Statistical Indicators
E-27
Breeding Value Udder Health

▪ Introduction

Clinical mastitis is one of the most significant animal diseases in dairy cattle. Certain management strategies have been developed that may help to reduce clinical mastitis on farms. Genetic selection is another strategy to reduce the incidence of mastitis. Although genetic selection is a slow process, it actually results in a permanent transformation of the genetic resistance to mastitis infections of the livestock.

Clinical mastitis is the direct visible form of mastitis. There is also subclinical mastitis, which only shows in a higher somatic cell count in the milk. When we want to breed against mastitis, it means directly that we want to improve the health of the udder. Therefore we have developed an index for udder health, the Udder Health Index (*UHI*), which may reduce both the incidence of clinical mastitis and of subclinical mastitis.

Hereditary improvement depends on four elements: reliability of breeding values, heritability, standard deviation and selection intensity. By using as much valid information as possible, the existing genetic differences are made more explicit and estimated as reliably as possible. This results in more stable estimations of genetic potential (breeding values). An important condition for the improvement of the genetic potential in livestock is the presence of sufficient genetic variation. For mastitis, the existence of genetic variation has been proven, which means that selection is possible.

Unfortunately, the low heritability of mastitis renders it more difficult to estimate breeding values for mastitis with a high reliability. However, a mastitis infection has a huge influence on the somatic cell count of the milk. The development of the somatic cell count of the milk during lactation is an indication whether or not a cow has contracted an infection. The main advantage of this procedure is that the somatic cell count of the milk is determined routinely during milk recording, so there is a continuous stream of reliable data available to estimate breeding values.

In the current breeding value estimation for *UHI* somatic cell count, data is used as well as clinical mastitis data. The clinical mastitis data have been used in the breeding value estimation since 2016. They are based on registrations by dairy farmers. Subclinical mastitis is derived from somatic cell count data. From those data a number of different somatic cell count traits have been defined. These extra traits are correlated to such an extent with clinical and subclinical mastitis, that it is possible to estimate reliable breeding values for clinical and subclinical mastitis.

With the help of the methodology we use, we are able to calculate an udder health index for sires with a daughter group from the test period with a reliability between 80% and 85%. This means that the breeding values of sires show a standard deviation that is approximately similar to 90% of the total genetic standard deviation.

This document describes the data, traits and the model used to define an index for udder health.

▪ Definition of udder health

What is a healthy udder? There are many answers to this question, varying from the type of the udder to the extent to which an udder is free of infections.

Udder infections are a major cost factor for dairy farmers. Therefore, with the breeding values for udder health the choice has been made to focus on preventing infections. This means that the breeding values will have to contribute to the goal of breeding a cow that is less sensitive to mastitis infections.

Mastitis is being caused by a number of different types of bacteria. *Staphylococcus aureus* may well be the most notorious, because of the persistent infections and the large damage it causes. We could also have chosen to focus on one single cause, such as *Staph. aureus.*, but then this could lead to a proliferation of breeding values. Besides, our dealings are with the cow and not with the bacteria: we want to breed a cow that is more resistant to udder infections all along the line.

So, a healthy udder is an udder that is not sensitive to clinical or subclinical mastitis, irrespective of the pathogen causing the infection.

▪ Traits and Breeding Goal

In publications, breeding values will be presented for two mastitis traits and the index: the breeding values for subclinical mastitis and clinical mastitis, and an udder health index. In the udder health index, clinical and subclinical mastitis have been given weight according to the economic damage they are causing. In total, seven traits have been defined that are being used in the breeding value estimation. Besides the two published breeding values, there are five traits that are being used to predict resistance against mastitis infections: the so-called indicator traits.

▪ Indicator traits

Research has proven that somatic cell counts from test days, show patterns from which potential contamination and infections may be deduced. So those patterns and other derived traits show a correlation with mastitis infections (clinical or subclinical), and therefore give us information on the susceptibility to infections of an animal, even before this animal gets an infection.

The five indicator traits are:
1. *SCS150*: the ^{2}log of the mean somatic cell count between day 5 and 150 of the lactation;
2. *SCS400*: the ^{2}log of the mean somatic cell count between day 151 and 400 of the lactation;
3. *Infection*: an indication (0/1) whether at least one somatic cell count higher than 150,000 cells/ml has been registered during a lactation between day 5 and 400 of the lactation; this trait registers *whether or not* there has been an infection.
4. *Severity*: the fraction of the total number of lactation test days until day 400 on which the somatic cell count was higher than 150,000 cells/ml (0, ..., 1); this trait registers how severe the infection was.
5. *Peak*: the number of identifiable peaks in the somatic cell count during a lactation until day 400, without specification of the peak pattern. A peak is based on three consecutive somatic cell count measurements, marking values up to 200,000 cells/ml as 'low' and values higher than 500,000 cell/ml as 'high'. Two types of peaks have been defined: low-high-low and low-high-high (referred to as -+- and -++).

