Mastitis Resistance Index: Selection for Udder Health

G. de Jong and L.M.T.E. Lansbergen

Royal Dutch Cattle Syndicate, P.O. Box 454, 6800 AL Arnhem, The Netherlands

Abstract

Direct and indirect selection against clinical masititis incidence was studied. Based on literature estimates and estimates from Dutch data a genetic parameter set was constructed. Traits used for indirect selection were somatic cell count, milking speed, and linear udder type traits. Based on selection index calculations a mastitis resistance index was constructed as a tool for selection against clinical mastitis.

From the index calculations it was concluded that indirect selection on clinical mastitis resulted in the same genetic progress as direct selection. Combining direct and indirect selection gave 15% higher response. The order importance of traits for indirect selection based on selection response for mastitis resistance was somatic cell count, udder traits and milking traits. Within the udder traits the order of importance was udder depth, fore udder attachment and teat length.

The relative weights of the traits in the index expressed in their own genetic standard deviation was 6, 16, 10, 17, 51 respectively for fore udder attachment, udder depth, teat length, milking speed and SCC.

Introduction

Mastitis is one of the most important diseases in dairy herds. Mastitis results in economic losses by decrease of milk production, including milk not delivered, treatment costs, labor costs, early culling and contamination of other cows. As mastitis infection causes high levels of somatic cells in the milk and most payment systems of milk include reduction of milk prices for milk with high levels of somatic cell counts (SSC), the reduction of mastitis incidence is of economic importance. Management factors and veterinary treatment get a lot of attention to reduce mastitis incidence. Reduction of SCC can also be enforced by genetic selection.

A clinical and a subclinical form of mastitis can be distinguished. Genetic correlation is less than unity (Emanuelson, 1988).

Selection on mastitis resistance requires selection on clinical and subclinical mastitis. As little is known on genetic parameters for subclinical mastitis and correlations of subclinical mastitis with other traits, a selection for clinical mastitis could be the best next. This seems justified because of the high positive correlation between clinical mastitis and subclinical mastitis.

Selection on clinical mastitis can be done directly and indirectly. For direct selection data on mastitis cases are needed and to be collected on the farms. In the Netherlands no registration of mastitis infections is available on national level. Further mastistis resistance has a low heritability of about 0.03.

In this study the alternative of indirect selection on mastitis resistance was investigated. For indirect selection breeding values for linear udder traits, SCC and milking speed are available.

Objective of the study was to define an index which makes it possible to select for clinical mastitis resistance. This index is subsequently called the mastitis resistance index or M-index.

Genetic parameters

The genetic parameters required for selection index calculations are listed in Table 1.

Parameters were based on literature and on analysis of data of dairy cows in the Netherlands.

For the type udder traits the heritabilities, genetic and phenotypic correlations were based on a genetic analysis of Dutch Black&White cow data. The genetic correlations between milking speed, SCC and udder traits were calculated from correlations between Dutch breeding values. The correlations between milking speed and udder traits were very low and set to zero. The heritabilities for milking speed (De Jong, 1993) and SCC (Fox, 1994) were based on Dutch data.

Heritability of mastitis resistance was to be found to be between 0.008 and 0.03 (Lund, 1994; Emanuelson, 1988; Lawstuen, 1988; Philipsson, 1995; Koenen, 1994; Groen, 1994). A heritability of 0.03 was used in the calculations.

Correlations for mastitis resistance with other traits used in Table 1 are based on literature values (see Table 2).

Udder depth shows that deep udders cause more mastitis. Genetic correlations with mastitis incidence are in the range of -0.69 to +0.18. Fore udder attachment was correlated with mastitis incidence with -0.57 to +0.18, which means that better attached udders reduce mastitis incidence. Correlation of suspensory ligament with mastitis incidence showed a variation from -0.51 to +0.26. Three studies showed that a stonger ligament results in less mastitis. Groen (1994), however found that strong suspensory ligaments give a higher mastitis incidence. Genetic correlation of mastitis incidence and teat placement was between -0.73 and -0.06, i.e. narrow teat placement reduces the chance on mastitis infection. Again Groen (1994) found opposite results.

