37th ICAR Session and Interbull Open Meeting, 31st May–4th June, 2010, Riga, Latvia

Combining test day SCS with clinical mastitis and udder type traits: A random regression model for joint genetic evaluation of udder health in Denmark, Finland and Sweden

***E. Negussie*[1*], *M. Lidauer*[1], *E. A. Mäntysaari*[1], *I. Strandén*[1], *J. Pösö*[2], *U. S. Nielsen*[3], *K. Johansson*[4], *J. – Å. Eriksson*[4], *G. P. Aamand*[5]**

[1]MTT Agrifood Research Finland, Biometrical Genetics, Jokioinen, Finland; [2]Faba Service, Vantaa, Finland; [3]Knowledge Centre for Agriculture, Aarhus, Denmark; [5]Swedish Dairy Association, Stockholm, Sweden; [5]NAV Nordic Cattle Genetic Evaluation, Aarhus, Denmark.

Abstract

Genetic associations during first three lactations between longitudinal test-day somatic cell score (TDSCS) and non-longitudinal udder health traits namely, four clinical mastitis (CM) and two udder type traits UA (Fore udder attachment) and UD (Udder depth) were estimated fitting a random regression model. Subsequently, a multi-trait rank reduced random regression test-day animal model was developed for the joint genetic evaluation of udder health traits in Denmark, Finland and Sweden. Compared to the currently used model, the new model offers efficient utilization of TDSCS information and provides proofs for both bulls and cows as well as harmonizes evaluation models used across the three countries.

1. Introduction

Udder health is traditionally one of the most important considerations in dairy genetic evaluation by the Nordic countries. In 2006, Denmark Finland and Sweden implemented a joint genetic evaluation for udder health traits. This joint evaluation is carried out by Nordic Cattle Genetic Evaluation (NCGE), a company that is responsible for cattle genetic evaluation across the three countries. The currently used joint udder health evaluation model is a multi-trait sire model that is based on lactation average records of SCS, four CM and 2 udder type traits (Johansson et al., 2006).

With a lactation average sire model, available information on udder health traits, particularly information on TDSCS may not be effectively utilized. Besides, upgrading the currently used sire model to an animal model that includes TDSCS is an important step so as to provide farmers with cow breeding values. Furthermore, the model provides monthly SCS management tools from herd-test-day solutions which can be used for herd management and monitoring purposes (See Koivula et al., 2007).

The objectives of the present study were to estimate the genetic associations between test-day SCS and CM and udder type traits during the first three lactations and subsequently to develop a joint model for the genetic evaluation of udder health based on a rank reduced random regression test-day animal model.

2. Material and methods

2.1. Variance components

2.1.1. Data

Data for the variance component analysis were from Danish Holstein herds including 17500 cows with first calving from 1994 to 2000. SCS was expressed as $\log_e$-transformed somatic cell count ($\log_e$SCC) from monthly test days measured in 1000cells/ml. TDSCS from the first, second and third lactations were included. The four clinical mastitis traits CM11, CM12, CM2 and CM3 covered the intervals: 15 d before to 50 d after first calving; 51 d to 300 d after first calving; 15 d before to 150 d after second calving; and 15 d before to 150 d after 3rd calving, respectively. Within these intervals, the absence or presence of mastitis was scored as “0” or “1”, respectively. In addition, two udder type traits fore udder attachment (UA) and udder depth (UD) were included in the analysis. Finally, information on CM cases and udder type traits for each cow extracted from the database were merged with TD SCS records for analyses.

Table 1. Description of the data used for the variance component estimation

No. animals	25,562
Cows with observations	17,525
Herds, no.	50
Mean test-day SCS, ($\log_e$ 1000cells/ml)	4.4; 4.80; 5.03†
Freq. of mastitis (%)	13.0; 12.0; 21.0; 26.0†
Mean udder type (UA,UD)	5.8; 6.3
Records, no. - TDSCS	158,711; 105,257; 56,021†
- CM traits	16,129; 16,093; 10,548; 8,732
- UA & UD	10,305; 10,293

† In 1st, 2nd and 3rd lactations, respectively.