Table 1. Example of a lactation test day list for a cow in second lactation. Refer to the text for an explanation of the derivation of the observations from the somatic cell count data.

lactation test day	Days in milk	somatic cell count (x 1,000 cells/ml)		Infection Intensity (> 150,000 cells/ml)	Peak
1	5	32			-
2	19	44			-
3	33	54			-
4	47	49			-
5	61	69			-
6	75	87			-
7	89	67			-
8	103	54			-
9	117	62	**mean scc**		-
10	131	49	**day 5 – 150:**		-
11	145	38	55		-
12	159	45			-
13	173	120			**-**
14	187	630		yes	**+**
15	201	558		yes	**+**
16	215	361		yes	0
17	229	213		yes	0
18	243	177		yes	-
19	257	150			-
20	271	185		yes	-
21	285	174		yes	-
22	299	162		yes	-
23	313	237	**mean scc**	yes	0
24	327	111	**day 150 – 400:**		-
25	341	114	231		-

Table 1 shows an example for a cow in second lactation. In this table the somatic cell counts for consecutive lactation test days (milk recording every two weeks) are listed.

The mean somatic cell count for the first part of the lactation (all test days between day 5 and day 150 of the lactation) was 55,000 cell/ml (see Table 1). For the second part of the lactation, day 151 until at the latest day 400 of the lactation, the mean somatic cell count was 231,000 cells/ml. So, for the traits *SCS150* and *SCS400* this cow has a score in this lactation of respectively:

SCS150: $^{2}\log$ (55,000) = 15.7
SCS400: $^{2}\log$ (231,000) = 17.8

Both the traits *Infection* and *Severity* are derived from the presence of lactation test days with an increased somatic cell count (somatic cell count > 150,000 cells/ml). In the table those days are marked with "yes". *Infection* is an "all or nothing" trait, that indicates *whether or not* there have been days in the lactation with a somatic cell count of more than 150,000 cells/ml.

In our example the cow gets a 1 for *Infection* (there have been days with somatic cell count > 150,000 cells/ml). *Severity* takes the number of lactation test days on which somatic cell count was higher than 150,000 cells/ml and divides this by the total number of lactation test days. For *Severity* this cow gets 9/25 = 36%.

Peak counts the number of identifiable peaks in somatic cell count. For *Peak* there has to be an obvious pattern of somatic cell counts on three consecutive lactation test days, namely low-high-high (- + +) or low-high-low (- + -). High (+) means a somatic cell count higher than 500,000 cells/ml and low (-) a somatic cell count lower than 200,000 cells/ml. Lactation test days on which the somatic cell count lies between those two limits are marked with (0). In the table we see one (- + +) pattern around day 187 of the lactation. For this lactation the cow gets *Peak* = 1. However, a cow may show several peaks in a lactation.
Table 2 shows the heritabilities and the genetic standard deviations for these indicator traits.

Table 2 Heritabilities (h^2) and genetic standard deviation (σ_g) for the traits that form the basis for the udder health index.

	Parity 1		Parity 2		Parity 3	
	h^2	σ_g	h^2	σ_g	h^2	σ_g
SCS150	0.088	40.706	0.098	48.135	0.087	48.301
SCS400	0.105	40.509	0.101	39.090	0.111	41.677
Infection	0.061	0.120	0.060	0.115	0.066	0.113
Intensity	0.094	8.602	0.094	9.434	0.096	10.198
Peak	0.050	0.102	0.055	0.124	0.061	0.136
SCM	0.022	0.066	0.026	0.071	0.041	0.094
CM	0.025	0.039	0.024	0.042	0.032	0.050

▪ Mastitis traits

Subclinical mastitis

For subclinical mastitis (*SCM*), the UGCN definition (UGCN (Dutch Udder Health Centre) project "Beest 5": Verbeteren van weerstand tegen mastitis via fokkerij, 2007) of low-low-high ('- - +') for the somatic cell count on three consecutive lactation test days is used. For heifers the limit value is 150,000 cells/ml, for cows the limit is a somatic cell count of 250,000 cells/ml. Subclinical mastitis is analysed as a 0/1 trait. If a cow or heifer shows the '- - +' pattern on three consecutive somatic cell count measurements during the lactation, the observation *SCM* becomes 1, in all other cases *SCM* is 0. No distinction is made between cows with only one infection and cows with several infections during the lactation. This is because we want to select against the presence of subclinical mastitis and not so much for cows with more or less cases of subclinical mastitis.

