Effects of Changes in Information Sources in an Udder Health Index on Genetic Correlations

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Introduction

Some Interbull member countries have expressed an interest in international genetic evaluations for an udder health index, either as an alternative or an addition to the current udder health routine evaluation. By an index trait is meant a composite of more than one trait, which after separate genetic evaluations are combined via, e.g., selection index methodology. To be able to conduct an international genetic evaluation for udder health indices, genetic correlations between countries are needed. These genetic correlations, however, first have to be examined, because they might change over time due to changes in the information sources.

The aim of this study was to estimate genetic correlations between udder health indices of different age classes within countries and evaluate if the genetic correlations change with age of the bull due to changes in the information sources.

The second aim was to estimate genetic correlations between milk somatic cell, clinical mastitis and the udder health index across countries for different age classes and investigate the impact of various time edits.

Material and Methods

Data

National genetic evaluation results for milk somatic cell, clinical mastitis and udder health index of Holstein bulls were received from Denmark, The Netherlands and Sweden. The Effective Daughter Contribution (EDC) for the udder health index was computed by the countries according to the procedure outlined in Appendix I. Information about udder health traits, received from Denmark and The Netherlands, was combined with the national conformation evaluations of these countries, as used in the Interbull February 2002 routine evaluation, in order to create a file with information about all traits included in the udder health index. For the across country estimation of genetic correlations between udder health traits, national genetic evaluation results for milk somatic cell of Holstein bulls from the USA were also used.

The breeding goals for udder health in Denmark, The Netherlands and Sweden are resistance to clinical mastitis (h^2 = 0.04, Sander Nielsen *et al*., 2000), mastitis resistance (h^2 = 0.03, De Jong & Lansbergen, 1996) and freedom from clinical mastitis (h^2 = 0.02, Philipsson, *et al.*, 1997), respectively. Information about recording and evaluation and the heritabilities of the udder health index traits (Denmark, The Netherlands and Sweden) and milk somatic cell (USA) is summarized in Table 1.

Table 1. Definition of the udder health index in Denmark (DNK), The Netherlands (NLD) and Sweden (SWE) and milk somatic cell in the USA.

	Udder health index traits	Data since	Days of lactation included	# Parities	h^2
DNK	UD, FU, DF[1]	1990		1	0.33, 0.24, 0.26
	SC	1990	10 – 180	1	0.11
	CM[2]	1990	-10 – 305	3	0.04
NLD	UD, TL, MS[3]	1981		1	0.40, 0.35, 0.30
	FU[3]	1981		1	0.29
	SC	1990	5 – 305	3	0.15
SWE	SC	1982	5 – 150	1	0.08
	CM	1983	-10 – 150	1	0.02
USA	SC	1987	6 – 305	5	0.10

All information on SC=milk somatic cell and CM=clinical mastitis, Mark *et al.* (2001)

1. UD=udder depth, FU=fore udder attachment and DF=dairy form.
   Source: Sander Nielsen *et al.* (2000)
2. CM in Denmark is divided in four separate traits: day -10 till 50 (first lactation), day -10 till 305 (first lactation), day -10 till 100 (second lactation) and day -10 till 100 (third lactation)
3. UD=udder depth, TL=teat length, MS=milking speed, FU=fore udder attachment
   Source: De Jong & Lansbergen (1996)

Selection Index

Genetic correlations between the udder health indices of bulls of three age classes were computed. These age classes were bulls born in 1985-1989, 1993, and 1996, corresponding approximately to bulls with first and second crop evaluations, bulls with the last full evaluation of first crop daughters and young bulls with a first evaluation, respectively.

The genetic correlations were calculated using selection index methodology. The index weights were calculated using the average EDC for each age class. The average EDC was used because factors causing changes in reliability were included this way, and not only the change in number of daughters. Further it was assumed that the average breeding values of the index traits did not change over time.

The genetic correlation between the indices of two age classes was calculated as:

$$R_{I,I'} = \frac{\mathrm{cov}(b_I \cdot X_I, b_{I'} \cdot X_{I'})}{\sqrt{(\mathrm{var}(b_I \cdot X_I) \cdot \mathrm{var}(b_{I'} \cdot X_{I'}))}} \qquad (1)$$

where

$\mathrm{cov}(b_I \times X_I, b_{I'} \times X_{I'}) = b_I' \times \mathrm{cov}(X_I, X_{I'}) \times b_{I'} = (b_I' \times P_I \times b_{I'})$

$\mathrm{var}(b_I \times X_I) = b_I' \times P_I \times b_I$

$\mathrm{var}(b_{I'} \times X_{I'}) = b_{I'}' \times P_{I'} \times b_{I'}$

b_I = a vector with the weightings factors of the index

P_I = P-matrix, containing variances and covariances of the index traits

The P-matrix of the index with the most information included was used to compute $\mathrm{cov}(X_I, X_{I'})$.