2.1.2. Model

The applied multi-trait random regression model (mt-RRM) combined longitudinal TDSCS and binary CM traits. The general description of the model in matrix form was:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{H}_h\mathbf{h} + \mathbf{K}_k\mathbf{k} + \mathbf{Z}_\mathrm{a}\mathbf{a} + \mathbf{Z}_\mathrm{p}\mathbf{p} + \mathbf{e}$$

where: **y** is a vector with observations on the nine different traits explained above. Vectors **b, h, k** contain the environmental effects whilst vectors **a**, and **p** contain additive genetic and non-genetic animal regression coefficients, respectively. Environmental effects in the model were calving age, herd environment and stage of lactation. Both additive genetic and non-genetic animal effects were modeled by a second order Legendre polynomial for TDSCS and intercept for the other traits leading to a 15×15 (co)variance matrix for each random effect to be estimated. Vector **e** contains the residuals of the 9 traits.

In order to facilitate accurate estimation, residual (co)variances between CM traits and TDSCS were assumed to be zero and the residual variance of CM and udder type traits was set to operationally low values so that part of this variance entered the permanent environmental component. This facilitated estimation of permanent environmental correlation between CM and the longitudinal trait (Negussie et al., 2008). The covariance components were estimated using DMU package (Madsen and Jensen, 2006).

3. Genetic evaluation

3.1. Data

A multi-trait random regression test-day animal model was developed for the joint genetic evaluation of udder health traits for Holstein (HOL), Red Dairy Cattle (RDC) and Jersey (JER) breeds. For each breed, the size of data used in the genetic evaluation is given in Table 2. The HOL data are by far the largest followed by RDC data which are the most heterogeneous. The JER data are mainly from Denmark with few herds from Sweden. The Finnish Ayrshire and Holstein data are included into both

RDC and HOL analyses due to many small mixed herds. Because TDSCS parameters were somewhat similar for the different breeds, each of the different breeds evaluations had different parameters where the CM and udder type (6x6) part comes from the estimates made for the breed. All traits were pre-corrected for heterogeneous variance due to year of calving and country.

Table 2. Size of the genetic evaluation data (in millions) for the different breeds

	HOL	RDC	JER
Cows with obs. (No)	6.5	4.1	0.6
Total observations	97.1	70.5	9.6
No. animal equations	100.0	61.3	9.3
No. total equations	217.1	137.1	18.1

3.2. The model

Separate genetic evaluations were made for HOL, RDC and JER breeds. The general description of the mt-RRM model that combines TDSCS and CM traits in the first three lactations with two udder type traits was as follows:

$$
\begin{bmatrix} y_{tdscs1} \\ y_{tdscs2} \\ y_{tdscs3} \\ y_{cm11} \\ y_{cm12} \\ y_{cm2} \\ y_{cm3} \\ y_{UA} \\ y_{UD} \end{bmatrix}
= [age] + [ym] + [hy5] + [ht] + [rc] +
\begin{bmatrix} & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ \tau_1 & \tau_2 & \tau_3 & \tau_4 & \tau_5 & \tau_6 & \tau_7 & \tau_8 \\ \tau_1 & \tau_2 & \tau_3 & \tau_4 & \tau_5 & \tau_6 & \tau_7 & \tau_8 \end{bmatrix}
+
\begin{bmatrix} \Sigma_{r=0}^{4} \phi_{\pi}(d)_r \beta_{S1} \\ \Sigma_{r=0}^{4} \phi_{\pi}(d)_r \beta_{S2} \\ \Sigma_{r=0}^{4} \phi_{\pi}(d)_r \beta_{S3} \\ \\ \\ \\ \\ \\ \\ \end{bmatrix}
+
$$

