Description of Model for Estimation of Breeding Values for Milk Somatic Cell Count

The same model as for milk production traits is used in evaluation of milk somatic cell count (SCC). Test Day Model is used, definition of effects as well as model equation is the same as for yield traits. Requirements for inclusion of animals are same too. Evaluation is performed separately for Holstein (HOL) and Simmental (SIM) population. (See description for Production traits).

Lactations with calving since January 1st 1995 are included. Lactation is used if at least 3 test day records of SCC are recorded.

Somatic cell count is expressed in thousands per 1 ml of milk. Only SSC values of <13;9999> are included into evaluation. Test day records for somatic cells are excluded from the evaluation if less than 80 % of samples within the same HTD have somatic cells analysis.

Transformation of values of SCC into somatic cell score (SCS) is performed before start of evaluation in order to have approximately normal distribution.

$$SCS = \log_2 (SCC / 100) + 3$$

After estimation of regression coefficients breeding values are computed for individual lactations. Total breeding values are computed as an average of individual BVs for all three lactations.

$$BV = (BV1 + BV2 + BV3) / 3.$$

Relative breeding values (RBV) are calculated according to this formula:

$$RBV = 100 - [(BV - x) / s * 12]$$

x   average BV for birth year 2005
s   standard deviation for birth year 2005

RBVs are standardized in parameters (100; 12) for bulls born in 2005. RBV is expressed in reverse scale so values above 100 mean less somatic cell count.
BV is published only in form of RBV.

Accuracy of estimation of breeding values is calculated in the same way as for milk production traits.

$$R = SW1 / (SW1 + k)$$

Genetic parameters used

	lactation	HOL	
		h^2	genetic variance
SCC	1st	0,207	19 350
	2nd	0,225	24 254
	3rd	0,187	23 493
	in total	0,301	21 464