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Predictive ability of different models for clinical mastitis in joint genetic evaluation for Sweden, Denmark and Finland

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Summary
Clinical mastitis (CM) and somatic cell count (SCC) in three lactations, and first lactation udder conformation traits (UC), are included in the joint genetic evaluations of Holstein and red cattle breeds in Sweden, Denmark and Finland since 2006. The aim of this study was to compare predictive ability of different multi-trait models for udder health on a Nordic level. Linear sire models including different number of udder health traits (CM, SCC, UC) were used to estimate breeding values (EBVs), based on data comprising 2.7 million Red Cattle cows recorded until 2002. Correlations were estimated between these EBVs and daughter group means for clinical mastitis recorded from 2003 and onwards. The comparison was made for 99 proven bulls born 1992-1995 and 486 young bulls born 1997-2000. Models including CM and at least one of the correlated traits SCC or UC gave the highest correlations between EBVs in early data and daughter group means in later data. Compared with the full model including all three traits, a model with only CM gave 9% weaker correlation between EBVs and daughter group means for CM. The corresponding difference was 17% weaker using a model including SCC and UC, and 39% weaker for a model with only UC for proven bulls.

Introduction
Clinical mastitis (CM) is one of the most common diseases in dairy cattle, causing economic losses to the farmers due to reduced milk yield, discarded milk, veterinary treatments, labour and replacement costs (Heringstad et al., 2000). It also reduces animal welfare considerably. In the Nordic countries, CM have long been recorded and included in the breeding goal and genetic evaluation. The heritability of CM is low, why also indirect selection through correlated traits with higher heritabilities, such as somatic cell count (SCC) or udder conformation traits (UC) is used. In the joint genetic evaluation of udder health traits in Sweden, Denmark and Finland, CM and SCC in three lactations, and first lactation records of fore udder attachment (UA) and udder depth (UD) are included since 2006. The aim of this study was to compare predictive ability of different multi-trait models for clinical mastitis, by estimating correlations between estimated early breeding values and later daughter group means or breeding values for Red Dairy Cattle (RDC) bulls in the Nordic cattle genetic evaluation.

Materials and Methods

Records 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) of Scandinavian Red breeds were used in genetic evaluations (Johansson et al., 2006). Mastitis data was available for Sweden and Finland since 1984 and for Denmark since 1990. Somatic cell count was available since 1984, 1988 and 1990 for Finland, Sweden, and Denmark, respectively. Udder conformation data since 1992 in Sweden and Finland and since1990 in Denmark was included.

All traits were pre-corrected for heterogeneous variance due to year of calving and country. The model for estimation of breeding values 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 periods were 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 Finncattle (FIC), were accounted for by regressions on population proportions. Heterosis was accounted for using the regression on expected total heterosis of all included populations.

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 an animal model.

The genetic parameters used for the 9 traits in the evaluation were presented by Johansson et al. (2006). Heritabilities are shown in Table 1. The genetic correlations used between CM-traits and SCC-traits were in the range 0.55 – 0.66, and between CM-traits and UC-traits -0.34 – -0.54. For computational reasons residual correlations between lactations were set to zero.

Table 1 contains the trait definitions and the different indices used in the study. The index definitions for CM traits and SCC traits are used in the routine evaluation from the Nordic Cattle Genetic Evaluation (NAV) while the index definition of ISCCUC was calculated from data using a regression of SCC and UC breeding values from the SCCUC evaluation on CM breeding values from single trait CM evaluation.

Table 1. Abbreviations, heritabilities (h^2), and definitions of traits included in the study

Trait abbrev.	h^2	Definition
		Trait definitions
CM11	0.032	Clinical mastitis (1) or not (0) between -15 and 50 days after 1st calving.
CM12	0.024	Clinical mastitis (1) or not (0) between 51 and 300 days after 1st calving.
CM2	0.032	Clinical mastitis (1) or not (0) between -15 and 150 days after 2nd calving.
CM3	0.034	Clinical mastitis (1) or not (0) between -15 and 150 days after 3rd calving.
SCC1	0.140	Log. somatic cell count average 5-170 days after 1st calving.
SCC2	0.133	Log. somatic cell count average 5-170 days after 2nd calving.
SCC3	0.115	Log. somatic cell count average 5-170 days after 3rd calving.
UA	0.240	Fore udder attachment score in 1st lactation.
UD	0.360	Udder depth score in 1st lactation.
		Index definitions
CM		Clinical mastitis: 0.25*CM11 + 0.25*CM12 + 0.3*CM2 + 0.2*CM3
SCC		Log somatic cell count: 0.5*SCC1 + 0.3*SCC2 + 0.2*SCC3
UC		Udder conformation: -1*(0.5*UA + 0.5*UD)
ISCCUC		Both indicator traits: b1*SCC+b2*UC, where b1 = 0.195 and b2 = 0.020

Two data sets were created; one with records until 2002 (early data) comprising 2 568 297 cows, the other with 563 815 cows having records from 2003 to 2006 (late data).

