

Statistical Indicators

E-18

Somatic Cell Score with Test Day Model

■ Introduction

Mastitis is one of the most important herd related illnesses in Dutch cattle management. Mastitis results in high economic losses due to a decrease in production (including non-delivered milk), treatment costs, labour costs, early culling and contamination of other cows. Furthermore, increasingly strict demands are made on the somatic cell count with respect to the payment for the milk.

Dairy farmers who participate in the milk recording system may also opt to have the somatic cell count in the milk of an individual cow analysed. The somatic cell count in milk is expressed as the number of cells per ml. When presented, the somatic cell count measured is divided by 1000, so that a somatic cell count of 50 means that there are 50,000 cells in one ml of milk. The dairy farmer is interested in the somatic cell count because the somatic cell count is used by the dairy industry as a quality criterion for milk delivered. A high somatic cell count means lower quality milk. This is expressed in a discount to the milk price paid when the somatic cell count is in excess of 400,000 cells per ml in the tank of milk delivered.

At the same time, the somatic cell count tells something about the health of the udder. There is a correlation between somatic cell count and infection or mastitis in the udder. If a cow has a high somatic cell count on the day of milk recording, this may mean that, at that moment, the cow's resistance system is fighting an infection in one or more parts of the body by producing extra white blood cells. Therefore, a high somatic cell count may point to mastitis. There may, however, be another (unknown) cause for it. If, at the same time, there are externally perceptible phenomena to the udder, milk or cow, it suggests clinical mastitis. Subclinical mastitis is only perceptible from changes in the somatic cell count and the presence of pathogens in the milk.

In this chapter, the Somatic Cell Score index will be described in detail.

■ Data in Somatic Cell Score evaluation

Starting in May 2003, the breeding values for somatic cell score are calculated using the Test Day Model based on testday somatic cell counts. Data edits and data suppliers are similar to the Testday Model for milk production (chapter E-7 of the CRV handbook). The only difference is the data-edit on milk yield. In the somatic cell score evaluation testdays with known somatic cell counts are used, regardless of the availability of milk yield.

■ Statistical Model

As the somatic cell count (SCC) measurements from individual test milk data are not normally distributed, this data cannot be used directly for the breeding value estimation. The SCC measurements are transformed in order to comply with the condition of normal distribution into somatic cell scores (SCS) for the breeding value estimation. The transformation is as follows:

$$SCS = 1000 + 100 * (\sqrt{\log(SCC/1000)}),$$

whereby SCC represents the somatic cell count from test milk data, expressed in the number of cells per ml. The SCS is used in the breeding value estimation. The SCS can be calculated back to the SCC via:

$$SCC = 1000 \times 2^{(SCS-1000)/100}$$

The relation between SCS and SCC is demonstrated in Figure 1.

The breeding value estimation for SCS is calculated with the Test Day Model as described in chapter E-7 of the CRV handbook. For SCS, the same fixed effects and random regression effects are used as for milk production traits. They are corrected for heterogeneity of variance in the same way that milk production traits are. With the Test Day Model, the breeding values of every animal are estimated for daily production for each day from day 5 through 305 in lactation 1, 2 and 3 for milk production traits. In the same way, the Test Day Model provides breeding values for SCS for every day from day 5 through 305 in lactation 1, 2 and 3. In that way, every animal obtains its own genetic curve in lactation 1, 2 and 3.

Table 1. Heritabilities (diagonal) and genetic correlations voor somatic cell count.

SCS	Lactation 1	Lactation 2	Lactation 3	Overall
Lactation 1	0.25			
Lactation 2	0.71	0.28		
Lactation 3	0.65	0.80	0.28	
Overall	0.89	0.92	0.89	0.37