Basically, *SCM* is calculated over the same period as the indicator traits above, from day 5 up to day 400 of the lactation. In the beginning of the lactation, the pattern covers more then one lactation: if a cow shows a somatic cell count above the limit value on its first lactation test day, the last two test days of the previous lactation are used to determine whether the somatic cell count pattern for subclinical mastitis '- - +' occurs. On the second test day of the lactation, the final test day of the previous lactation is included. Therefore, the patterns '- - dry +' and '- dry - +' are equivalent to '- - +'. This is also the case if the final test days of the previous lactation are later than day 400 of the previous lactation.

On the first and second lactation test day of heifers, the previous days are set to unknown ('0'). However, on the first and second lactation test day of heifers it is assumed, for pattern identification, that '0' is the same as '-', so the patterns '0 0 +' (on the first test day) and '0 - +' (on the second test day) are seen as a subclinical infection.

Clinical mastitis
Starting April 2016, clinical mastitis registrations by dairy farmers have been added to the breeding value estimation. Besides that, research for the UGCN project 'Beest 5' has indicated that the genetic value for resistance against clinical mastitis infections can be predicted reliably from the indicator traits and the potential for resistance against subclinical mastitis (see Table 8 for the genetic correlation between the traits).

In Table 2 the heritabilities and the genetic standard deviations for clinical and subclinical mastitis per parity are given.

Index Udder Health
From the breeding values *CM* and *SCM* an index is composed in which the economic damage of a clinical case of mastitis and a subclinical case of mastitis have been incorporated. Besides the breeding values *CM* and *SCM*, this index is published to give a complete picture of udder health. For information on the composition of the index see under ('Udder Health Index').

▪ Data

Observations
There is no data available on clinical mastitis. The breeding value estimation uses the somatic cell count that has been measured on the lactation test day. The data is entered on test day level, but analysed on lactation level. This means that the traits are valid for the complete lactation, but are derived from the data of all available test days in that lactation.

The day productions have to meet the following requirements:
- A cow has to be herd book registered (S) and the sire of the cow has to be known;
- Only official (controlled) day productions are included; day productions that have been collected by farmers on their own account are valid too;
- Only day productions of lactation 1-3 of a cow are included;
- Only day productions from day 5 up to the end of lactation are included;
- A cow must have a known herd on the test day;
- Age at calving has to be at least 610 days;
- At least 1 valid lactation test day with somatic cell count measurement has to be known.
- There is an extra requirement for the pattern traits (*Peak* and *SCM*), which states that within a lactation there should be no more than 84 days between consecutive test days with a somatic cell count. If this requirement is not met, the records for the traits *Peak* and *SCM* for this lactation are set to 'missing'.

Pedigree
Family relations between animals are included in the breeding value calculations. Animals that are related share a certain amount of DNA, therefore, the family of an animal forms an extra source of information on the genetic potential of this animal. In the first place this applies to parents and progeny of an animal, but it also applies to (half) brothers and sisters, ancestors (through parents and grand parents) and grandchildren (through direct progeny). Such a network of relations covers several generations and is a valuable addition to information from parents and from own observations.

Every pedigree ultimately ends with parents that are unknown. These unknown parents are grouped (*phantom group*), and the average genetic potential of this group is used as a predictor for the progeny.
In breeding, animals of other breeds are used within a breed and therefore many genetic (family) relations have developed between breeds. An example is the use of Holstein Friesians in the

Dutch Friesian breed and in the MRY population. The numerous genetic relations between breeds make it possible to calculate breeding values simultaneously for different breeds.

Phantom groups

If a parent is unknown, this parent is replaced by a "phantom parent". Phantom parents can be combined into phantom groups or genetic groups. A phantom group gives a "replacement" genetic value of an unknown parent. The genetic value of a phantom group is determined by all animals that are linked to this group. It is important to combine animals into a group that will most probably have the same genetic potential. The factors that may cause a difference in genetic potential in the breeding value estimation and therefore are important for the definition of phantom groups, are:

1. Breed

A different group is formed for every breed. In practice, this means about 30 different breed groups. A crossbred is assigned to the group of which it has the highest blood portion. If the blood portions are the same, there are two situations:

- for 50%/50% FH/HF crossbreds and 50%/50% MRY/HF-crossbreds there are two different "breed"-groups; they are not linked to one of the parent breeds;
- in the case of the other 50%/50% crossbreds, the animal is assigned to one of the parent breeds, based on the breeding direction of the crossbred. Three directions are distinguished: dairy, dual-purpose and beef. The breeding direction determines which of the parent breeds is leading. In which the breed that belongs to the breeding direction beef is leading, then the breed that belongs to the breeding direction dual-purpose and finally the breed that belongs to the breeding direction dairy. If both breeds have the same breeding direction, the first breed in the breed code is leading.