Genetic correlation between mastitis resistance, which is opposite of mastitis incidence, and udder traits were assumed to be 0.40 for udder depth, 0.35 for fore udder attachment, 0.15 for teat placement and 0.10 for suspensory ligament (Table 1). These values are used in selection index calculations.

Rear udder height was not correlated with clinical mastitis incidence. Teat length had a genetic correlation with mastitis incidence of +0.72, i.e. long teats give more mastitis. Dutch data with about 1500 cows showed a correlation of -0.87, which means that long teats are preferred to avoid mastitis. Due to the low genetic correlations found for rear udder heigth with mastitis incidence this udder trait was not used in the index calculations.

Index calculations

Index calculations were made with mastitis resistance as breeding goal (H). Mastitis resistance was defined as the reverse trait of clinical mastitis incidence. In the index (I) milking speed (MS), SCC, udder depth (UD), fore udder attachment (FU), suspensory ligament (SL), teat placement (TP) and teat length (TL) were used. The formula of the breeding goal is:

$$H = v_1 {*} MR$$

The formula of the index is:

$$I = b_1{*}BV_{FU} + b_2{*}BV_{UD} + b_3{*}BV_{TP} + b_4{*}BV_{SL} + b_5{*}BV_{TL} + b_6{*}BV_{MS} + b_7{*}BV_{SCC} \quad [1]$$

where BV is breeding value.

Selind was used to determine b-values. Different combinations of selection index traits were tested for response of mastitis resistance. Results of different combinations of traits in the selection indices can be found in Table 3.

Using mastitis resistance data of 100 daughters of a bull results in an index having a correlation (R_{IH}) of 0.656 with the breeding goal mastitis resistance. This is direct selection on mastitis resistance. When separate indirect traits are used the response and R_{IH} are lower. SCC gives 93 percent of the response compared with direct selection. Milking speed and udder traits give respectively 43 and 61 percent of the response when compared with direct selection. This shows clearly that SCC is the best single indirect trait for mastitis resistance and milking speed is the least informative trait. When using milking speed, udder traits and SCC in the index the response is 1 percent higher than direct selection for MR. The highest reponse was found when direct and indirect selection was combined: 15 percent higher response than with only direct selection.

When taking a closer look at the five udder traits it is obvious that one trait is more informative than the other. In Table 4 selection indices are defined with milking speed and SCC plus one or more udder traits. When including one type udder trait in the index jointly with milking speed and SCC, the index with udder depth gave the highest reponse with 0.297 (number of mastitis infections during lactation), followed by the index including fore udder attachment with a genetic response of 0.292. Both responses were close to the response of the index including all the type udder traits jointly with milking speed and SCC: 0.298. Third best alternative is a combination of SCC, milking and teat length, giving a response of 0.288. Adding teat placement or suspensory ligament to the index already including milking speed and SCC improved the response sligthly. The index with milking speed, SCC, udder depth, fore udder attachment and teat length gave the same response as the index with all the seven traits combined.

This results in an index for indirect selection on udder health containing the traits milking speed, SCC, udder depth, fore udder attachment and teat length:

$$I_{uh} = 0.0065*BV_{FU} + 0.0174*BV_{UD} - 0.0108*BV_{TL} - 0.0164*BV_{MS} - 0.6725*BV_{SCC} \quad [2]$$

Conclusion

Indirect selection for mastitis resistance gave the same genetic response as direct selection. Such an indirect selection is based on combining the traits milking speed, SCC, udder dept, fore udder attachment and teat length (see Equation 2). Other udder type traits such as suspensory ligament and teat placement did not increase the genetic response on mastitis resistance.

A combination of direct and indirect selection gave 15 percent higher response than only direct selection.

The relative weights of the traits in the index expressed in their own genetic standard deviation was 6, 16, 10, 17, 51 respectively for fore udder attachment, udder depth, teat length, milking speed and SCC.