Linear sire models including different number of udder health traits (CM, SCC, UC) were used to estimate breeding values (EBVs) in the early dataset.

Information on mastitis, as progeny means or breeding values, from the late dataset (2003-2006) was used to study the predictions made from the first dataset. The progeny means included only daughters in the country where the sire had most records. Daughters with records in the first dataset were omitted in the second. The number of records that the daughter group means were based on is shown for each trait in Table 2.

Two different groups of bulls were studied: 99 bulls born 1992-1995 and 486 bulls born 1997-2000. Bulls in these two groups had different amount of information on udder health of daughters available in the two data sets. Only bulls with at least 20 first lactation daughters in total and at least 10 daughters with third lactation CM-records between 2003 and 2006 were included. Bulls born 1992-1995 were required to have at least 200 daughters in total with first lactation records of CM or SCC to be included in the analysis.

The 99 bulls born 1992-1995 were proven bulls with records from first crop daughters in the first data set from which EBVs were estimated, and records from second crop daughters in the second data set from which daughter group means for clinical mastitis were calculated. The average group contained 1533 first lactation daughters.

The 486 bulls born 1997-2000 were young bulls, and for these EBVs estimated from the first data set was mainly based on pedigree index, whereas daughter group means in the second data set was calculated based on first crop daughter records of clinical mastitis. The average group contained 142 first lactation daughters.

Estimation of correlations

Different sets of breeding values for mastitis from early data were correlated with clinical mastitis information (daughter group means or breeding values) in late data. Correlations were estimated on residuals after fitting a model that contained main effects of sire birth years and countries. When CM was included in the analysis of early data the CM breeding values were used for correlation with late data. If CM was not included as a trait in the multiple-trait model, indices were calculated and correlated with daughter group means and EBVs for CM in the later data, see Table 1.

Table 2. Number of bulls and number of daughters with records for clinical mastitis in first (CM11, CM12), second and third lactations (CM2, CM3) included in the calculation

		No of bulls**		Average no of daughters 2003-2006**	
Country	Trait	Proven bulls (1992-1995)*	Young bulls (1997-2000)*	Proven bulls (1992-1995)*	Young bulls (1997-2000)*
Sweden	CM11	28	198	2537	139
	CM12	28	198	2359	134
	CM2	28	198	1465	87
	CM3	28	198	561	42
Denmark	CM11	13	91	1158	71
	CM12	13	91	1103	69
	CM2	13	91	715	43
	CM3	13	91	320	20
Finland	CM11	58	197	1134	178
	CM12	58	197	1107	174
	CM2	58	197	833	128
	CM3	58	197	394	61

**Bulls with at least 10 daughters with 3rd lactation records

* Birth year of bulls.

Results

Estimated correlations between EBVs in early data (records until 2002), and EBVs or daughter group means in late data (records 2003 – 2006), are presented in Table 3. The differences between different multi-trait models, containing different combinations of information on mastitis (direct or indicator information), are illustrated in Figures 1 and 2.

Estimated correlations, that should reflect the accuracy of the model in the prediction of mastitis occurrence, were as expected higher for proven bulls than for young bulls. Correlations between EBVs in early and late data were stronger than correlations between EBVs in early data and daughter group means in late data.

Multiple-trait models including CM gave generally higher correlations than models without CM. When correlating early EBVs and daughter group means for young bulls, however, only CM gave a slightly lower correlation than a combination of the indirect traits SCC and UC.

The highest correlations were found when CM was combined with at least one of the traits SCC and UC.

