

Predicting Mastitis Resistance Breeding Values from Somatic Cell Count Indicator Traits

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Abstract

A new breeding value estimation procedure for mastitis traits has been implemented in the Dutch/Flemish dairy genetic evaluation. This breeding value estimation uses incidences of subclinical mastitis together with five indicator traits derived from test day somatic cell counts to predict the breeding value for resistance against subclinical and clinical mastitis (SCM and CM, resp.). The mastitis breeding values are combined in an udder health index, using weights reflecting the mean economic losses of occurrence of (sub)clinical mastitis. Results show a marked improvement in reliability of the new udder health index over the previous one. The mean reliability for bulls with 100 or more lactating daughters was 85%, where this used to be around 50%. Correlations between mastitis resistance breeding values, the new udder health index and the old one show that the new index is better suited for breeding for mastitis resistance generally (correlations between index and CM was 0.95, between index and SCM was 0.91), where the old index predominantly emphasised subclinical mastitis (correlations 0.78 with CM and 0.91 with SCM). The genetic trend for mastitis traits shows improvement in the last decade, after somatic cell counts breeding values were introduced and after adding udder health traits in the Dutch total merit index NVI.

Introduction

Until recently the Dutch/Flemish national dairy genetic evaluation made use of two traits indicating udder health: somatic cell count (SCC) and an udder health index (UGZ; de Jong and Lansbergen, 1996). The latter consisted of SCC and four udder conformation traits. However, the index had a relatively low reliability: Approximately 50% on average for bulls with >100 daughters.

De Haas *et al.* (2008) suggested some alternative traits, derived from test day somatic cell counts, to predict breeding values for resistance against clinical (CM) and subclinical (SCM) mastitis. Together with direct observational data on occurrences of infections (clinical or subclinical) their research suggested it should be possible to construct an udder health index with a markedly increased reliability (~85%).

Following the suggestion by de Haas *et al.* (2008) a new breeding value estimation procedure was set up incorporating five somatic cell count derived traits and traits for direct observations on subclinical and clinical mastitis.

As of April 2009 the Dutch national evaluation publishes three mastitis resistance breeding values: CM, SCM and UDH. These breeding values are a significant improvement over the earlier udder health breeding values used. The purpose of this paper is to report some results of the implementation of this breeding value estimation in Dutch dairy cattle.

Methods

Breeding values

In the Dutch evaluation the udder health index (UDH) and two main breeding values are published: Clinical mastitis incidence (CM) and subclinical mastitis incidence (SCM). Observations on subclinical mastitis infections are derived from test day somatic cell count patterns (de Haas *et al.*, 2007).

To increase the reliability of breeding values for the two main mastitis resistance traits, breeding values for five indicator traits (de Haas *et al.*, 2008) are calculated:

- 1) Mean somatic cell score in the first part of the lactation (4 to 150 days),
- 2) Mean somatic cell score in the last part of the lactation (days 151 to 400),
- 3) Presence of infection (0/1, where '1' indicates the presence of at least one test day where the SCC was $> 150,000 \text{ ml}^{-1}$)
- 4) Severity of infections (number of test days where SCC was $> 150,000 \text{ ml}^{-1}$ divided by the total number of lactation test days)
- 5) Number of peaks during lactation (number of times when the SCC shows a changes from $< 200,000$ to $> 500,000 \text{ ml}^{-1}$ on consecutive test days)

Statistical model

The breeding values for the five indicator traits and two mastitis traits are estimated for lactations 1, 2 and 3 in a MT Animal Model comprising 21 traits in total. The statistical model used is:

$$Y_{ijklmnopq} = HY_j + YM_k + Age_l + Ntd_m + DAR_n + het_o + rec_p + animal_q + error_{ijklmnopq}$$

where (effects are fixed unless stated otherwise):

- $Y_{ijklmnopq}$ = The observation on the i -th trait
 HY_j = Herd x Year effect
 YM_k = Year x Month effect
 Age_l = Age at calving
 Ntd_m = Numbers of test-days in this lactation
 DAR_n = Number of days at risk
 het_o = The effect of heterosis
 rec_p = The effect of recombination
 $animal_q$ = The random additive genetic effect.

At this point in time no reliable data stream exists to introduce direct observations on CM into the genetic evaluation. Hence, breeding values for CM are estimated from the correlation structure of this traits with other predictive traits.

Index

For each trait the lactation breeding values are combined into a single overall breeding value using weights established in the Dutch test-day model:

$$BV_i = 0.41 \cdot BV_{i1} + 0.33 \cdot BV_{i2} + 0.26 \cdot BV_{i3}$$

To calculate the UDH index, the overall breeding values of CM and SCM are used. These BV's are published on a relative scale with mean 100 and standard deviation of 4.