Application in the Netherlands

In april 1996 the mastitis resistance index (M-index) has been introduced to facilitate selection for mastitis resistance. The index is presented as a relative breeding value with a mean of 100 and a standard deviation of 4. As a result of this standardisation, the following equation for the mastitis resistance index is obtained:

$$\begin{aligned} \text{M-index} = & - 6.063*I_{SCC} - 0.193*(I_{MS}-100) + \\ & + 0.173*(I_{UD}-100) + \\ & + 0.063*(I_{FU}-100) - \\ & + 0.108*(I_{TL}-100) + 100 \quad [3] \end{aligned}$$

where

M-index = index for mastitis resistance with mean 100 and standard deviation 4

I_{SCC} = index for somatic cell count (on ^{2}log-scale)

I_{MS} = index for milking speed (mean 100, sd 4)

I_{FU} = index for fore udder attachment (mean 100, sd 4)

I_{UD} = index for udder depth (mean 100, sd 4)

I_{TL} = index for teat length (mean 100, sd 4)

Faster milking cows have on average higher somatic cell count due to more mastitis infections in the udder (Figure 1). But the phenotypic figures also show that slow milking animals have on average a higher somatic cell count. Based on Figure 1 it seems that slow milking and fast milking cows have higher somatic cell count in their milk than average. This could mean that the lowest incidence of mastitis also is found with average milking speed.

Figure 2, with the relationship between breeding values of bulls for milking speed and breeding values for SCC, shows a decline of SCC with the reduction of milking speed. But the decline of SCC for milking speed breeding values below 100 is less than above 100. This could be due to the low number of bulls with breeding values below 100.

The relationship between low milking speed and SCC, and therefore mastitis resistance, is not completely understood. Hence, when calculating the M-index the indexes for milking speed below 100 are set to 100.

Discussion

This paper shows the results of several index calculations for indirect selection on mastitis resistance. The basis for these calculations are the parameters of Table 1. Definitive values were based on literature estimates and estimates in Dutch data sets. The question is how rubust the index is. The results from the index were robust with varying the genetic correlations between mastitis resistance and traits used for indirect selection. The order of importance of traits in the index did not change when correlations were changed with 0.10 upwards.

Index calculations clearly identify the most important traits for indirect selection on mastitis resistance. Somatic cell count is by far the most important trait, followed by the udder traits and milking speed. Changes in genetic parameters, as far as they are likely to change, will change the weighting factors for the traits but it is expected they will not immediately change the order of importance of the traits.

Further, in this paper parameters are used which hold for clinical mastitis. Little is known on correlations between the index traits and subclinical mastitis. It is assumed that selection on clinical mastitis also will decrease the incidence of subclinical mastitis.

Literature

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Table 1. Parameters used to calculate the udder health index. In upper triangle phenotypic correlations, on diagonal heritabilities, in lower triangle genetic correlations. The last column shows the genetic standard deviation of the traits

	MR	FU	TP	UD	SL	TL	MS	SCC	sd
MR	**0.03**	0.10	0.10	0.10	0.10	0.10	-0.20	-0.40	0.45*
FU	0.35	**0.29**	0.38	0.47	0.20	-0.13	0.00	-0.10	4.50
TP	0.15	0.60	**0.33**	0.25	0.33	-0.23	0.00	-0.10	4.50
UD	0.40	0.72	0.28	**0.40**	0.23	-0.14	0.00	-0.10	4.50
SL	0.10	0.32	0.44	0.34	**0.21**	-0.11	0.00	-0.10	4.50
TL	-0.15	-0.26	-0.28	-0.26	-0.30	**0.35**	0.00	-0.10	4.50
MS	-0.30	0.00	0.00	0.00	0.00	-0.30	**0.30**	0.10	4.50
SCC	-0.70	-0.30	-0.10	-0.35	-0.05	0.10	0.30	**0.12**	0.38

MR = mastitis resistance (low-high); FU = fore udder attachment (loose-strong); TP = teat placement (wide-narrow; UD = udder depth (deep-shallow); SL = suspensory ligament (weak-strong); TL = teat length (short-long); MS = milking speed (slow-fast); SCC = somatic cel count on ^{2}log-scale (low-high); sd = genetic standard deviaton.

* genetic standard deviation based on mastitis resistance defined as mastitis incidence (number of mastitis infections) during the lacation.