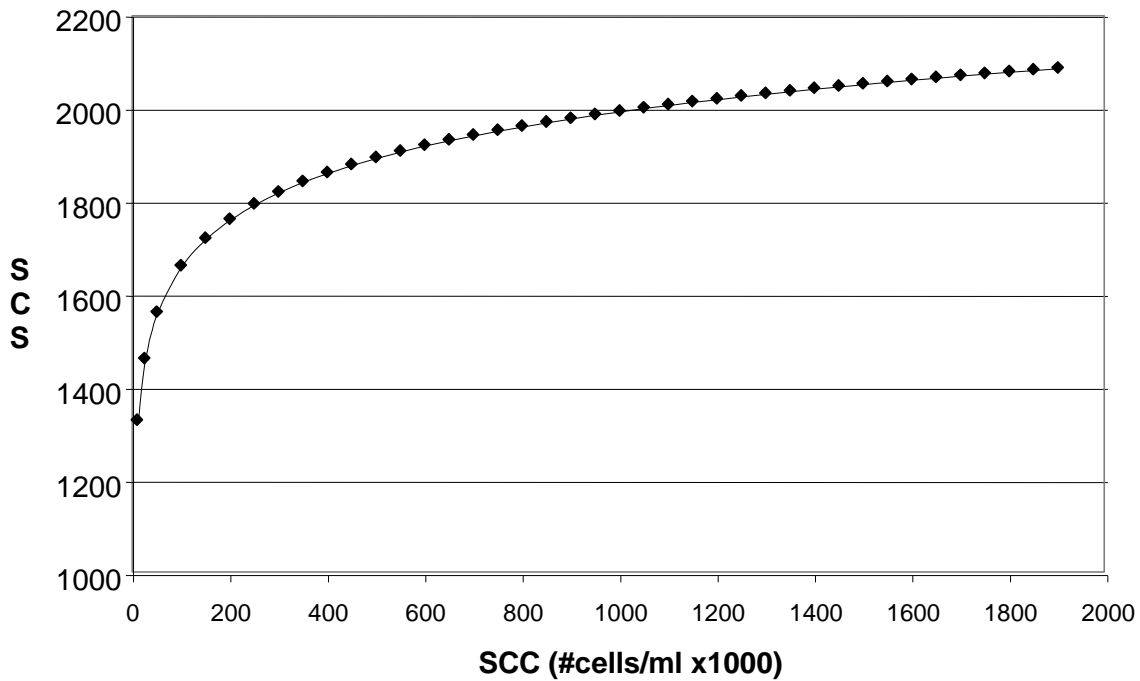


Figure 1. Somatic cell score (SCS) as a function of somatic cell count (SCC)

The genetic standard deviations for SCS on a daily basis are expressed in Figure 2, including the standard deviations of permanent environment, the herd curves, and the rest. The heritabilities for SCS on a daily basis are expressed in Figure 3 and, on average, are 0.37 and within lactation 1, 2 and 3 are 0.25, 0.28, and 0.28 respectively. The heritabilities and genetic correlation on lactation level are shown in table 1.

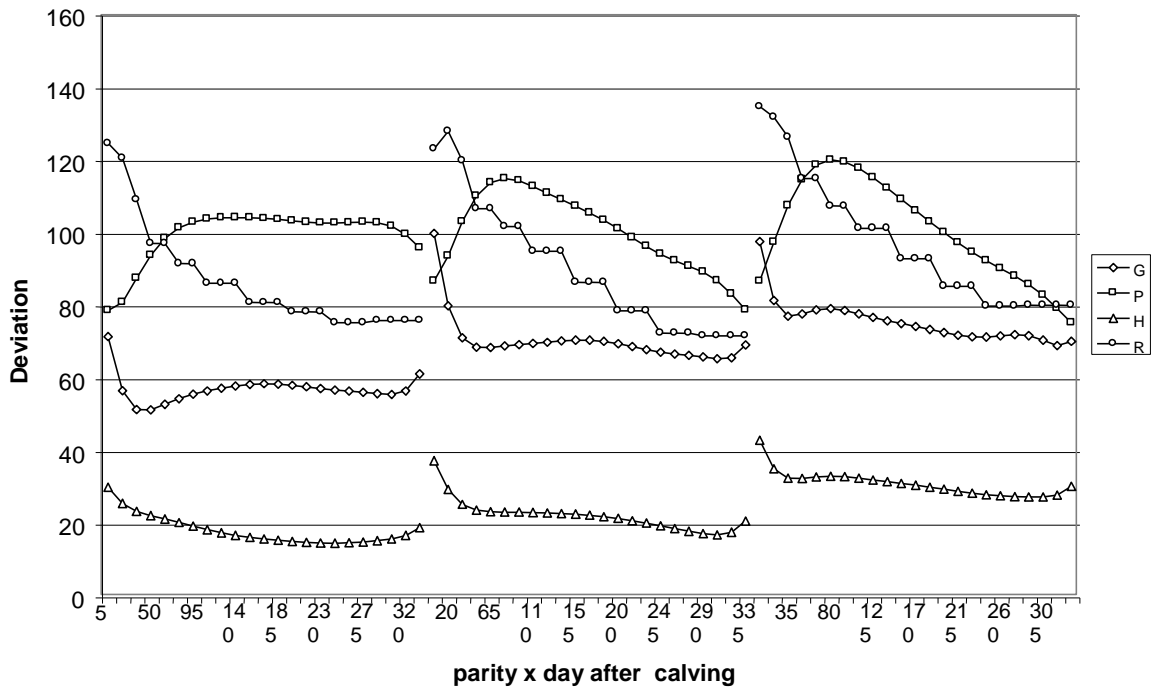


Figure 2. Genetic (G), permanent environment (P), herd curve (H) and the rest (R) standard deviations for SCS on a daily basis