2. Year of birth

Every year of birth forms a group. Animals that have been born before 1950 are linked to the year of birth 1950.

The minimum number of animals (parents) per phantom group is 100. If the number of 100 is not reached, phantom groups are put together. Years of birth are put together until the number of 100 has been reached or until a maximum of 10 years of birth has been put together. If a breed is so small that it has less than 20 animals, the phantom group is added to the rest group. This rest group consists of all sorts of phantom groups that have too little animals to be able to realize a reliable estimation if viewed apart.

The influence of the phantom group estimation on the cow or sire index gradually decreases as the phantom group moves more generations away from the animal in question, and/or as the animal itself gets more information from progeny and/or own lactation(s).

▪ Statistical model

The breeding values for the mastitis resistance traits are estimated with an animal model, according to the BLUP technique (Best Linear Unbiased Prediction). An animal can have a higher potential for getting an infection without actually getting infected, therefore the information on subclinical and clinical infections is completed with information from the breeding values for the underlying traits. For this, the correlations between all traits are used (see Table 9). Hence, the breeding value estimation is a 'multiple trait' breeding value estimation.

All traits are analysed with the same statistical model:

$$Y_{ijklmnopqr} = HY_j + YM_k + age_l + n\_td_m + NRD_n + het_o + rec_p + inb_q + animal_r + e_{ijklmnopqr}$$

The effects in the model

The effects in the model are:

$Y_{i.}$ = observation for trait *i* (CM, SCM or indicator trait)
HY_j = herd*year class of observation
YM_k = year*month class of observation
age_l = calving age (10 day classes)
n_td_m = number of registered lactation test days
NRD_n = number of risk days in lactation (number of days between 1st and final test day)
het_o = heterosis effect
rec_p = recombination effect
nb_q = inbreeding coefficient
$animal_q$ = additive genetic effect (breeding value) of the animal
$e_{ijklmnopq}$ = rest term of $Y_{i.}$, the part which cannot be explained with the model.

*Herd*year class*
The level of observations differs per herd. And within a herd, the situation around the traits may also change. Therefore, in the herd*year class a herd effect is estimated for each year. A year runs from 1 January until 31 December. The attribution of an observation to a herd depends on the type of the trait (see Table 3). In the majority of cases this is the same herd for all traits, but the correct attribution of an observation to a herd is a point of attention for animals that move during their lactation.

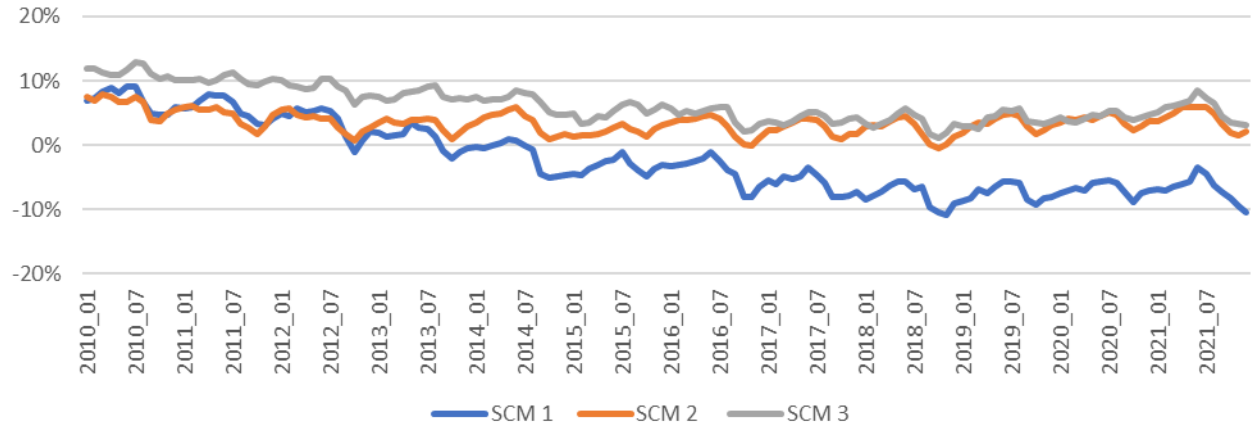
Table 3. Attribution of traits to herds when a cow is moved to another herd during a lactation.