Table 2. Genetic correlations between mastitis incidence and udder type traits, milking speed and SCC

	Lawstuen (1989)	Lund (1994)	r bv DK-US[1]	Groen (1994)	
FU	-0.57	-0.18	-0.35	0.09	- = loose -> more mastitis
TP	-0.73	-0.13	-0.06	0.11	- = wide -> more mastitis
UD	-0.69	0.11	-0.45	0.18	- = deep -> more mastitis
SL	-0.51	-0.32	-0.02	0.26	- = weak -> more mastitis
RU	0.07	-0.14	-0.02	-	- = low -> more mastitis
TL	-	+0.72	-0.10	-	+ = long -> more mastitis
MS	-0.57	-0.29	-	-	- = slow -> more mastitis
SCC	-	0.27	-	0.77	+ = high -> more mastitis

[1] correlations between Danish breeding values for mastitis and US breeding values for udder traits. Personal communication with G.W. Rogers.

Table 3. Genetic response (Resp) and correlation between index and aggregate genotype (R_{IH}) with an index consisting of different combinations of udder traits, milking speed (MS), somatic cell count (SCC) and mastitis resistance (MR). UDD stands for all udder type traits. Calculations are based on 100 daughters per bull for all traits

Index	Resp	R_{IH}	% of MR
MR	0.295	0.656	100
MS	0.127	0.283	43
UDD	0.180	0.399	61
SCC	0.274	0.609	93
MS+UDD	0.227	0.505	77
MS+SCC	0.280	0.622	95
UDD+SCC	0.292	0.648	99
MS+UDD+SCC	0.302	0.670	102
MR+MS+UDD+SCC	0.338	0.752	115

Table 4. Weighting factors, genetic response and correlation between index and aggregate genotype (R_{IH}) with an index consisting of one or more udder traits, milking speed (MS), somatic cell count (SCC) and mastitis resistance (MR). Calculation based on 100 daughters per bull for all traits

	Weighting factors								
Index	FU	TP	UD	SL	TL	MS	SCC	Response	R_{IH}
SCC+MS+UDD	.0075	.0012	.0198	-.0027	-.0115	-.0164	-.6710	0.302	0.670
SCC+MS+FU	.0206	-	-	-	-	-.0156	-.7076	0.292	0.649
SCC+MS+TP	-	.0092	-	-	-	-.0144	-.7691	0.283	0.628
SCC+MS+UD	-	-	.0242	-	-	-.0163	-.6786	0.297	0.660
SCC+MS+SL	-	-	-	-.0063	-	-.0142	-.7765	0.281	0.625
SCC+MS+TL	-	-	-	-	-.0162	-.0191	-.7510	0.288	0.639
SCC+MS+FU+UD	.0080	-	.0189	-	-	-.0164	-.6725	0.298	0.662
SCC+MS+FU+UD+TL	.0065	-	.0174	-	-.0108	-.0164	-.6725	0.301	0.669
SCC+MS+FU+UD+TP	.0055	.0034	.0196	-	-	-.0163	-.6758	0.298	0.662
SCC+MS+FU+UD+SL	.0084	-	.0194	-.0024	-	-.0164	-.6708	0.298	0.662