$$
\begin{bmatrix} \\ \\ \\ hy_{cm\,11} \\ hy_{cm\,12} \\ hy_{cm\,2} \\ hy_{cm\,3} \\ hy_{ua} \\ hy_{ud} \end{bmatrix}
+
\begin{bmatrix} htd_{s1} \\ htd_{s2} \\ htd_{s3} \\ \\ \\ \\ \\ \\ \\ \end{bmatrix}
+
\begin{bmatrix} \Sigma_{r=0}^{2} \phi_{\alpha}(d)_r p_{S1} \\ \Sigma_{r=0}^{2} \phi_{\alpha}(d)_r p_{S2} \\ \Sigma_{r=0}^{2} \phi_{\alpha}(d)_r p_{S3} \\ p_{CM11} \\ p_{CM12} \\ p_{CM2} \\ p_{CM3} \\ p_{UA} \\ p_{UD} \end{bmatrix}
+
\begin{bmatrix} \Sigma_{r=0}^{2} \phi_{\alpha}(d)_r a_{S1} \\ \Sigma_{r=0}^{2} \phi_{\alpha}(d)_r a_{S2} \\ \Sigma_{r=0}^{2} \phi_{\alpha}(d)_r a_{S3} \\ a_{CM11} \\ a_{CM12} \\ a_{CM2} \\ a_{CM3} \\ a_{UA} \\ a_{UD} \end{bmatrix}
+
\begin{bmatrix} e_{s1} \\ e_{s2} \\ e_{s3} \\ e_{cm11} \\ e_{cm12} \\ e_{cm2} \\ e_{cm3} \\ e_{ua} \\ e_{ud} \end{bmatrix} .
$$

Where $\mathbf{y}_i$… are vectors of observations on TDSCS1, TDSCS2, TDSCS3, CM11, CM12, CM2, CM3, UA and UD traits, respectively.

Fixed effects: Fixed effects of the model include calving age×country (**age**), calving-year×calving-month×country (**ym**), herd×5-year period (**hy5**), τ_i fixed effects (τ) specific to UA and UD traits, total heterosis (**h**t) and recombination loss (**r**c) and regression coefficients (β) describing the shape of the lactation curve within production 4-year period×month×country classes modeled by a third order orthogonal Legendre

Polynomial plus an exponential term. The modeling of fixed effects was the same for all traits with the exception of specific fixed effects modeled for the udder type traits and the lactation curve which was modeled only for test-day SCS traits.

The covariables for coefficients $\beta_{..r}$ (r=0,…,4) were:

$$\phi_\pi(d) = [c_0 \; c_1 \; c_2 \; c_3 \; \exp(wd)]^T,$$

where c_0 c_1 c_2 c_3 represent coefficients of the third-order orthogonal Legendre polynomial at DIM (d) and w =-0.09 is coefficient of the exponential term of the Wilmink function (Wilmink, 1987).

Random effects: Random effects in the model were herd×year of calving (for CM and udder type traits) and herd-test-day (htd) for TDSCS traits. The non-genetic random animal effects **p**, were modeled by 15 regression coefficients whilst the additive genetic effects **a**, by 12 random regression coefficients.

Rank reduction: To reduce the dimensionality of the model and thereby develop a computationally less demanding model rank reduction was made. Because the permanent environment (**Pe)** co-variance matrix was closely full, rank reduction was made only on the correlation matrices of the genetic (**G**) co-variance matrix. Here the rank of the genetic co-variance matrix was reduced from 15 to 12 resulting in 12 unique genetic random regression coefficients for each animal.

3.3. BLUP evaluation

The system was solved by preconditioned conjugate gradient (PCG) method (Strandén and Lidauer, 1999), using parallel computing (Strandén and Lidauer 2001) on 4 Intel Xeon 3.0 GHz CPU's. From mt-RRM, an animal gets 12 RRM breeding value coefficients from which 305-breeding values were computed. Corresponding EBVs for TDSCS, CM and udder type traits of animal *i* were calculated as:

$EBV_{Si} = \sum_{d=1}^{305} \phi_\alpha^T(d)\hat{\mathbf{a}}_i$ and

$EBV_{CMi}=\hat{\mathbf{a}}_i$ and $EBV_{UDDi}=\hat{\mathbf{a}}_i$, respectively. Estimated breeding values for TDSCS and CM traits were then combined into indices $TDSCS_{com}$ and CM_{com} by giving appropriate weights for lactations as agreed by the NCGE weighting procedures for udder health traits.