MACE

Genetic correlations between countries for udder health traits were estimated with an EM-REML applied to a reduced set of MACE equations (Klei & Weigel, 1998). Pedigree information was taken from the Interbull February 2002 routine evaluation. National breeding values were first de-regressed within country. For the estimation of genetic correlations well connected subsets of common bulls, as well as bulls that belong to 3/4-sib groups that have relatives with evaluations in more than one country, were created. Number of common bulls was more than 80 for all country pairs, and there were at least 50 bulls with a breeding value in all countries. Seven combinations of milk somatic cell, clinical mastitis and the udder health index were created and for each of these seven combinations, five analyses were carried out. For the first analysis no edit on birth year was applied. To investigate whether there was a time trend, bulls born before 1980 (analysis 2), born after 1995 (analysis 3), born after 1992 (analysis 4) and born after 1989 (analysis 5) were excluded in the other analyses.

Results and Discussion

Average EDC for the udder health index traits increased with age (Table 2), as expected. Table 2 also shows the influence of trait definition (Table 1) on average EDC for different udder health index traits. Young bulls (1996) only have information from first lactation. Average EDC's for bulls born in 1993 change only for milk somatic cell and clinical mastitis, reflecting information from three lactations (conformation traits are only scored in first lactation). The increase in average EDC for all udder health index traits of older bulls (1985-1989) is due to information becoming available from second crop daughters.

Table 2. The average Effective Daughter Contribution (EDC) for udder health index traits for three age classes of bulls in Denmark (DNK), The Netherlands (NLD) and Sweden (SWE).

	DNK			NLD			SWE	
Birth year	COD[1]	SC	CM	CON	FU	SC	SC	CM
1985-1989	48	266	596	265	139	604	264	305
1993	38	89	216	74	72	167	114	133
1996	38	63	107	58	58	95	84	96

1. COD = includes udder depth, fore udder attachment and dairy form; EDC's are the same, SC = milk somatic cell, CM = clinical mastitis, CON = includes udder depth, teat length and milking speed; EDC's are the same, FU = fore udder attachment

Index weights were also affected by information becoming available at different times and changed over time (Table 3). The b-values of clinical mastitis in Denmark were high because the breeding goal trait was included in the index. This also holds for Sweden, but because the heritability of clinical mastitis was lower and the correlation between milk somatic cell and clinical mastitis in Sweden was higher (0.50 vs 0.70), the influence was less. The b-values of the conformation traits and milking speed in the udder health index of The Netherlands did not change over time. The b-values for milk somatic cell ranged from -0.686 till -0.551.

Table 3. The b-values for udder health index traits of Denmark (DNK) and Sweden (SWE) for three age classes of bulls.

	DNK					SWE	
Birth year	UD[1]	FU	DF	SC	CM	SC	CM
1985-1989	-0.011	-0.001	0.007	0.020	0.779	0.110	0.473
1993	-0.021	-0.003	0.014	0.031	0.571	0.121	0.306
1996	-0.030	-0.005	0.021	0.038	0.400	0.118	0.250

1. UD = udder depth, FU = fore udder attachment, DF = dairy form, SC = milk somatic cell, CM = clinical mastitis.

Genetic correlations (Table 4) between udder health indices of age classes were less than unity, as a result of changing b-values over time. The lowest correlations were between old bulls (1985-1989) and young bulls born in 1996, especially in Denmark and Sweden.

Table 4. Genetic correlations between the udder health index of three age classes of bulls within Denmark (DNK), The Netherlands (NLD) and Sweden (SWE).

	DNK		NLD		SWE	
Birth year	1993	1996	1993	1996	1993	1996
1985-1989	0.92	0.85	0.96	0.93	0.89	0.84
1993		0.92		0.97		0.94

The genetic correlation of the single trait milk somatic cell between countries did not change much over time (Table 5). Again the influence of number of parities is shown. The genetic correlation between milk somatic cell in Denmark and milk somatic cell in Sweden was near unity and constant, which could be expected as both countries consider first lactation in the genetic evaluation. The genetic correlation with milk somatic cell in The Netherlands (three parities) and USA (five parities) changed more. This might be due to the different number of parities considered and the non-unity correlation between parities.

Table 5. Genetic correlations of milk somatic cell between Denmark (DNK), The Netherlands (NLD), Sweden (SWE) and USA for five groups of bulls.