The average damage of a case of clinical mastitis is estimated at €196.- (Huijps *et al.*, 2008). Included are the costs of production loss, veterinary costs, extra labour and removal of heavily infected animals (15% of the infected animals). The average damage for subclinical mastitis is €83,- per case (Halasa *et al.*, 2008). This damage is based on an average production loss per case. On the absolute scale SCM and CM are expressed in incidences of infections per lactation. Hence, the UDH index is calculated from CM and SCM weighted with the mean economic damage in euros (Huijps *et al.*, 2008; Halasa *et al.*, 2008) of one occurrence of (sub)clinical mastitis:

$$UDH = (-83) \cdot SCM + (-196) \cdot CM$$

Transformed to the relative scale in which all values are published, the UDH index is:

$$BV_{UDH} = 100 + 0.477 \cdot (BV_{SCM} - 100) + 0.641 \cdot (BV_{CM} - 100)$$

where BV_x denotes the breeding value of trait x on the relative scale $\sim N(100,4)$. Note the scale reversal, indicating that higher breeding values imply decreased mastitis incidence.

Parameters

Table 1 shows the overall heritability and genetic standard deviation of the traits combined for three lactations. Table 2 shows per lactation the heritabilities and correlations of SCM and CM.

Table 1. Overall heritabilities and genetic standard deviations of traits used in the new Dutch udder health evaluation.

Trait	h^2	σ_g
SCS150	0,165	43,255
SCS400	0,173	38,794
Infection	0,120	0,110
Severity	0,158	8,864
Peaks	0,112	0,113
SCM	0,056	0,068
CM	0,060	0,039
UDH	0,089	0,051

Table 2. Heritabilities (**diagonal**) and genetic correlations (off-diagonals) of CM and SCM per lactation.

	lactation 1		lactation 2		lactation 3	
	SCM	CM	SCM	CM	SCM	CM
SCM1	0.022	0.588	0.695	0.611	0.687	0.516
CM1		0.025	0.542	0.676	0.356	0.671
SCM2			0.026	0.554	0.816	0.501
CM2				0.024	0.375	0.806
SCM3					0.041	0.257
CM3						0.032

Analysis

Correlations were calculated between the new breeding values (CM, SCM and UDH) and the old Dutch udder health index (UGZ) and the Dutch somatic cell count (SCC). Genetic trends were calculated from breeding values of Holstein Friesian breeding bulls with at least 100 lactating daughters. Genetic trends for breeds were calculated from cow breeding values where each breed-by-year class had > 100 individuals.

Results and Discussion

Relative breeding values

On the relative scale in which the breeding values are published, a deviation of one standard deviation (4 points) is similar to a change of incidence of 6.8% (for SCM) and of 4.0% (for CM). The matching economic costs/benefits correspond to €5.68 and €7.52 per cow per lactation, respectively. In the udder health index one standard deviation

corresponds to € 11.82 per animal per lactation. The expected response of selection on UDH in breeding bulls is a decrease in subclinical mastitis of 4%, a decrease in clinical mastitis of 2.5% and an economic benefit of €8,35 per cow per lactation.

Reliabilities

Reliabilities were on average 85% for bulls with >100 daughters and >95% for breeding bulls with >2000 daughters distributed over three lactations (Table 3). This was a considerable improvement over the previous udder health index. As a result the standard deviation of the sire breeding values increased from 2.5 for UGH to 4.4 for UDH. This implies a wider range of breeding values and hence the potential for more accurate selection and increased response to selection.

Reliabilities for CM breeding values were comparable to those of SCM, even though no direct observational data on clinical infections was available. The system of breeding value estimation described in this paper is ready to incorporate such data when it becomes available in the future. However, research showed that adding direct observational data on clinical mastitis would increase the reliability of the CM breeding value with 2 to 3% (de Haas *et al.*, 2007), indicating that the present set up predicts CM breeding values adequately.

Table 3. Reliability for breeding values SCM, CM and UDH in different sire types. Numbers of daughters in **bold** are set beforehand, other numbers are averages for the sire category concerned.

	Number of daughters			Reliability		
	1st lac	2d lac	3rd lac	SCM	CM	UDH
Y1	80-120	0	0	69	67	70
Y2	150-250	74	0	79	76	80
B1	150-250	139	93	87	83	87
B2	900-1100	766	526	95	94	95
B3	8000-12,000	7436	5452	95	95	95
B4	>12,000	23133	>6,000	98	98	98

The categories are: Y1) young bulls with around 100 first lactation daughters only; Y2) young bulls with around 200 first lactation daughters, but no third lactation daughters; B1) bulls with an average of 200 daughters in first lactation; B2) bulls with 1,000 daughters in first lactation; B3) bulls with around 10,000 daughters in first lactation; B4) bulls with more than 12,000 daughters in first lactation and at least 6,000 daughters in lactation 3.