Estimates of breeding values from the new mt-RRM were then compared with the currently used multi-trait lactation average sire model. The model was validated with the Interbull testing procedures and computational aspects were assessed.

In addition, to assess the effects of the new mt-RRM, comparison between mt-RRM and multi-trait Lactation Average Animal model (mt-LAM) was made. For this, LAM parameters were derived from Holstein mt-RRM parameters and then correlations between EBVs and SD of EBVs for the different groups of animals were calculated. The analyses of breeding values involved four different groups of Holsteins. The first group was "old proven" bulls: these were bulls that had their progeny tests available and were born between 1993 and 1995 and were required to have at least 100 daughters. The second group was "young" bulls: these were bulls born between 2000 and 2002 and had at least 20 daughters. The third and fourth group included “older cows” and “young cows” which were born in 1998 and 2004, respectively, and had at least one observation.

4. Results and discussion

4.1. Genetic parameters

Heritability: Estimates of genetic parameters for the four CM, two udder type traits and for selected DIM of TDSCS traits in the first three lactations are given in Table 3. The heritabilities for CM11, CM12, CM2 and CM3 ranged from 0.03 to 0.07. As expected, estimates from later lactations were higher than the estimates from the first lactations. This goes with higher incidences of CM in the later lactations and use of linear model where the heritability of binary traits is the functions of the frequencies. Literature estimates involving later lactations are generally rare. For Danish Red cattle, Lund et al. (1999) reported heritability of 0.05 and 0.02 for CM traits defined as 10 d before to 50 d after calving and 50 d to 350 d after calving, respectively. The estimates from our study also falls within the range of (0.04 – 0.06) reported by Nielsen et al., (1997) for Red Danish and Danish Friesians.

Table 3. Estimated heritabilities (diagonal), genetic (below diagonal) and phenotypic correlations (above diagonal) for CM, udder type traits and for selected days in milk of test-day SCS by mt-RRM for Danish Holstein.