Trait	Attribution (herd) *)	Date	Period (days lactation)
SCS150	Herd where longest part of the period has been spent.	First test day of period	5 – 150
SCS400	Herd where longest part of the period has been spent.	First test day of period	151 – 400
Infection	Herd where peak (first increase) has been observed.	First test day of SCC increase	5 – 400
Intensity	Herd where peak (first increase) has been observed.	First test day of SCC increase	5 – 400
Peak	Herd where peak (first increase) has been observed.	First test day of SCC increase	5 – 400
SCM	Herd where the infection has been observed.	First test day of SCC increase	5 – 400
CM	Herd where the infection has been observed.	Registration date of infection	-15 – 400

*) If the observation is negative (valid record but no observation), the observation is attributed to the herd where the longest part of the period has been spent.

*Year*month class*
The infection pressure differs per season and from year to year (Figure 1). To take this into account, a class is attributed to every lactation based on the year and month of calving (the start of the lactation under consideration). To avoid confounding this effect with herd*year, each month-group starts on the 15th of the corresponding month.

Figure 1. Year*month effect from January 2010 to June 2021 for subclinical mastitis in the first lactation (above), second lactation (middle) and third lactation (below).



Age at calving
It has been shown that there is a certain dependence of the mastitis traits on the age of calving of an animal. Animals are divided into age classes with a difference of 10 days between them. The classes run from 610 to 2040 days (1.7 – 5.6 year) in age.

Number of registered lactation test days and Number of days at risk
The chance to notice an infection by looking at the development of the somatic cell count, decreases with an increasing interval between test days. The other way around, there is more chance to miss an infection with six weeks milk recording than with three week milk recording.
However, independent of the potential of a cow, the chance of at least one infection during the lactation increases with the length of the lactation. Meaning, the chance of an infection between day 5 and day 120 of the lactation is smaller than the chance of an infection between day 5 and day 305.

Both effects are a result of elapsed time (between test days and during the lactation) and don't state anything about the genetic potential of a cow. Therefore the two effects have been included in the model: 1) the number of lactation test days and 2) the number of days at risk between the first and last lactation test day.

The number of registered lactation test days tells us something about the length of the lactation until then, or about the interval between test days. It is irrelevant which of the two it is, because both have the same effect: A higher number of test days also increases the chance of finding something. To count the number of test days, only test days with a valid somatic cell count observation are included.
Correction for the number of days at risk has to make sure that the final remaining difference between the various test day schemes is removed.

Heterosis and recombination effect
Heterosis and recombination effects play a role with crossbreeding. They are genetic effects that are not passed on to the offspring. Research showed that corrections need to be made for these effects. The extent of heterosis is defined as the difference in level of the trait in the crossbred with the difference of the parent breeds. Recombination is the loss of the usually positive effect of

heterosis and occurs when the earlier obtained crossbred product is crossed back with one of the parent breeds. This is described in E-chapter 7 in more detail.

Inbreeding coefficient
The amount of inbreeding can affect the incidence of reproduction disorders. The higher the inbreeding coefficient the larger the negative effect, this is called inbreeding depression. By including the inbreeding coefficient as an effect in the model, the negative effects of inbreeding on incidence of reproduction disorders are taken into account.

Animal
This is the additive genetic effect or breeding value, the effect that matters in the end. The variable *animal* contains the (genetic) contribution of an animal to the observation and determines the breeding value of an animal. In addition, all information coming from ancestors and progeny is used to determine the breeding value.

▪ Udder health index

The breeding values that are meant for publication are, respectively: *SCM*, *CM* and *UHI*, in which *UHI* is the udder health index, existing of *SCM* and *CM*. Even though breeding values for all traits (including the indicator traits) are estimated separately for the first three lactations, per trait only one breeding value is rendered for the overall trait. The breeding value for the overall trait is an index in which weights per parity are attributed to the lactation breeding values in the way they have been established in the Test Day Model for production traits:

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

Table 4 shows the heritabilities and standard deviations of the overall traits.

Table 4 Heritabilities (h^2) and standard deviations (σ_g) of the (absolute) breeding values for the overall traits. The three lactation breeding values for every trait have been weighed into a single index for that trait. Heritability and standard deviation of the udder health index are also included.