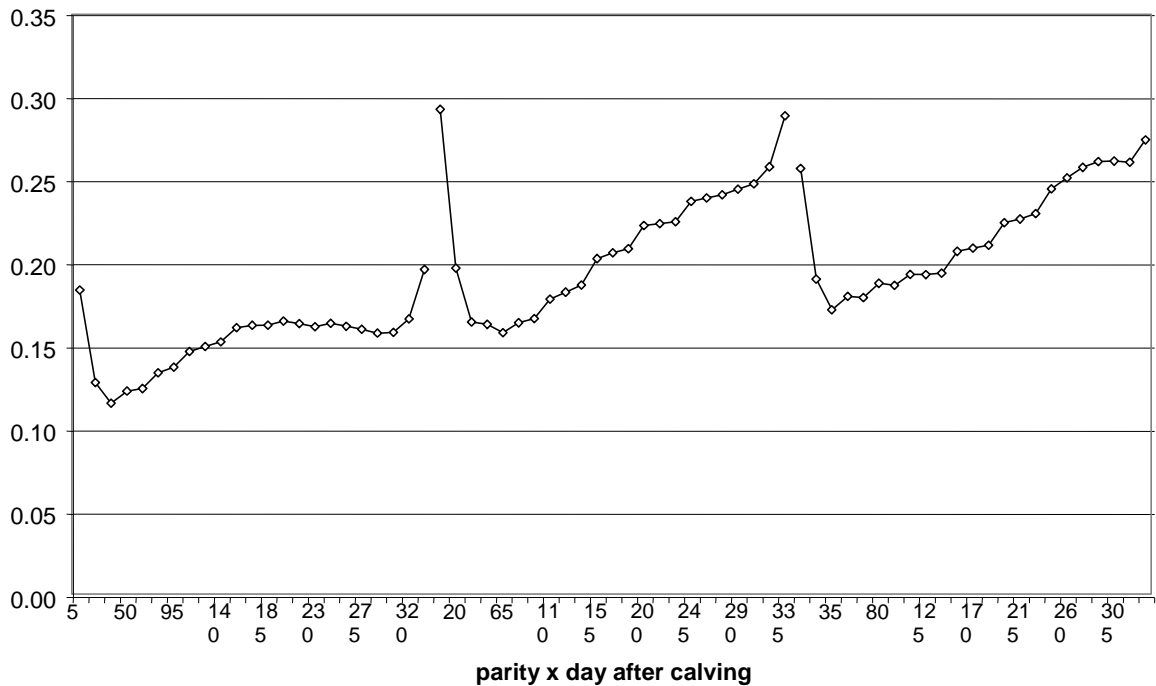


Figure 3. Heritabilities for SCS on a daily basis

The breeding values for SCS on a daily basis are not published. However, from these day-

breeding values, the 305 day breeding values are calculated by adding the day-breeding values from day 5 up to and including day 305. Afterwards the breeding values for lactations 1, 2 and 3 are combined in the same way into a comprehensive breeding value for SCS in 305 days as is done with milk production traits, specifically:

$$BV_{305,\text{total}} = 0.41 \times BV_{305,\text{lactation 1}} + 0.33 \times BV_{305,\text{lactation 2}} + 0.26 \times BV_{305,\text{lactation 3}}$$

Other derived traits, like persistency and late maturity as they relate to milk production traits, are not (yet) calculated for somatic cell score.

Heritability traits for 305-days SCS are 0.24, 0.30 and 0.30 for lactation 1, 2 and 3 respectively and 0.35 for the total 305-day SCS. The genetic correlations for 305-days SCS in different lactations are 0.64 (lactation 1 & 2), 0.52 (lactation 1 & 3), and 0.67 (lactation 2 & 3). The genetic standard deviation for 305-days SCS in lactation 1, 2 and 3 is 15512, 18490, and 19335 respectively and for the total 305-days SCS is 15088.