Table 3. Estimated correlations between clinical mastitis (means or estimated breeding values) for proven and young bulls in the late data (records until 2002), and estimated breeding values from different models in early data (records 2003 – 2006)**

	Sire daughter group means Late data		Sire estimated breeding values Late data	
Multiple-trait definition Early data	Proven bulls (1992-1995)*	Young bulls (1997-2000)*	Proven bulls (1992-1995)*	Young bulls (1997-2000)*
CM, SCC, UC	0.64	0.36	0.75	0.44
CM, SCC	0.64	0.31	0.75	0.42
CM, UC	0.62	0.36	0.73	0.44
CM	0.58	0.25	0.71	0.38
SCC, UC	0.53	0.28	0.58	0.34
SCC	0.45	0.23	0.53	0.32
UC	0.39	0.12	0.36	0.12

*Birth year of bulls, proven bulls have their first daughter group in early data, whereas young bulls have their first daughter group in the late data.
**Abbreviations as in Table 1

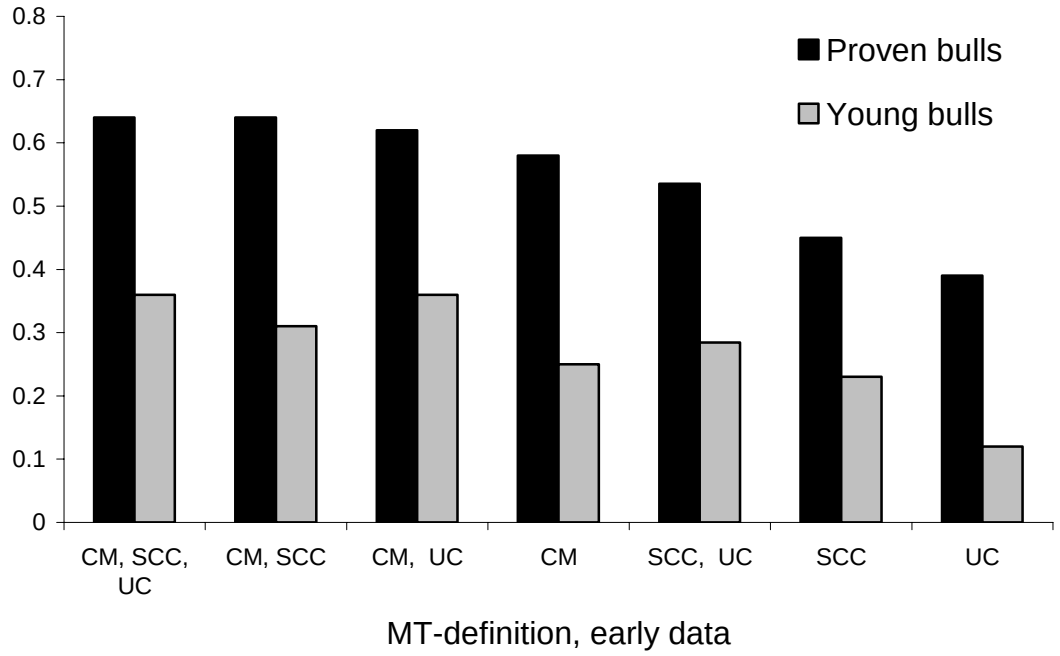

Figure 1. Correlations between EBVs from different models in early data and progeny group means for clinical mastitis in late data.

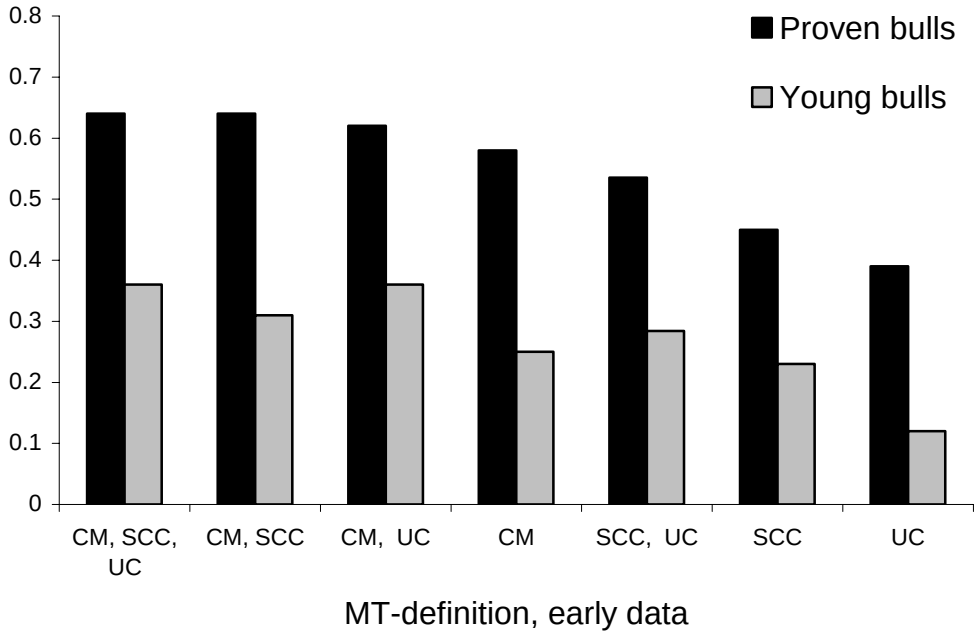

Figure 2. Correlations between EBVs from different models in early data and EBVs for clinical mastitis in late data.