	DNK			NLD		SWE
Birth year	NLD	SWE	USA	SWE	USA	USA
All	0.90	0.99	0.87	0.94	0.89	0.91
1980-	0.91	0.99	0.87	0.95	0.89	0.91
1980-1995	0.91	0.99	0.88	0.95	0.89	0.91
1980-1992	0.91	0.99	0.88	0.95	0.89	0.92
1980-1989	0.94	0.99	0.91	0.95	0.91	0.92

The genetic correlation between milk somatic cell in The Netherlands and clinical mastitis in Sweden (Table 6) changed only slightly over time. In contrast, the time trend was stronger for the udder health index, for which the genetic correlations varied between 0.63, for bulls born after 1980, and 0.90, when only bulls born between 1980 and 1990 were included (clinical mastitis in Denmark). The large difference in the genetic correlation between milk somatic cell in The Netherlands and the udder health index in Sweden when all bulls were included or only bulls after 1980, might be due to the fact that in the file of Sweden relatively more bulls were born before 1980 (15% vs 2-5% in the other countries). Genetic correlations for clinical mastitis in Denmark and udder health traits in the other countries were almost the same as for the Danish udder health index. This was as expected, because clinical mastitis is almost the same trait as the udder health index, since clinical mastitis is nationally evaluated in a multiple-trait evaluation and it is also included as one of the index traits.

Table 6. Genetic correlations between milk somatic cell (SC) and the udder health index (UHI) of The Netherlands (NLD) and clinical mastitis (CM) in Denmark and Sweden and the udder health index (UHI) in Sweden (SWE) for five groups of bulls.

	NLD (SC)			NLD (UHI)		
Birth year	DNK (CM)	SWE (CM)	SWE (UHI)	DNK (CM)	SWE (CM)	SWE (UHI)
All	0.52	0.58	0.84	0.61	0.65	0.83
1980-	0.53	0.60	0.90	0.63	0.66	0.86
1980-1995	0.52	0.59	0.90	0.60	0.65	0.86
1980-1992	0.58	0.63	0.91	0.77	0.76	0.91
1980-1989	0.60	0.60	0.89	0.90	0.83	0.97

Conclusion

The genetic correlations between udder health indices of different age classes within countries changed. Genetic correlation between udder health indices and milk somatic cell and clinical mastitis across countries also changed over time. The inclusion of udder health indices in current international genetic evaluations is therefore not recommended, because of changing trait definition with age.

The udder health index showed a higher genetic correlation across countries with clinical mastitis than with milk somatic cell. For countries without direct information on clinical mastitis, an udder health index based on indirect information (milk somatic cell, conformation traits) can be used to improve udder health.

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Appendix: Computation of EDCs for index traits

Computation of EDC's for index traits we suggest to apply the following procedure. Note that the procedure is not exact, since it ignores residual correlations between the underlying traits making up the index trait.

Step 1: Converting EDCs to reliability figures

For each of the underlying traits the EDC's can be converted into a reliability figure as follows:

$$REL_{s,i} = \frac{w_{s,i}}{w_{s,i} + k_i}$$

where:

$w_{s,i}$ = weighting factor (EDC) for sire s and trait i

k_i = variance ratio for trait i: (4 - h^2_i)/h^2_i

Step 2: Combine sources of information

Let the composite trait for sire s be a linear function of EBVs of underlying traits:

$$CT_s = b_1 EBV_{s,1} + \ldots + b_n EBV_{s,n} = \mathbf{b'EBV}_s$$

Then the reliabiality of the composite trait for sire s is:

$$REL_{CT,s} = \frac{\mathbf{b'P}_s\mathbf{b}}{\mathbf{b'Gb}},$$

where:

$$\mathbf{P}_s = \begin{bmatrix} REL_{s,1} & \cdots & r_{1i}REL_{s,1}REL_{s,i} & \cdots & r_{1n}REL_{s,1}REL_{s,n} \\ \vdots & \ddots & & & \vdots \\ r_{1i}REL_{s,1}REL_{s,i} & & REL_{s,i} & & r_{in}REL_{s,i}REL_{s,n} \\ \vdots & & & \ddots & \vdots \\ r_{1n}REL_{s,1}REL_{s,n} & \cdots & r_{in}REL_{s,i}REL_{s,n} & \cdots & REL_{s,n} \end{bmatrix},$$

$$\mathbf{G} = \begin{bmatrix} 1 & \cdots & r_{1i} & \cdots & r_{1n} \\ \vdots & \ddots & & & \vdots \\ r_{1i} & & 1 & & r_{in} \\ \vdots & & & \ddots & \vdots \\ r_{1n} & \cdots & r_{in} & \cdots & 1 \end{bmatrix},$$

$r_{1,i}$ = genetic correlation between trait 1 and i.

Step 3: Convert reliability for composite trait to EDC's

$$w_{CT\,s} = k_{CT} \frac{REL_{CT\,s}}{1 - REL_{CT\,s}},$$

where:

$w_{CT,s}$ = weighting factor (EDC) for the composite trait to be submitted in the data file

k_{CT} = variance ratio for the composite trait: (4 - h^2_{CT})/h^2_{CT}