	TDSCS1					**TDSCS2**					**TDSCS3**										
DIM	30	60	160	210	310	30	60	160	210	310	30	60	160	210	310	**CM11**	**CM12**	**CM2**	**CM3**	**UA**	**UD**
30	**0.08**	0.51	0.37	0.32	0.23	0.18	0.18	0.17	0.16	0.13	0.13	0.15	0.14	0.14	0.12	0.14	0.11	0.05	0.04	-0.05	-0.08
60	0.97	**0.10**	0.46	0.42	0.26	0.20	0.22	0.21	0.20	0.16	0.14	0.17	0.17	0.17	0.14	0.11	0.14	0.06	0.05	-0.05	-0.09
160	0.80	0.92	**0.14**	0.58	0.33	0.23	0.27	0.27	0.26	0.21	0.15	0.20	0.22	0.22	0.18	0.05	0.16	0.08	0.05	-0.06	-0.09
210	0.75	0.89	1.00	**0.15**	0.39	0.24	0.28	0.29	0.28	0.23	0.15	0.20	0.23	0.23	0.20	0.04	0.16	0.08	0.05	-0.06	-0.10
310	0.70	0.78	0.86	0.88	**0.10**	0.22	0.26	0.28	0.29	0.26	0.14	0.18	0.21	0.21	0.21	0.10	0.06	0.07	0.05	-0.06	-0.10
30	0.90	0.94	0.88	0.85	0.77	**0.13**	0.61	0.44	0.38	0.28	0.23	0.25	0.23	0.22	0.18	0.05	0.09	0.21	0.09	-0.05	-0.09
60	0.83	0.91	0.94	0.93	0.84	0.97	**0.15**	0.57	0.52	0.34	0.25	0.29	0.29	0.28	0.24	0.06	0.10	0.20	0.10	-0.06	-0.10
160	0.68	0.81	0.94	0.95	0.87	0.86	0.96	**0.16**	0.61	0.42	0.24	0.30	0.33	0.33	0.30	0.07	0.10	0.15	0.10	-0.05	-0.11
210	0.64	0.77	0.91	0.93	0.87	0.81	0.93	0.99	**0.16**	0.46	0.23	0.30	0.34	0.34	0.32	0.07	0.10	0.13	0.10	-0.05	-0.11
310	0.59	0.68	0.77	0.79	0.85	0.72	0.81	0.90	0.93	**0.13**	0.20	0.25	0.29	0.30	0.32	0.06	0.10	0.09	0.08	-0.05	-0.11
30	0.87	0.90	0.83	0.80	0.68	0.97	0.92	0.81	0.77	0.71	**0.11**	0.64	0.38	0.29	0.23	0.05	0.06	0.12	0.21	-0.05	-0.08
60	0.85	0.90	0.88	0.86	0.74	0.97	0.96	0.88	0.84	0.73	0.98	**0.15**	0.55	0.48	0.36	0.06	0.07	0.13	0.20	-0.05	-0.10
160	0.76	0.86	0.91	0.90	0.81	0.92	0.97	0.94	0.91	0.78	0.91	0.97	**0.15**	0.64	0.48	0.08	0.08	0.12	0.14	-0.05	-0.11
210	0.72	0.83	0.91	0.91	0.84	0.90	0.96	0.97	0.95	0.83	0.87	0.94	0.99	**0.14**	0.51	0.07	0.08	0.11	0.12	-0.05	-0.11
310	0.56	0.68	0.80	0.83	0.86	0.74	0.85	0.94	0.97	0.98	0.72	0.77	0.84	0.89	**0.13**	0.06	0.09	0.11	0.08	-0.05	-0.11
CM11	0.57	0.56	0.49	0.47	0.46	0.56	0.53	0.47	0.46	0.46	0.55	0.53	0.50	0.49	0.45	**0.05**	0.03	0.05	0.05	-0.05	-0.10
CM12	0.62	0.65	0.62	0.61	0.55	0.68	0.68	0.62	0.60	0.55	0.67	0.68	0.66	0.65	0.56	0.66	**0.03**	0.07	0.04	-0.03	-0.06
CM2	0.63	0.66	0.63	0.61	0.55	0.70	0.69	0.63	0.61	0.56	0.69	0.70	0.67	0.66	0.57	0.67	0.97	**0.06**	0.11	-0.03	-0.06
CM3	0.62	0.64	0.59	0.57	0.51	0.68	0.66	0.60	0.58	0.54	0.67	0.67	0.64	0.63	0.54	0.68	0.81	0.93	**0.07**	-0.01	-0.04
UA	-0.22	-0.23	-0.21	-0.21	-0.22	-0.20	-0.20	-0.20	-0.21	-0.24	-0.18	-0.17	-0.17	-0.18	-0.22	-0.37	-0.22	-0.15	-0.13	**0.27**	0.32
UD	-0.39	-0.40	-0.37	-0.36	-0.37	-0.36	-0.37	-0.36	-0.36	-0.40	-0.35	-0.33	-0.32	-0.33	-0.37	-0.56	-0.38	-0.28	-0.25	0.80	**0.41**

The heritability of test-day SCS during first lactation ranged from 0.08 to 0.15 (Table 3). In early lactation, the estimates were less than 0.09 and increased gradually reaching 0.15 in mid to late stages of lactation at about 210 days after calving. In the second and third lactations, similar trends were observed, although generally the estimates were slightly higher than those of first lactation ranging from 0.11 to 0.016. These estimates are in line with earlier studies (Koivula et al., 2004; Silvestre et al., 2006) which reported lower estimates of heritability for the early stages of first lactation. It is also in line with de Roos et al. (2003) who reported heritability ranging from 0.12 to 0.19 for early lactation Dutch Holstein. The heritability of the two udder type traits were 0.27 and 0.41. These estimates are similar to estimates of 0.26

and 0.36 reported for Danish Holstein by Sorensen et al. (2001).