Discussion

For proven bulls all multi-trait models where CM was included gave far better prediction of clinical mastitis in future daughters, compared with models without this goal trait. Including also SCC or UC in the MT-model increased the correlations between EBVs in early data and daughter group means or EBVs in late data further. The advantage of using all three traits together seemed small from looking at the estimated correlations only. One reason could be that CM and either SCC or UC give sufficient information, and that the value of including additional information from another correlated trait is low. However, a clear benefit of including UC in the evaluation is that it provides an early indication of udder health, as it is measured rather early in first lactation daughters. It should be kept in mind that the records of UC are from first lactation only, whereas records from three lactations of somatic cell count are included in the SCC.

For young bulls the scenery is different. In this case, the prediction is based on pedigree information only. The more information available, the higher heritabilities of the traits, the better predictions can be made. Consequently, including UC in the multi-trait models seem to give better predictions especially for young bulls. Philipsson et al. (1994) found that it was more efficient to select for a correlated trait with higher heritability (SCC) than directly on clinical mastitis if the progeny groups were small (less than 100 daughters). With large daughter groups, direct selection on clinical mastitis was more efficient, however. They also found that a combination of both measures was the most efficient in both cases.

Nielsen et al. (1996) compared the efficiency of including information on different udder health traits in the Danish evaluation of mastitis resistance. Similarly to our

results, they found that all indices including clinical mastitis gave higher correlation between the index and aggregate genotype for mastitis resistance than indices based on SCC, udder conformation or SCC and udder conformation traits together.

For both young and proven bulls, the predictive value for UC alone for clinical mastitis seemed rather low in our study. The included information on UC was from first lactation only, whereas CM and SCC data was from three lactations. Also, records of UC are available for fewer animals compared with SCC. This will influence the comparisons. In addition, the genetic correlations between UC and CM are lower than between SCC and CM. Nielsen et al (1996) found that udder depth and fore udder attachment together were as effective as SCC for evaluation of mastitis resistance. Different progeny group sizes in the different countries may at least partly explain this difference. Including UC provides additional values as information related to udder health becomes available earlier. This is of importance in the practical situation when selecting bulls. The main part of the selection will take place when most of the daughters in the daughter group only have first lactation records.

It would be interesting to continue this study and also make comparisons between models using only first lactation records for both SCC and UC, or information from all three lactations for both indicator traits.

The results from proven bulls seem more stable than those from young bulls. There are, however, advantages and disadvantages of using both groups of results. In this dataset the number of proven sires is not large. This means that the influence of each sire on the correlation is relatively important. Proven bulls have randomly sampled daughter groups in early data but have been selected in the late data. Young bull daughter groups, found in the late data, are randomly sampled, but information on the bull in early data is only of pedigree type, which, as mentioned above, is more influenced by differences in heritability of the traits than the latter progeny information. The selection on udder health has been rather mild which may give advantages for proven bull results in this study.

As expected, the correlations with breeding values in early data were higher and more stable when using estimated breeding values compared with progeny means in the late dataset. All alternatives that included CM in early data MT-model gave somewhat higher correlations when correlating breeding values with breeding values rather than daughter group means. To calculate the progeny group means for CM from lactation means in the late data the same index weights were used as when making the official index from estimated breeding values. The index weights are not optimal when making progeny group means. The index for CM weighted the lactation means somewhat differently and this was more important when CM was included in the model for early data. Thus correlations to sire group means may be a little too low for alternatives that include CM in model for early data. A more detailed study on the separate lactational traits could shed light on this.

The setup of the current study is somewhat similar to the setup used in Interbulls' validation method 3. One obvious set of correlations to compare would then be those between breeding values from the reduced dataset, here called the early data, and the breeding values from the full data (early and old data). This was avoided here since it

seemed in preliminary studies that autocorrelations from data used in both evaluations influenced the results and gave unrealistically high correlations.

Conclusions

Including direct information on clinical mastitis in the genetic evaluation improves the prediction of clinical mastitis in future daughters.

Including information on somatic cell score or udder conformation together with clinical mastitis increases the predictive ability of the multi-trait model. The combination of clinical mastitis and udder conformation information gave comparatively high predictive value, especially for young bulls.

Both proven bull correlations and young bull correlations proved to be informative when discriminating between models for prediction.

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