■ Publication

The breeding value for somatic cell score is a relative breeding value that is presented with an average of 100 and a standard deviation of 4. A breeding value above 100 means that the daughters of the bull have a below average somatic cell count. Each point increase in breeding value coincides with 2938, 3331, 3512 and 2958 lower 305-days SCS in lactation 1, 2, 3 and total. In the case of equal genetic ability for every day this coincides with 9.76, 11.07, 11.67 and 9.83 lower SCS per day respectively. The number of cells per ml that corresponds with this depends on the level of the somatic cell count.

An example: the average somatic cell count of the cows in the base population Z (see next paragraph for definition) on day 5 of lactation 1 is 165421 cells per ml. These cows have an average breeding value of exactly 100, since they compose the base population. The $SCC = 165421$ cells/ml gives $SCS = 1000 + 100 \times (2 \log(165421/1000)) = 1737.22$. When these cows are mated with a bull that has a breeding value of 110, the offspring will have an average breeding value of 105. If all other circumstances remain the same, the average SCS of the offspring is equal to $1737.22 - 5 \times 9.76 = 1688.42$. This corresponds with $SCC = 118.127$, or 47.294 cells/ml less. When a different breeding value from a bull, for example 90 or 110 is the starting point, or a different SCC is assumed, one will also end up with a different number of cells per ml.

For the daughters of a bull with breeding values of 100, 90, or 110 for every lactation, the SCS and SCS are calculated for every day and in every lactation, based on the average SCC and SCS of the cows in the base population Z (Figure 4 and 5). The line for 'sire 100' also reflects the average SCC and SCS for the cows in the base population Z.

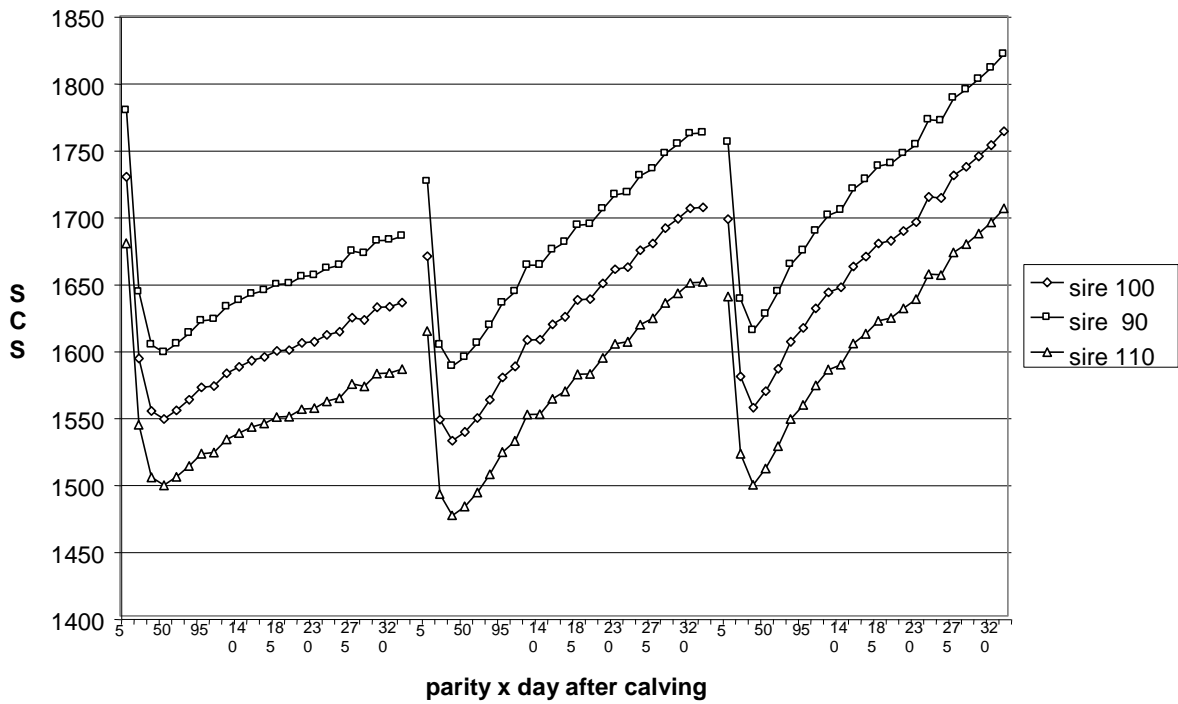


Figure 4. Average SCS of cows from the base population Z (= sire 100) plus the additional effect of a sire with a breeding value of 90 and 110 for each lactation