Genetic & phenotypic correlations: Genetic correlation between TDSCS traits and CM in first, second and third lactations ranged from 0.46-0.57, 0.56-0.70 and 0.57-0.70, respectively. The general trend was that correlations in early part of lactations (between DIM 30 and 60) were slightly higher than correlations at the later stages of lactations. The estimates from our study are within the range of most values (0.40-0.70) reported in literature for genetic associations between CM and SCS traits (Carlén et al., 2004; Negussie et al., 2008).

The genetic correlations between TDSCS and udder type traits during the different stages of lactations ranged from -0.17 to -0.24 for UA and from -0.32 to -0.40 for UD. On the other hand, correlations between the different CM traits and udder type traits ranged from -0.13 to -0.37 for UA and from -0.0.25 to -0.56 for UD. Phenotypic associations between TDSCS and CM traits ranged from 0.04 to 0.21 depending on the stages of lactations. Correlations were in general stronger in the early stages of lactations compared to those in the later stages. Phenotypic correlations between TDSCS and type traits were slightly lower than those with CM traits.

4.2. Analysis of breeding values

The comparison between the new (mt-RRM) and the currently used (mt-LAM sire) models shows that for HOL bulls (≥50 daughters) born from 1990 to 2003, the correlation between EBVs ranged from 0.93-0.96, 0.93-0.98 and 0.93-0.97 for Denmark, Finland and Sweden, respectively. For RDC bulls (≥50 daughters), the correlations between EBVs were from 0.92-0.96, 0.93-0.97 and 0.93-0.97 for Denmark, Finland and Sweden, respectively. In view of the changes made in the model and parameters, the results obtained are expected.

The analyses of breeding values involving the four different groups of animals are in Table 4. The Table shows that correlations between EBVs for CM_{comb} were higher for older groups of bulls (~0.98) than for young cows (0.92-0.93) and bulls (0.95). One of the reasons for this is the use of test-day model (test-day SCS), which allows better modeling of the herd environment and thereby improves the accuracy of young cow and bulls EBVs. Older proven bulls with large numbers of daughters, however, get relatively accurate EBVs from both models. Thus, the apparent advantage of mt-RRM comes from better evaluation of cows and young bulls with fewer numbers of daughters. As a consequence, some changes might be expected in the ranking of young bulls and cows.

Standard deviations (SD) of EBVs for CM_{comb} from mt-RRM and mt-LAMs models are also on Table 4. For the different groups of animals, the SD of EBVs from the mt-RRM was higher than that from mt-LAM. Especially, the difference between the models in the SD of EBVs were larger for the younger groups of animals which could be due to the better utilization of information by the test-day model which in turn revealed more genetic variation.

Table 4. Standard deviations (SD) of EBVs for combined CM traits (CM_{comb}) † from mt-RRM and mt-LAM for different groups of Holstein: old bulls (born 1993-95, with 100 daughters), young bulls (born 2000-2002, with ≥20), and old and young Holstein cows with at least one observation (born 1998 and 2004).

Groups		Bulls/cows No.	MODEL	
		No. Bulls/Cows	mt-RRM	mt-LAM
Bulls				
Old	CM_{comb}	118	0.054	0.052
Young	CM_{comb}	957	0.052	0.046
Cows				
Old	CM_{comb}	195284	0.028	0.026
Young	CM_{comb}	108097	0.027	0.024

† Values for CM_{comb} are based on combining EBVs for CM11, CM12, CM2 and CM3 with their respective weights

Table 5. Number of equations (N_{eq}), iterations until convergence (N_{conv}), solving time† for the multi-trait random regression (mt-RRM) and lactation average models (mt-LAM)

Model	Model	N_{eq} (millions)	$N_{conv.}$	Solving time (hrs.)
mt-LAM (animal)	HOL	66.4	5500	27
	RDC	38.5	4500	19
mt-RRM (animal)	HOL	100.0	3000	17
	RDC	61.1	2700	10

† Intel Xeon 3.8 GHz Dual Core CPU

5. Conclusions

Udder health evaluation benefits from a multi-trait evaluation that combines information from the different sources. In this study, estimation of variance components using a model that combines TDSCS with CM and udder type traits lead to the development of a joint genetic evaluation model for udder health evaluation in Denmark, Finland and Sweden. Assessment of the models performances showed that the new model a) makes efficient use of available information b) offers breeding values for both bulls and cows c) harmonizes udder health evaluation models used across the three countries and finally d) provides herd-test day solutions which can be used in herd management and monitoring purposes.