Trait	**h^2**	**σ_g**
SCS150	0.165	43.255
SCS400	0.173	38.794
Infection	0.120	0.110
Intensity	0.158	8.864
Peak	0.121	0.113
SCM	0.056	0.068
CM	0.060	0.039
UHI	**0.089**	**0.051**

Also, an udder health index was created in which the economic damage of clinical and subclinical mastitis have been incorporated. 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, both *CM* and *SCM* are expressed in the interval [0.1]. In other words, a breeding value of +0.01 corresponds on average with a 1% higher incidence of mastitis in the group progeny. On an absolute scale the index would look like this:

$$I_{abs} = (-83) * BV_{SCM,\ abs} + (-196) * BV_{CM,\ abs}$$

However, both *CM* and *SCM*, as well as the index *UHI* are published as a relative breeding value with a mean of 100 and a standard deviation of 4. Therefore the weights for *SCM* and *CM* also have to be translated to the relative scale.

Given the economic damage of a case of *SCM* or *CM* (Table 5), the variances of, and covariances between *CM* and *SCM*, the genetic standard deviation of the index is €11.82. The genetic standard deviation (sdG) of the economic damage of *SCM* and *CM* is € 83.- * 0.0682 = € 5.66 en €196 * 0.0385 = € 7.55, respectively. Because the index is expressed on the same relative scale as *SCM* and *CM*, the relative weights of both can be calculated easily:

$W_{rel,SCM}$ = sdG€(SCM)/ sdG€(Index) = € 5.66 / € 11.82 = 0.477
$W_{rel,CM}$ = sdG€(CM) / sdG€(Index) = € 7.55 / € 11.82 = 0.641

So the udder health index is calculated from the relative breeding values *CM* and *SCM* according to the formula:

$$BV_{UHI,rel} = 100 + 0.477 * [BV_{SCM,rel} - 100] + 0.641 * [BV_{CM,rel} - 100]$$

This relative breeding value or index has an average of 100 and a standard deviation of 4, just like the breeding values *CM* and *SCM*.

Table 5 Calculation of the weights for *SCM* and *CM* for an udder health index on a relative scale (average 100, standard deviation 4). *W_Econ* is the economic damage of an infection. The variance/covariance matrix on the absolute scale for *CM* and *SCM* is included under *(co-)var*, as is the predicted variance of *UHI*; *sdG* is the genetic standard deviation of *CM* and *SCM* on an absolute scale. The standard deviation of the economic damage, expressed in euros, is under *sdG€*. The weighing for *SCM* and *CM* on the relative scale that follows from it, is under *W_Rel*.

	(co-)var SCM	CM	W_Econ	sdG	sdG€	W_Rel
SCM	0.00465	0.00155	€ 83.-	0.0682	€ 5.66	0.477
CM	0.00155	0.00148	€ 196.-	0.0385	€ 7.55	0.641
UHI (SCM + CM)	€139.60				€ 11.82	

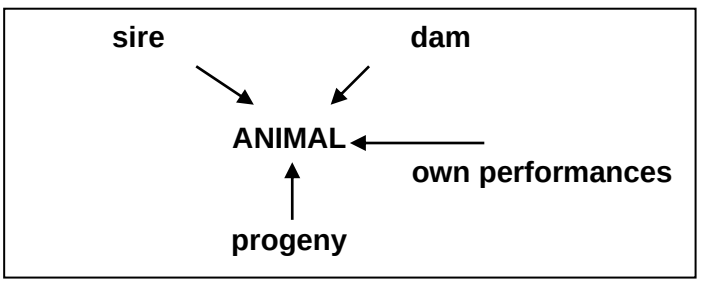
W_Econ have been rendered as positive amounts, because the breeding values are reversed: higher breeding values indicate lower incidences. So amounts have to be seen as economic benefits.

▪ Reliability

Breeding values are estimates of the genetic potential. The word ‘estimate’ indicates that there is a certain inaccuracy in a breeding value. The reliability of a breeding value indicates how much difference there may be between the estimated breeding value and the real genetic value.

The reliability depends on the amount of available information for an animal. There are three information sources:
1. own performance
2. progeny
3. parents

Information on the udder health of (half) sisters, grandparents, etc. is included through the parents, and information from granddaughters etc, is included through the progeny.



In Figure 2 an impression is given of the reliabilities of the breeding values *CM* and *SCM*, and of the udder health index *UHI*. In Figure 2 the reliability of sires born between 2001 and 2003 is considerably lower, because there are less daughters and less lactations known for these sires. In general the conclusion may be that a sire with 100 daughters or more, scores an average reliability of 86% for the index *UHI* and for the breeding value subclinical mastitis, and 83% for the breeding value clinical mastitis.