Heterosis

Heterosis only played a small part in mastitis traits. For SCM the heterosis effect in the first parity was 1.0% less cases of infection. For parity two and three this was 0.7% and 0.8% less infections, respectively. Hence, the heterosis effect was less than 15% of the genetic standard deviation.

Correlations

Correlations between traits were moderate to high (Table 4). The lowest correlation (0.75) was found between CM and SCM, indicating these are independent traits. With the exception of UDH, CM correlated markedly less with all other traits. In contrast, SCM correlated high with all other traits, except CM. Particularly SCC showed a markedly higher correlation with SCM than with CM, indicating that selection on SCC puts emphasis on SCM infections, even though these are economically less damaging than CM infections.

Table 4. Correlations between udder health breeding values. UDH = udder health index (new), CM = clinical mastitis, SCM = subclinical mastitis, SCC = somatic cell count, UGZ = udder health index (old).

	CM	SCM	SCC	UGZ
UDH	0.95	0.91	0.90	0.89
CM		0.75	0.78	0.78
SCM			0.92	0.91

The old udder health index UGZ showed a similar pattern of correlations: High for SCM, only moderate for CM. The new index UDH correlated highly with both CM and SCM. Hence, the breeding goal under UDH is defined somewhat broader, putting equal emphasis on both CM and SCM infections, whereas UGZ tended to put the emphasis on SCM infections only.

Genetic trend

The genetic trend in bulls for the new mastitis resistance BV's (Figure 1) clearly shows the

effects of incorporating mastitis related breeding values into the national breeding goal. Until the mid-90's the trend is slightly negative. From 1995 the breeding value for SCC was introduced, which is marked by a flat trend for bulls born between 1995 and 2000. From 2002 onwards udder health (UGZ) was incorporated in the Dutch total merit index, which resulted in a slightly positive trend for bulls born from 2000 onwards.

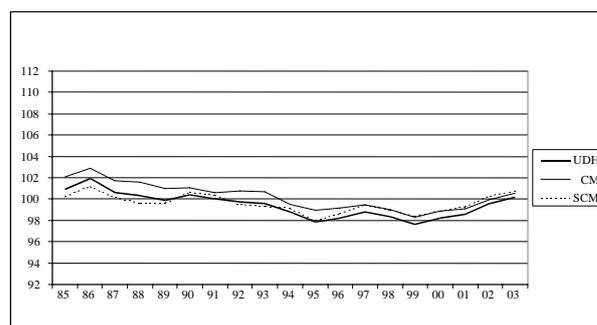


Figure 1. Genetic trends of clinical (CM) and subclinical (SCM) mastitis and udder health (UDH) for HF bulls with >100 lactating daughters born between 1985 and 2003.

Per breed genetic trends in cows (Figure 2) were in all cases nearly flat, but negative nonetheless. Considerable differences between breeds could be observed. Montbeliardes and Dutch Friesian cattle showed best average breeding values (mean BV: 105.7 for MON and 102.2 for DF), while Jersey cattle showed lowest mean breeding values (mean BV: 95.5).

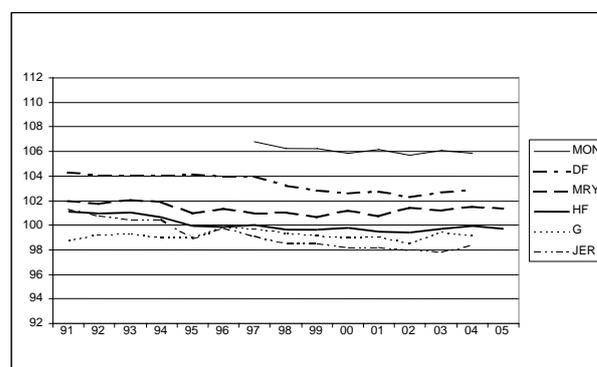


Figure 2. Average breeding values UDH for cows, born between 1991 and 2005 according to breed: Montbeliardes (MON), Dutch-Friesian (DF), Maas-Rijn-Yssel cattle (MRY), Holstein Friesian (HF), Groninger (G) and Jerseys (JER).

Conclusion

The new UDH index has a broader breeding goal than the previous index, which tended to focus on subclinical mastitis alone. The new breeding values are more reliable. Hence a greater range in breeding values could be observed, enabling better selection of bulls for these traits. In the future this should translate into herds that are more resistant to mastitis infection, reducing costs of veterinary services and production loss, while at the same time lowering SCS because of decreased incidence of infection.

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