

Genetic Evaluation of Udder Health Traits for Denmark, Finland and Sweden

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Introduction

Denmark, Finland and Sweden have agreed to make joint genetic evaluations for dairy cattle. One of the goals is to strengthen the selection for health traits which traditionally have been considered as an important target for genetic improvement by the Nordic farmers. Originally the motivation for the health trait selection mainly came from economical considerations. Today animal welfare issues are also important.

Selection is carried out continuously during a bulls' lifetime, but the main part takes place when breeding values from milk production traits are at hand. Breeding values for clinical mastitis have then comparatively large prediction errors, because of low heritability. Inclusion of clinical mastitis traits measured during a shorter early period is thus favourable, as well as the inclusion of correlated traits with high heritability. Therefore, including somatic cell count in and some udder conformation traits with higher heritabilities and relatively strong correlations to mastitis are beneficial for the genetic evaluation (Nielsen *et al.*, 1996).

Heringstad *et al.* (2003,) and Heringstad, (2004 pers. com.) estimated genetic variance components for mastitis in a sub-set of Nordic Holstein data, and performed a first analysis of mastitis in three lactations on Nordic level. The experience gathered in their work was used as the starting point of the current developments. The aim of this study was to present the model developments that were made to form a Nordic evaluation for udder health.

Material and Methods

Data from first to third lactation on clinical mastitis (CM) and Somatic Cell Count (SCC), and from first lactation on udder depth (UD) and fore udder attachment (UA) was used in the genetic evaluation for udder health. Table 1 gives the number of sires of cows for Red Breeds and Holstein in each country. Mastitis data started for Finland and Sweden in 1984 and for Denmark in 1990. Somatic cell count data started in 1984 for Sweden, in 1988 for Finland and 1990 for Denmark. Udder conformation traits are added from 1990 in Denmark, 1992 in Finland and 1992 in Sweden

CM was defined as a mastitis treatment (1) or not (0) within a certain time period. The following traits were calculated and used in the analysis:

CM11 was an observation on mastitis from 15 days before to 50 days after first calving,
CM12 was an observation mastitis on from 51 to 300 days after first calving,
CM2 was an observation on mastitis from 15 days before to 150 days after second calving,
CM3 was an observation on mastitis from 15 days before to 150 days after third calving,
SCC1 was an observation on somatic cell count from 5 to 170 days after first calving,
SCC2 was an observation on somatic cell count from 5 to 170 days after second calving,
SCC3 was an observation on somatic cell count from 5 to 170 days after third calving,
UA was an observation on fore udder attachment in first lactation, and
UD was an observation on udder depth in first lactation.

Table 1. Number of sires and number of cows for Clinical Mastitis (CM), Somatic Cell Count (SCC), Fore Udder Attachment (UA) and Udder Depth (UD)

	Trait	No of sires		No of first lactation records	
		Holstein	Red Breeds	Holstein	Red Breeds
Denmark	CM	9460	1308	1557321	231502
	SCC	9885	1315	2011067	312407
	UA/UD	6537	1141	418400	71888
Finland	CM	1056	2651	338229	1365049
	SCC	1056	2652	370037	1515397
	UA	988	1717	60161	136192
	UD	988	1717	60141	136123
Sweden	CM	2987	2877	1141021	1282405
	SCC	2987	2877	1040254	1312975
	UA/UD	1537	1198	96960	107087
NAV	CM	13503	6836	3036571	2878956
	SCC	13928	6844	3421358	3140779
	UA	9062	4056	575521	315167
	UD	9062	4056	575501	315098

All traits were pre-corrected for heterogeneous variance due to year of calving and country. The model was a multi trait-, multi lactation model with herd*year effects as random. The only genetic random effect was for sires. Included as fixed class effects were herd*period, calving age*country, and year*month of calving*country. The period was 5 years long. For the Red Breeds effects of Original Red Danes (RDM), Danish Friesian (SDM), Finnish Ayrshire (FAY), Norwegian Red (NRF), American Brown Swiss (ABK), American Holstein (HOL), Swedish Red Cattle (SRB), Canadian Ayrshire (CAY) and Fincattle (FIC), and for the Holsteins the American Holstein, were accounted for by regressions on population proportions. Heterosis was accounted for using the regression on expected total heterosis of all included populations in both Holsteins and Red breed.

Separate genetic evaluations were made for Holsteins and Red Breeds. To make Finnish contemporary group sizes larger FAY and Finnish Holstein were included in both evaluations. Separate age effects, population effects and heterosis effects were then accommodated for in the population not under

evaluation. The udder conformation observations were edited in the type evaluation and corrected for heterogeneous variance. The model for udder conformation traits in udder health evaluation was almost the same as the one in type evaluation (Fogh *et al.*, 2004), except that we used a sire model instead of animal model.