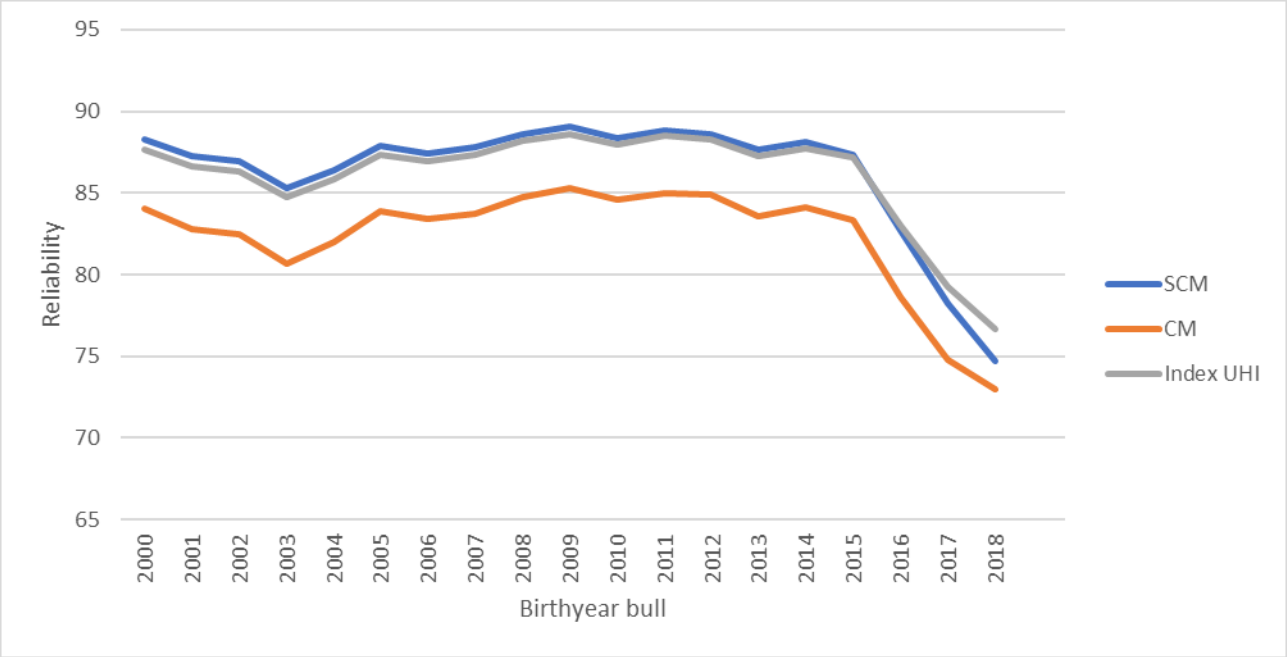


Figure 2. Average reliability of the breeding values for UHI, CM and SCM of sires, born between 2000 and 2018, with 100 or more descendants (based on data up to and including August 2008).

▪ Base

See chapter ‘Bases for breeding values and base differences’.

▪ Publication

Presentation

The breeding values for the mastitis traits (*CM*, *SCM* and *UHI*) are published with an average of 100 and a standard deviation of 4. It is important to remember that values above 100 are advisable. A breeding value for *CM* of more than 100 indicates that clinical mastitis will appear *less often* in the daughter group. A breeding value for *UHI* of more than 100 will decrease the presence of both clinical and subclinical mastitis.

The breeding values *CM* and *SCM* are expressed on an absolute scale in incidences (chance of infection per cow per lactation). On the relative scale, on 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 descendant per lactation, respectively. In the udder health index one standard deviation corresponds to € 11.82 per descendant per lactation.

So a breeding value above 100 means a more than average resistance against mastitis. A bull with a breeding value for resistance against subclinical mastitis of 104 will have a group of daughters in which clinical mastitis occurs ½ * (104 –100) * 1.7% = 3.4% less. This corresponds to economic benefits of € 2.84 per daughter per lactation. A breeding value of 104 for the index *UHI* means that on average per daughter about ½ * (104 –100) * € 2.96 = € 5.91 per lactation can be saved on costs linked to subclinical and/or clinical mastitis.

The expected response of selection on UHI in breeding bulls shows a decrease per generation in subclinical mastitis of 4%, a decrease in clinical mastitis of 2.5%, and an economic benefit of € 8,35 per cow per lactation.

▪ Publication Requirements

See chapter ‘Publication rules sires’.

Table 6 Overview of the heritabilities (diagonal, bold), genetic correlations (above the diagonal) and rest correlations (under the diagonal) for the 21 traits in the breeding value estimation udder health.