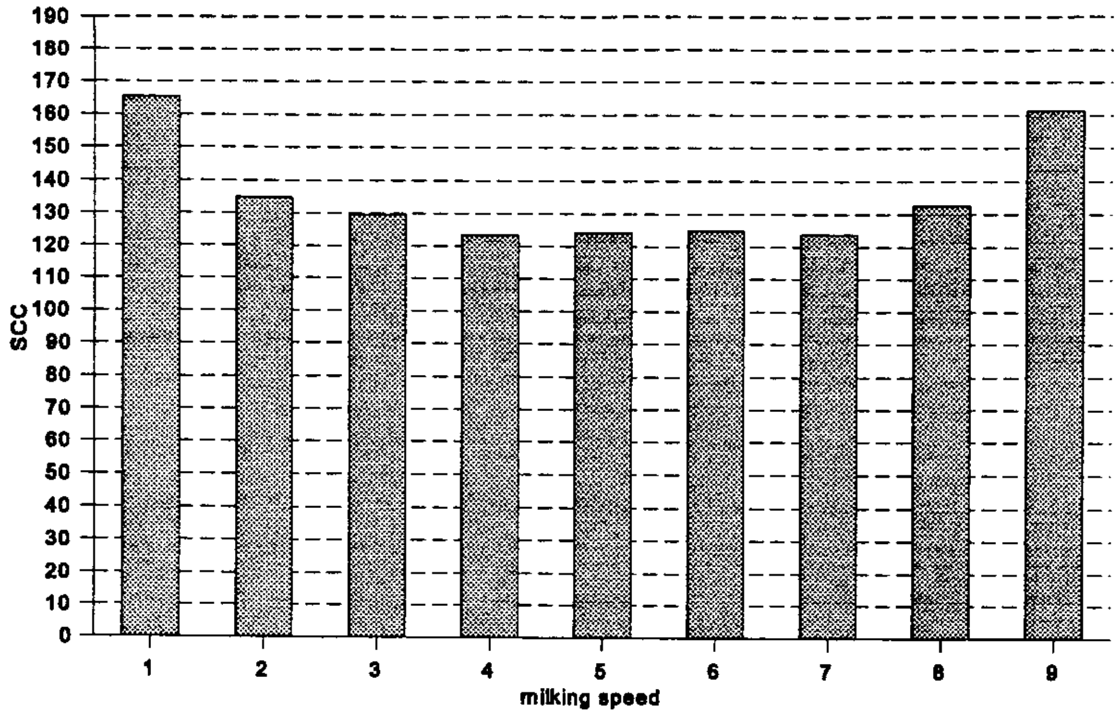

Figure 1: Relationship between somatic cell count (phenotypic) and score for milking speed (1=slow, 9=fast, phenotypic), based on 118691 first lactation cows.

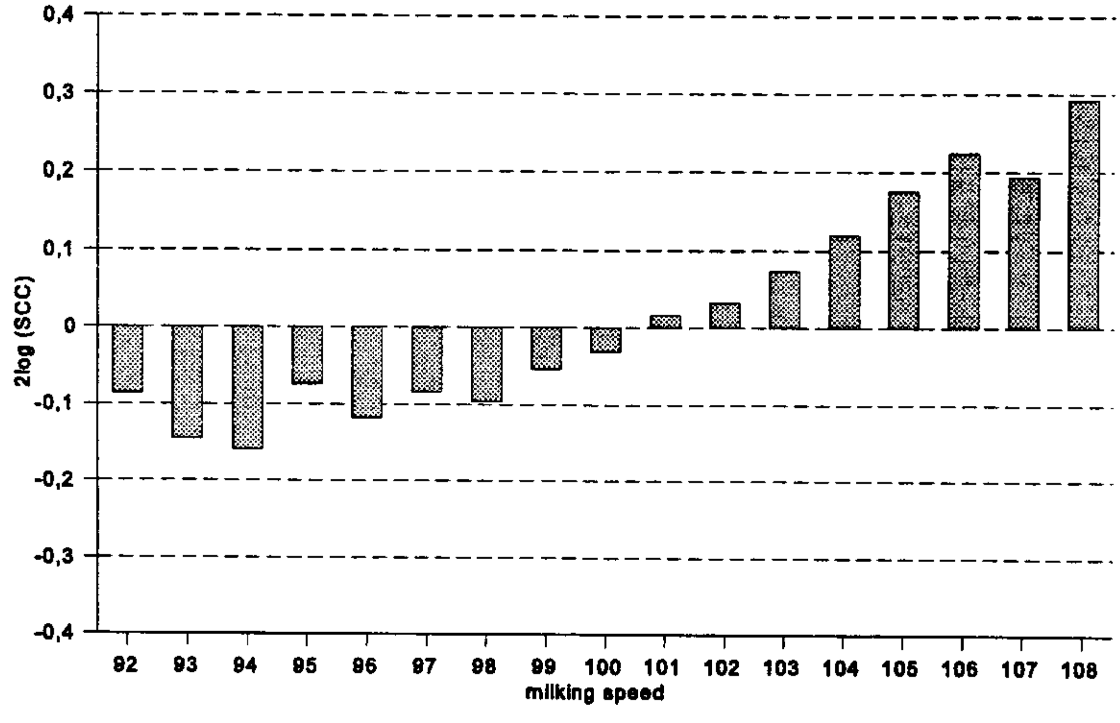

Figure 2: Relationship between breeding values of bulls for milking speed (above 100 is faster than average) and somatic cell count.