} the fix herd-test-day effect *i* (HTD) within lactation *l*

f_{jlm} coefficient *m* of regression of fixed lactation curve *j* in lactation *l*

β_{jlm} term *m* of the Wilmink function of the fixed laktation curve *j* in lactation *l* with $\beta_{..1}=1$, $\beta_{..2}=d$ and $\beta_{..3}=e^{-0.05d}$, *d* represents day of lactation

a_{klm} and p_{klm} random coefficients of regression *m* in lactation *l* of cow *k* for genetic and permanent environmental effects

b_{klm} term *m* of Legendre Polynom function with three parameters $b_{..1} = 1$, $b_{..2} = \sqrt{3}z$ and $b_{..3} = \frac{1}{2}\sqrt{5}\left(3z^2 - 1\right)$ and $z = \left(d - 5\right)/150 - 1$ for lactation *l* of cow *k*

e_{ijklo} residual effect

The phenotypic performance is generally divided in following components: P = G + E + e. The phenotype (P) will be split into a genetic (G) and an environmental (E) component. Effects not explained in the statistical model are summarized in a residual effect (e).

The residual effect contains phenotypic measures not explained by environmental or genetic effects. It can be assumed that extremely high error terms are caused by unique events during a lactation, e.g. mastitis. If this really has an effect on the error terms, they are able to represent a trait to indicate mastitis events.

Figure 1 shows the trend of test-day breeding values, phenotypic measures and residuals of an example cow with a mastitis event during her lactation. Cell count and residuals increase during the mastitis event while it cannot be completely covered by the SCS-EBV. The EBV will be estimated as curve over the complete lactation and single events, as mastitis events are not included by the formula which describes the lactation curve. Single events can only be found in the data when residual effects and SCS peaks are analysed. Lactations without mastitis show an even curve of error terms without large deviations. Lactations with mastitis show one or two peaks in the trend of error terms and cell count. The relation between SCS-EBV, phenotypic cell count and residual is demonstrated by a single lactation derived from actual data in figure 1.

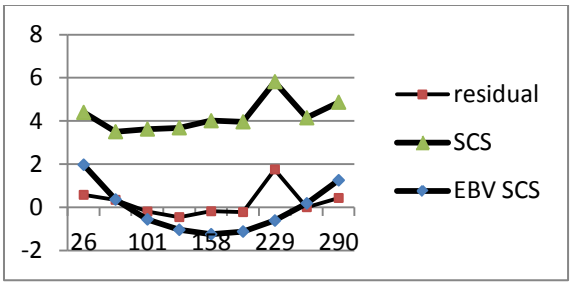

Figure 1. Trend of phenotypic measures, breeding values for SCS and residuals within a lactation with one mastitis event.

Totally four traits were analysed and compared, two of them based on residuals:

N_RES: number of extreme test-day residuals within lactation

STD: standard deviation of residuals (error term) of SCS-EBV within lactation

N_SCS: number of extreme test-day somatic cell scores within lactation

RZS: Relative EBV for SCS expressed as partial index

The four traits were chosen as a consequence of the trend analysis as shown in figure 1. It was clear how a mastitis event influences the trend of SCS and the residuals within a lactation. The tresholds for the two extreme parameters N_RES and N_SCS were defined using a univariate analysis (SAS: proc univariate) in order to define quantiles for the parameters. 95% quantiles were defined and observations above chosen to be indicators for mastitis.

To validate the prediction potential of the four traits data of actual mastitis observations collected in the German health trait projects GKUH and BHNP were used (Stock *et al.*, 2013). Within these projects detailed health data including mastitis are collected. The number of lactations with mastitis recording is shown in table 1. In difference to many other projects not only mastitis was actively recorded on daily base but mastitis-free, too. The relatively high incidence rate for mastitis of 12017 affected cows in first lactation compared to 14784 mastitis free cows must be interpreted in the context of this precise definition of mastitis-free.

Table 1. Mastitis records from health trait recording.