There exists some differences between countries in terms of the incidences of mastitis and hence heritabilities. This may cause some problems in the evaluation process. To address this issue, the ideal solution would be to evaluate CM traits by a threshold model which could alleviate this country dependant variation in the incidences of CM traits. For this, in the near future, development of a model that takes the distributional characteristics of binary traits (CM traits) into consideration in the form of a Linear-Threshold mt-RRM test-day animal model would be a logical alternative.

6. References

Carlén E., Strandberg, E., Roth, A., 2004. Genetic parameters for Clinical mastitis, somatic cell score, and production in the first three lactations of Swedish Holstein cows. J. Dairy sci. 87:3062-3070.

de Roos, A. P. W., A.G.F. Harbers, and G. de Jong. 2003 Genetic parameters of test day somatic cell score estimated with a random regression model. Interbull Bull. No. 31:97-101.

Heringstad, B., Klemetsdal, G., Ruane, J., 2000. Selection for mastitis resistance in dairy cattle: A review with focus on the situation in the Nordic countries. Livest. Prod. Sci. 64, 95–106.

Johansson, K., Eriksson, S., Pösö J., Toivonen, M., Nielsen, U. S., Eriksson, J.-Å., and Aamand, G. P. 2006. Genetic evaluation of udder health traits for Denmark, Finland and Sweden. Interbull Bulletin No. 35:92-96.

Koivula M., Negussie, E., Mäntysaari, E. A., 2004. Genetic parameters for test-day somatic cell score at different lactation stages of Finnish dairy cattle. Livest. Prod. Sci. 90, 145-157.

Lund, M.S., Jensen, J. and P. H. Peterson. 1999. Estimation of genetic and phenotypic parameters for clinical mastitis, somatic cell production deviance, and protein yield in dairy cattle using Gibbs sampling. J. Dairy Sci. 82:1045–1051.

Madsen, P., Jensen, J., 2006. A Users's Guide to DMU. A package for analysing multivariate mixed models. Version 6, release 4.6. Danish Institute of Agricultural Sciences, Denmark.

Negussie, E., Koivula, M., Mäntysaari, E. A., Lidauer, M., 2006b. Genetic evaluation of somatic cell score in dairy cattle considering first and later lactations as two different but correlated traits. J. Anim. Breed. Genet. 123, 224-238.

Negussie, E., Strandén, I., M., Mäntysaari, E. A., 2008. Genetic association of Clinical mastitis with test-day somatic cell score and milk yield during first lactation Finnish Ayrshire cows. J. Dairy Sci. 91:1189-1197.

Nielsen, U. S., G.A. Pedersen, J. Pedersen and J. Jensen. 1997. Genetic correlations among health traits in different lactations. Interbull Bulletin No. 15:68-77.

Strandén I., Lidauer, M., 1999. Solving large mixed linear models using preconditioned conjugate gradient iteration. J. Dairy Sci. 75, 2017-2022

Wilmink, J.B.M. 1987. Adjustment of test-day milk, fat, and protein yields for age, season, and stage of lactation. Livest. Prod. Sci. 16:335-348.

Silvestre, A., F. Petim-Batista, A. Martins, A. Ferreira, A. Martins, S. Pinto, J. Carvalheira, and J. Colaco. 2006. Genetic parameter estimates of Portuguese dairy cows for SCS using a spline test-day model. Proc. 8th WCGALP, Belo Horizonte, Brazil. CD-ROM Commun. No. 01-82.

Sorensen, M. K., Jensen, J. and Christensen, L. G. 2001. Udder confirmation and mastitis resistance in Danish first-lactation cows: Heritabilities, genetic and environmental correlations. Acta Agriculturae Scandinavica. Section A – Animal Science. 50:72-82.