The genetic parameters used for the 9 traits in the evaluation are presented in Table 2. They were modified according to an Interbull procedure for bending (Jorjani 2003). Estimates were collected from different studies (Heringstad 2004, pers. comm., Nielsen, 2000, Negussie, 2004, Carlén, 2003 and de Haas, 1998) on the evaluated populations. For computational reasons residual correlations between lactations were set to zero.

Trend validation was carried out on each trait within country and over countries using validation method 3 (Boichard *et al.* (1995). In the selection for mastitis, all four breeding values for mastitis, standardized to the same phenotypic standard deviation, were weighted to a mastitis trait (CM) using the following equation: $CM = 0.25CM11 + 0.25CM12 + 0.3CM2 + 0.2CM3$.

Table 2. Genetic parameters used in the genetic evaluation. Genetic correlation under, residual correlation above, and heritabilities on the diagonal

	SCC1	SCC2	SCC3	CM1	CM12	CM2	CM3	UA	UD
SCC1	0.140			0.20	0.20				
SCC2	0.90	0.133				0.20			
SCC3	0.82	0.97	0.115				0.20		
CM1	0.66	0.58	0.55	0.032	0.02			-0.05	-0.05
CM12	0.66	0.58	0.55	0.65	0.024			-0.03	-0.06
CM2	0.55	0.62	0.56	0.77	0.79	0.032			
CM3	0.47	0.55	0.62	0.76	0.79	0.91	0.034		
UA	-0.19	-0.19	-0.19	-0.36	-0.35	-0.35	-0.34	0.240	0.13
UD	0.30	-0.30	-0.30	-0.50	-0.54	-0.54	-0.54	0.65	0.360

Results

Figure 1 shows trends in estimated sire breeding values for CM of Holstein and Red Breeds. The Holstein had an increasing, unfavourable trend whereas the Red Breeds showed no obvious trend.

Figures 2 and 3 give correlations between sire breeding values from the NAV model and from Interbull (mean EBVs of the three country scales) run February 2006. For both breeds correlations fluctuate around 0.9.

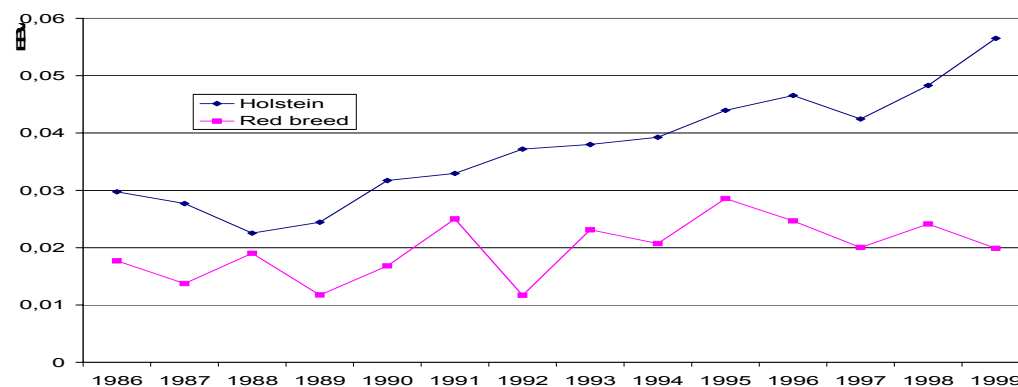


Figure 1. Genetic trends for CM. Average sire breeding values.

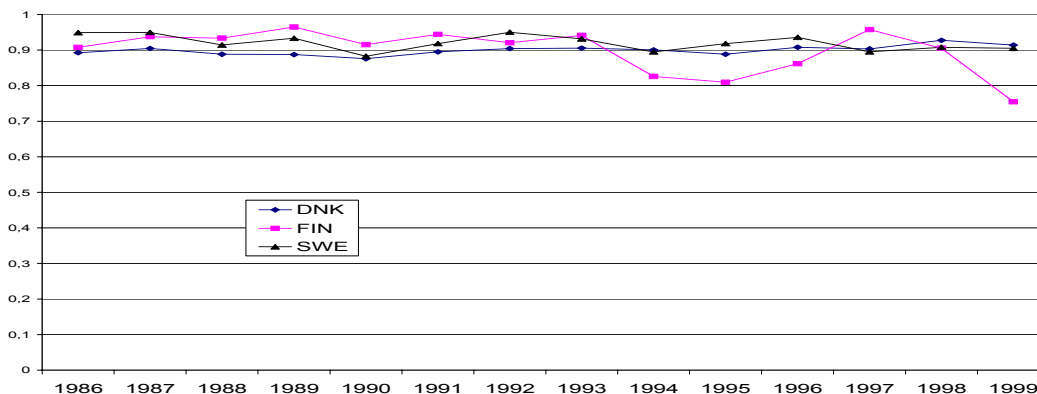


Figure 2. Correlations between estimated sire breeding values from the NAV-model (CM) and from Interbull run February 2006. Holstein.