Lactation	Mastitis events	No mastitis	All
1	12017	14784	26801
2	11943	10757	22700
3	10375	6622	16997
All	32163	34335	66498

Results and Discussion

The residual effects derived from the genetic evaluation of SCS were combined with real phenotypic measures of mastitis. An overview of variation of residuals, number of extreme residuals and cell counts and additional the mean relative breeding value SCS (RZS) in lactations with and without mastitis events is shown in table 2. Calculated for a complete lactation, the differences in standard deviation of error terms with and without mastitis are statistically significant. The standard deviation of error terms increases with the occurrence of mastitis.

Table 2. Means for analysed traits in lactations with different numbers of mastitis events.

Number of mastitis events within lactation	Standard deviation of residuals (error term)*	N_SCS	N_RES	RZS (relative breeding value for udder health)
0	0.74	0.22	0.35	105.7
1	1.16	0.55	0.61	103.1
2	1.39	1.11	1.01	100.1

*) all values are statistically significant different with p=0.001

The influence of the defined traits on the target traits were analysed using R-Square analysis and are shown in table 3. STD has the highest determination on the number of mastitis events, followed by the number of extreme SCS values. The two other traits have only low additional impact on the R-Square value.

Table 3. R-Square values of analysed traits to determine their influence on mastitis.

R-Square	STD	N_SCS	RZS	N_RES
0.1537	X			
0.2012	X	X		
0.2138	X	X	X	
0.2145	X	X	X	X

Based on these results the two traits STD and N_SCS were chosen to become alternative traits to mastitis. For these traits, genetic parameters were estimated using following genetic model:

Y = hy + lact.nr. + sire + e

The model was chosen to be a sire model in order to get a better convergence. Parameters were estimated using the software VCE6 (Groeneveld *et al.*, 2010), results are shown in table 4. Heritabilities found for STD and N_SCS are .09 and .04 resp. The genetic correlation between these two traits is .76. The heritability for N_SCS is similar to estimates for number of excessive values in literature. Urioste *et al.* (2012) estimated on the large Swedish data base for N-Peaks a heritability of .12 and for mastitis .08. The genetic correlation between both traits was .79. Miglior *et al.* (2012) found on a Canadian data base a correlation of standard deviation of raw SCS to clinical mastitis of .82. So STD is different from the raw measure N_SCS and at the same time behaves very similar to direct mastitis in other studies. This can be seen as a strong indication that STD is an appropriate measure for direct mastitis.

Table 4. genetic parameters estimates for the two alternative traits.

	STD	N_SCS
STD	0.09	0.76
N_SCS	0.22	0.04

Heritabilities on, genetic correlation above and phenotypic correlation below diagonal

The found heritability of .09 for STD is at the upper bound found in other studies (Govignon-Gion *et al.*, 2012: .02; Miglior *et al.*, 2012: .04; Urioste *et al.*, 2012:.08) and used in Scandinavian routine evaluation (.03-.07). This could indicate that STD has even advantages compared to mastitis recorded directly. STD is based on objective measures and available for all cows. Per definition direct mastitis can be only recorded if detected and often only if reported by a veterinarian i.e. treated.

Conclusions

Information on cell count in Germany is available for all cows and the entire lactation (all test-days). Recording of mastitis has started on regional base in projects but data will not be available on the majority of cows during the next years. Except from Scandinavia most countries face the same problem. There is strong indication that STD is a measure for direct mastitis. STD is available for all cows in national SCS routine evaluations, is a clearly different trait from phenotypic SCS measures and shows similar correlations to SCS measures as direct mastitis in other studies. In conjunction with the relative high heritability of .09 this could offer very effective perspectives for routine evaluation for mastitis without additional data recording. A routine evaluation for mastitis defined as STD could easily be implemented in all countries with SCS evaluation. STD as mastitis measure is already available for actual and historical data. All daughter proven bulls would get mastitis proofs and therefore genomic prediction would be possible with the same reference population as for SCS. Because country correlations in MACE for SCS are high the same can be expected for mastitis measured as STD.

Reasonable high country correlations of STD in MACE for mastitis would be another indirect validation of STD as a measure for mastitis. Therefore genetic evaluation for STD on the entire German population will be calculated and provided for an Interbull test run.

Nevertheless with German data a final validation that STD is a better measure for mastitis than SCS is not possible yet. It would be helpful to further evaluate STD in joint projects with countries having a solid data base for direct mastitis.

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