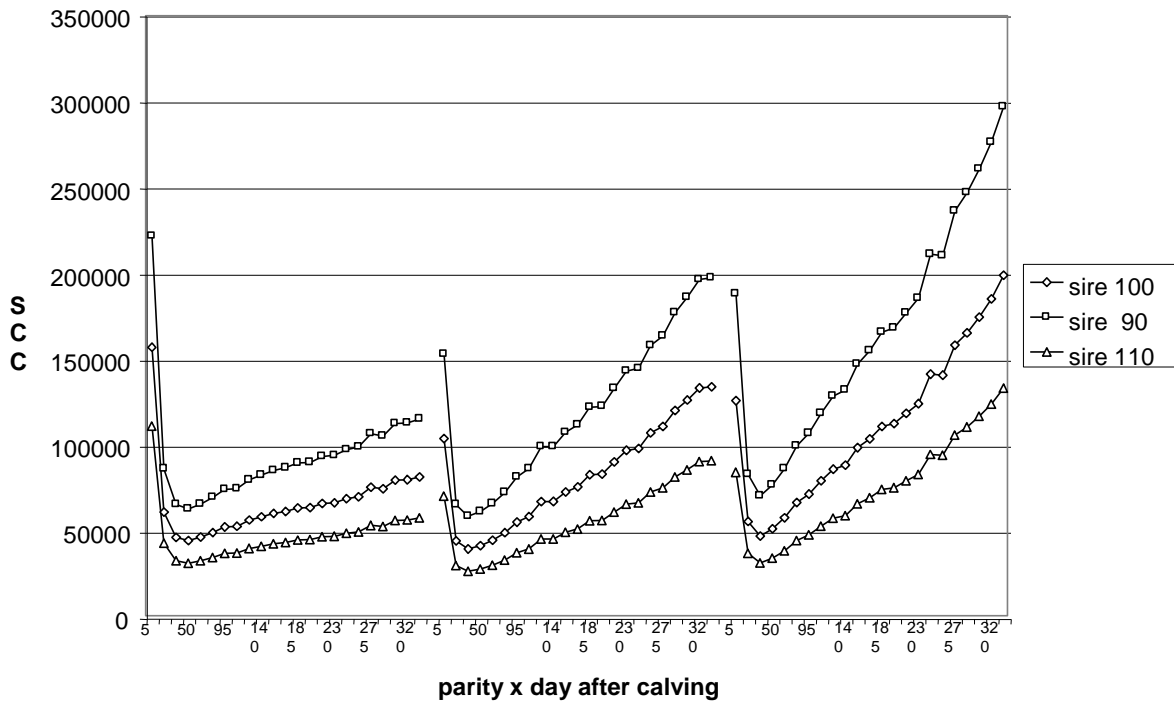


Figure 5. Average SCC of cows from the base population Z (= sire 100) plus the additional effect of a sire with a breeding value of 90 and 110 for each lactation

Breeding values for somatic cell score for bulls are published at the same time as the breeding values for milk production. This means that milk production data from a minimum of 15 daughters that have passed day 120 of lactation 1 must be available.

■ Base

Breeding values for somatic cell count of sires are published on the 2010 base. This base is determined by the cows that were born in 2005. For the breeding values for somatic cell count 3 bases have been defined: a Black&White base, a Red&White base and a Local base. The definitions of these bases are as follows:

Black&White base (Z):

The herd book registered cows that were born in 2005 with at least 87.5% HF blood and 12.5% or less FH blood with Black&White color, with at least one observation in the breeding value estimation;

Red&White base (R):

The herd book registered cows that were born in 2005 with at least 87.5% HF blood and 12.5% or less MRIJ blood with Red&White color, with at least one observation in the breeding value estimation;

Local base (Y):

The herd book registered cows that were born in 2005 with at least 87.5% MRIJ blood and 12.5% or less HF blood, with at least one observation in the breeding value estimation;

An observation is defined as a testday for somatic cell count.

Every 5 years, in a year divisible by 5, the reference year for the base is moved 5 years.

The bulls from the Black&White base are used to determine the standard deviation of the breeding values for all bases. The standard deviation of the breeding values from the base animals is calculated followed by standardization of this standard deviation to an average reliability of 80% for the breeding values. Because of this 4 points breeding value corresponds to 0.9 x genetic standard deviation of the concerning trait. Using one standard deviation for the 3 bases has as advantage that only the level differs between the bases and no difference exists between the standard deviations. Table 2 shows the base differences for somatic cell count.

Table 2. Base differences for somatic cell count

	Z → R	R → Y	Z → Y
Somatic cell count	-1	1	0
Somatic cell count lactation 1	-1	1	0
Somatic cell count lactation 2	-1	1	0
Somatic cell count lactation 3	-1	1	0