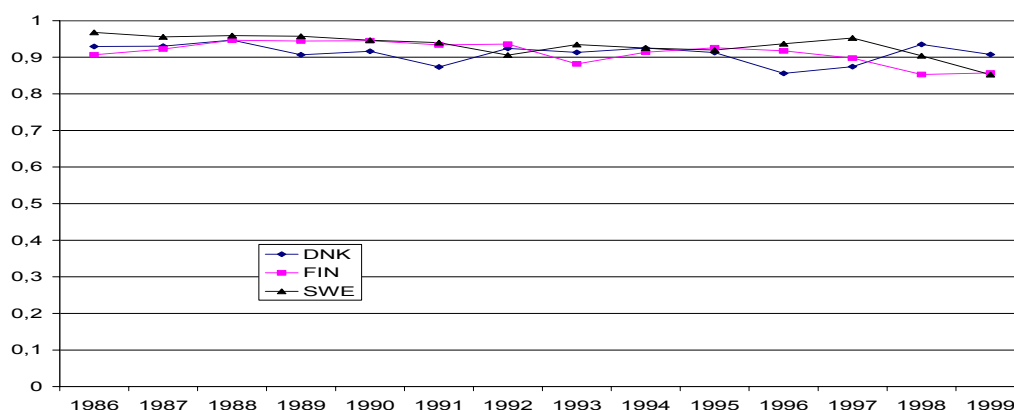


Figure 3. Correlations between estimated sire breeding values from the NAV-model (CM) and from Interbull run February 2006. Red Breeds

The model validation requirements set up by Interbull (estimated bias less than 0.02xgenetic standard deviation) was met for both CM and SCC, see table 3. Only one trait, SCC for Red Danes was outside the limits at

country level. The standard deviations of sire breeding values are given in table 4. The Danish sires had somewhat higher standard deviation of breeding values than Finnish and Swedish sires.

Table 3. Results from model validation¹.

	Breed	Denmark	Finland	Sweden	NAV
CM	Holstein	-0.00022	-0.00093	0.00055	0.00035
SCC	Holstein	-0.00177	-0.00115	0.00183	-0.00096
CM	Red Breeds	0.00019	-0.00054	0.00076	0.00001
SCC	Red Breeds	0.00365	-0.00070	0.00051	0.00056

¹Limits: CM=0.00153, SCC=0.00304

Table 4. Standard deviation of estimated breeding values for CM in percent of genetic standard deviation for sires born 1990 to 1999.

Breed	Denmark	Finland	Sweden
Holstein	60.7	52.1	54.9
Red Breeds	56.5	51.3	50.0

Discussion

In this project we have developed a joint Nordic evaluation that is expected to give accurate breeding values for udder health as early as possible. The model validation showed that the model was unbiased.

The correlations between EBV:s from this Nordic model and the corresponding Interbull run was around 0.90 which indicates that there will be rather large changes when the new developments are put into use. The main reasons are the model improvements made and the harmonization of models and data editing. It is worth notice that all countries used

different models and different traits in their national evaluations. The between country genetic correlations estimated by Interbull also indicate that the mastitis traits were rather different in the different countries. For the mastitis traits they were between 0.83 and 0.90. A part of those differences will now disappear. It would be interesting to know the size of these correlations on breeding values from the new evaluation used within country. It is however clear that the new model has the opportunity to utilise the data better, both within and across the Nordic country borders. The differences in standard deviation of sire breeding values require some further attention. For RDM especially, we can expect a higher

variation among sires because of the heterogeneous genetic background. One other reason may be that the simple pre-correction of heterogeneous variance is not working properly. There are of course special problems with mastitis traits since they are of categorical nature and further developments should rely on more realistic assumptions. The present model utilises relatively simple techniques and models. The reason is that the important step is to make the harmonisation. This will lead to a working evaluation on Nordic level. From this basis it is easier to develop and test more advanced techniques such as test day or mixture models which can improve the udder health evaluation further.

Conclusions

The developmental work has lead to a model giving accurate breeding values as early as possible in the life of a AI-bull. The information about udder health in Denmark, Finland and Sweden is utilised better than in the current national developments. The new genetic evaluation is good platform for further developments.

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