		1st lactation							2nd lactation							3rd lactation						
lactation		SCS150	SCS400	Inf	Intens	Peak	SCM	CM	SCS150	SCS400	A_Inf	Intens	Peak	SCM	CM	SCS150	SCS400	Inf	Intens	Peak	SCM	CM
1st	SCS150	**0.088**	0.889	0.879	0.928	0.825	0.836	0.745	0.861	0.705	0.652	0.736	0.813	0.558	0.645	0.827	0.684	0.554	0.734	0.728	0.440	0.638
	SCS400	0.538	**0.105**	0.926	0.936	0.770	0.916	0.713	0.857	0.875	0.834	0.881	0.766	0.768	0.590	0.779	0.861	0.810	0.859	0.708	0.691	0.495
	Inf	0.623	0.609	**0.061**	0.930	0.717	0.916	0.553	0.851	0.838	0.870	0.883	0.722	0.735	0.530	0.767	0.833	0.758	0.833	0.687	0.697	0.497
	Intensity	0.781	0.829	0.686	**0.094**	0.764	0.911	0.660	0.874	0.802	0.779	0.838	0.742	0.667	0.548	0.796	0.745	0.678	0.832	0.718	0.579	0.511
	Peak	0.571	0.509	0.392	0.487	**0.050**	0.769	0.790	0.853	0.705	0.581	0.655	0.888	0.688	0.874	0.869	0.677	0.573	0.760	0.836	0.406	0.786
	SCM	0.212	0.451	0.664	0.295	0.169	**0.022**	0.588	0.863	0.875	0.828	0.895	0.779	0.695	0.611	0.753	0.817	0.788	0.872	0.720	0.687	0.516
	CM	0.000	0.000	0.000	0.000	0.000	0.000	**0.025**	0.659	0.511	0.454	0.493	0.768	0.542	0.676	0.720	0.556	0.504	0.658	0.664	0.356	0.671
2nd	SCS150	0.186	0.216	0.151	0.199	0.116	0.091	0.000	**0.098**	0.824	0.742	0.859	0.894	0.720	0.774	0.951	0.816	0.737	0.884	0.915	0.609	0.762
	SCS400	0.161	0.254	0.173	0.198	0.101	0.130	0.000	0.535	**0.101**	0.930	0.954	0.689	0.898	0.558	0.785	0.930	0.913	0.915	0.769	0.829	0.539
	Inf	0.126	0.176	0.130	0.153	0.082	0.087	0.000	0.546	0.615	**0.060**	0.941	0.583	0.864	0.435	0.695	0.903	0.893	0.905	0.646	0.812	0.472
	Intensity	0.183	0.268	0.189	0.261	0.141	0.122	0.000	0.792	0.824	0.667	**0.094**	0.686	0.816	0.575	0.796	0.906	0.899	0.935	0.756	0.798	0.572
	Peak	0.119	0.132	0.107	0.141	0.107	0.062	0.000	0.583	0.556	0.365	0.511	**0.055**	0.601	0.873	0.915	0.755	0.635	0.769	0.886	0.513	0.791
	SCM	0.070	0.123	0.093	0.112	0.050	0.069	0.000	0.276	0.512	0.471	0.427	0.358	**0.026**	0.554	0.736	0.895	0.866	0.865	0.731	0.816	0.501
	CM	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.024**	0.833	0.638	0.481	0.693	0.830	0.375	0.806
3rd	SCS150	0.177	0.189	0.123	0.147	0.080	0.080	0.000	0.232	0.273	0.167	0.244	0.163	0.126	0.000	**0.087**	0.803	0.682	0.856	0.962	0.580	0.862
	SCS400	0.127	0.196	0.144	0.151	0.065	0.108	0.000	0.240	0.374	0.258	0.312	0.185	0.203	0.000	0.536	**0.111**	0.908	0.915	0.772	0.869	0.530
	Inf	0.099	0.128	0.080	0.091	0.043	0.055	0.000	0.152	0.239	0.187	0.199	0.115	0.137	0.000	0.527	0.589	**0.066**	0.884	0.663	0.862	0.444
	Intensity	0.161	0.202	0.141	0.174	0.088	0.096	0.000	0.257	0.335	0.224	0.337	0.195	0.174	0.000	0.801	0.828	0.650	**0.096**	0.822	0.769	0.647
	Peak	0.092	0.115	0.079	0.112	0.052	0.053	0.000	0.154	0.192	0.112	0.177	0.153	0.116	0.000	0.594	0.555	0.337	0.499	**0.054**	0.631	0.837
	SCM	0.087	0.104	0.089	0.085	0.032	0.073	0.000	0.087	0.188	0.151	0.149	0.077	0.131	0.000	0.223	0.454	0.451	0.362	0.307	**0.041**	0.257
	CM	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.032**

▪ Literature

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