Predicting Mastitis Resistance Breeding Values From Somatic Cell Count Indicator Traits

H. Eding[*] and G. de Jong[*]

Introduction

De Haas et al. (2008) suggested using traits derived from test day somatic cell counts, to predict breeding values for resistance against clinical (CM) and sub-clinical (SCM) mastitis. Together with direct observational data on occurrences of infections (clinical or sub-clinical) 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 sub-clinical and clinical mastitis.

The old index (UGZ) consisted of breeding values for SCC and milking speed, supported by breeding values for udder related conformation traits (fore udder attachment, teat length and udder depth). The breeding goal of the UHZ was CM resistance. As of April 2009 the Dutch national evaluation publishes three mastitis resistance breeding values: CM, SCM and UDH, estimated using a system as suggested by de Haas et al. (2008). The purpose of this paper is to report some results of the implementation of this breeding value estimation in Dutch dairy cattle.

Material and methods

Breeding values. In the new evaluation the udder health index (UDH) and two main breeding values are published: Clinical mastitis incidence (CM) and sub-clinical mastitis incidence (SCM). Observations on sub-clinical 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) SCS150: Mean somatic cell score in the first part of the lactation (4 to 150 days)
2) SCS400: Mean somatic cell score in the last part of the lactation (days 151 to 400)
3) INF: Presence of infection (0/1, where '1' indicates the presence of at least one test day where the SCC was > 150,000 ml^{-1})
4) SEV: Severity of infections (number of test days where SCC was > 150,000 ml^{-1} divided by the total number of lactation test days)
5) NPK: Number of peaks during lactation (number of times when the SCC shows a change from <200,000 to >500,000 ml^{-1} on consecutive test days)

[*] Animal Evaluation Unit, CRV, P.O. Box 454, 6800 AL Arnhem, The Netherlands

The breeding values for these traits are not published. Instead they are used to predict the breeding values of interest (CM and SCM). Table 1 shows the overall heritability and genetic standard deviation of the traits combined for three lactations.

Table 1: Overall heritabilities (lactation 1 –3) and genetic standard deviations of udder health traits.

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**

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:

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

Where (effects are fixed unless stated otherwise):
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. Breeding values for CM are estimated from the correlation structure of this trait with other predictive traits. The occurrence of SCM is scored from patterns in test day SCC associated with SCM.

Index. The average damage of a case of CM 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. The average damage for SCM is € 83,- per case (Halasa *et al.*, 2008). 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 weighed with the mean economic damage in Euro of one occurrence of (sub)clinical mastitis as $UDH = (-83) \cdot SCM + (-196) \cdot CM$ .Transformed to the relative scale in which all values are published (mean 100, s.d. 4), the UDH index is:

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

Note the scale reversal, giving higher index values to decreased mastitis incidence.

Analysis. Mean reliabilities were calculated for different types of bull breeding values, where types were defined according to number of daughters in three lactations, raging from young bulls (Y) with 80 to 250 daughters in first lactation, to breeding bulls (B) with at least 12,000 daughters in first and at least 6,000 in third lactation. Correlations were calculated between the new breeding values (CM, SCM and UDH) and the old Dutch udder health index (UGZ) and the somatic cell count (SCC). Genetic trends were calculated from breeding values of Holstein Friesian breeding bulls with at least 100 lactating daughters.

Results and discussion

Correlations between mastitis traits and indicator traits were moderate to high (0.44 to 0.87), but showed varying emphases. SCS150 and NPK correlated well with CM (~ 0.85) and less with SCM (~ 0.60) On the other hand, SCS400 and INF correlated more with SCM (~0.86) then with CM (0.53 and 0.44, resp). This indicates that the five indicator traits all provide differentiated information on mastitis traits.

Table 2: 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.

Reliabilities were on average 85% for bulls with >100 daughters and >95% for breeding bulls with >2000 daughters distributed over three lactations (Table 2). As a result the standard deviation of the sire breeding values increased from 2.5 for UGH to 4.4 for UDH, implying more accurate selection and increased response to selection. Reliabilities for CM were comparable to SCM, even though no direct observational data were available. The system of breeding value estimation is ready to incorporate such data. However, research showed that adding direct observational data on clinical mastitis would increase the reliability of CM with 2 to 3% (de Haas *et al*., 2007), indicating that the present set up predicts CM breeding values adequately.

Correlations between mastitis traits were moderate to high (Table 3). The lowest correlation (0.75) was found between CM and SCM. With the exception of UDH, CM correlated markedly less with all other traits. SCM correlated high with all other traits, except CM. Particularly SCC showed a higher correlation with SCM than with CM, indicating that selection on SCC puts emphasis on SCM infections.

Table 3: 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 high correlation with SCM, but only a moderate correlation with CM. This is in contrast with the original breeding goal of UGZ, which was developed specifically to increase resistance against CM.

The new index UDH correlated highly with both CM and SCM. Hence, the breeding goal under UDH puts equal emphasis on both CM and SCM infections, whereas UGZ puts more emphasis on SCM infections.

The genetic trend in bulls for the new mastitis BV's (Figure 1) clearly shows the effects of mastitis related breeding values in 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.

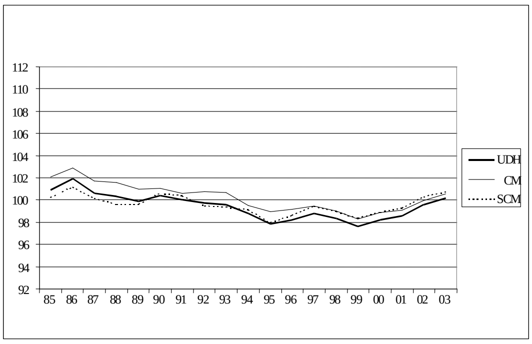

Figure 1: Genetic trends of clinical (CM) and subclinical (SCM) mastitis and udder health (UDH) for HF bulls with >100 lactating daughters born between 1985 and 2003

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

Conclusion

The new UDH index has a broader goal then the old UGZ index and is more reliable, improving 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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