Feasibility of International Genetic Evaluations of Dairy Sires for Somatic Cell Count and Clinical Mastitis

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1. Introduction

Selection of foreign sires involves risk when genetic values for breeding goal traits are unknown. Information to support objective selection decisions concerning foreign sires are confined to the information from Interbull=s routine evaluations for production and conformation traits. Functional traits are associated with efficiency of production by their direct influence on costs of production, and are generally considered to be an important factor in maximizing profit from dairy operations. As a consequence, several countries perform national genetic evaluations for various functional traits (Groen *et al.*, 1997), and international genetic evaluations should be considered to enable comparisons between sires across countries for these traits as well.

Several studies have estimated genetic correlations between somatic cell count (SCC) in different Holstein populations (Fikse, 1995; Kolmodin, 1999; Mrode & Swanson, 1997; Reklewski *et al.*, 1998; Rogers *et al.*, 1998). However, these studies considered a limited number of countries. Genetic relationships among more populations and with more up to date methods need to be investigated, before international genetic routine evaluations for traits associated with udder health can be considered.

The main objective of this study was therefore to investigate the feasibility of international genetic evaluations using Mace (Schaeffer, 1994) for traits associated with udder health. In that context it is important to study:

- Data availability and degree of harmonisation in trait definitions and evaluation procedures;
- Connectedness of available data;
- Genetic correlations between traits in different countries;
- Behaviour of Mace for traits with low heritability.

2. Materials

National genetic evaluation results of Holstein bulls for SCC were obtained from Canada (CAN), Germany (DEU), Denmark (DNK), Finland (FIN), France (FRA), the United Kingdom (GBR), the Netherlands (NLD), Sweden (SWE) and the United States (USA). Furthermore, national genetic evaluation results of Holstein bulls for clinical mastitis were available from the three Nordic countries (DNK, FIN and SWE). National genetic evaluation results of Ayrshire bulls were obtained from Finland and Sweden for both clinical mastitis and SCC. All national genetic evaluations were from 1999 except those from Finland and Sweden, which were from 1998.

Bulls were in this study required to have a national proof based on at least 50 daughters to be included in further analysis to obtain similar reliabilities among bulls as in Interbull=s routine evaluations for production traits. The number of evaluated bulls with at least 10 and 50 daughters in each country respectively is shown in Table 1.

Table 1. Number of evaluated bulls with at least 10 (top) and 50 (bottom) daughters respectively in data received from different countries

Holstein												Ayrshire			
SCC									Mastitis			SCC		Mastitis	
CAN	DEU	DNK	FIN	FRA	GBR	NLD	SWE	USA	DNK	FIN	SWE	FIN	SWE	FIN	SWE
4975	8635	3527	989	8080	1597	5224	1797	17917	3458	799	1797	3610	2481	2682	2481
3692	7655	3271	902	6184	1143	4454	1652	9094	1958	726	1652	3502	2336	2592	2336

3. Methods

National genetic evaluation procedures were reviewed based on information found in literature and information provided from organisations responsible for the national evaluations. Number of common bulls (bulls with evaluations in more than one country) was determined for each country pair to get an impression of the amount of genetic ties between countries.

Different methods were used to estimate genetic correlations:

- Interbull-REML: EM-REML for Mace (Sigurdsson *et al.*, 1996);
- REML for R-Mace: EM-REML for a reduced set of Mace equations (Klei & Weigel, 1998).

Both EM-REML programs use deregressed national evaluations as input, and include pedigree information. Deregression of national evaluations was done separately for each trait according to the procedure described by Jairath *et al.* (1998) that accounts for all effects subsequently included in Mace. Well connected subsets of bulls were created for the estimation of genetic correlations. These subsets consisted of all bulls with multiple evaluations and bulls which are members of a 3/4 sib group, with members having evaluations in more than one of the countries considered in a particular analysis. No edit on birth year was practised. Bivariate analyses were done for Interbull-REML, whereas multivariate analysis were done for REML for R-Mace. Different batches created for multivariate analyses are summarised with the results.

4. Results and Discussion

4.1 Review of national genetic evaluation procedures

Data included in and methods used in the national genetic SCC evaluations are summarised in Table 2.

Table 2. Summary of national genetic evaluation procedures for SCC and mastitis used in various countries[1]

Trait	Country	Trait definition	Data incl. since	Days of lact. included	# Parities	Method of evaluation[2]	h^2
SCC	CAN	$\log_2$ test-day SCC	1988	5-305	3	MT RR TDM	.29
	DEU	$\log_2$ test-day SCC	1990	4-365	3	MT FR TDM	.12
	DNK	Lact. mean of $\log_e$ test-day SCC	1990	10-180	1	ST[3] SM	.11
	FIN	Lact. mean of $\log_{10}$ test-day SCC	1978	5-305	3	ST AM RP	.15
	FRA	Lact. mean of $\log_2$ test-day SCC	1989	5-350	3	ST AM RP	.15
	GBR	Lact. mean of $\log_e$ test-day SCC	1991	5-305	5	ST AM RP	.11
	NLD	Lact. mean of $\log_2$ test-day SCC	1990	5-305	3	ST AM RP	.15
	SWE	Lact. mean of $\log_{10}$ test-day SCC	1983	5-150	1*	ST SM	.08
	USA	Lact. mean of $\log_2$ test-day SCC	1987	6-305	5	ST AM RP	.10
Mastitis	DNK	Clinical mastitis[4] scored in 2 categories	1990	-10-180	1	ST[3] SM	.04
	FIN	Clinical mastitis and culling due to udder diseases scored in 2 categories	1983	-7-150	3	ST SM RP	.05
	SWE	Clinical mastitis and culling due to udder diseases scored in 2 categories	1983	-10-150	1	ST SM	.02

1) References are persons responsible for nat'l evaluations and Interbull (1996); 2) MT=Multi-trait (different parities are considered as different traits); ST=Single-Trait; TDM=Animal Model using test-day records; AM=Animal Model; SM=Sire Model; RP=Repeated observations; RR= Random Regression; FR= Fixed Regression; 3) Normally mastitis and SCC are analysed in a multi-trait model, but for this study both traits were analysed in univariate analysis. 4) Not due to culling *) Age between 22 and 36 months.

Objective and consistent measures of SCC are practised in countries providing data for this study, but several inconsistencies among national genetic evaluation models and amount of data included in respective evaluations are evident from Table 2. Both Sire Models and Animal Models based on lactation averages as well as Test-day Models are used. Number of parities included range from one to five and in some countries late lactation stages are not considered. In most countries daily log transformed SCC values are averaged before they are analysed.

For mastitis there are also inconsistencies in parities included in different evaluations. In Denmark the number of parities have been raised to three for mastitis after data was made available for this study (Nielsen et al., 2000). Definition of clinical mastitis among the three Nordic countries also differs. Clinical mastitis diagnoses are recorded by veterinarians in the Nordic countries, but in Denmark farmers can also diagnose and record clinical mastitis. All three countries use a Sire Model for genetic evaluation.

Heritabilities for SCC used in the various national genetic evaluations differ substantially, and range from .29 in Canada to .08 in Sweden. This may to some extent be explained by differences in the evaluation models and data included in the evaluations. Different effects corrected for previous to or in analysis are summarised for different national evaluations in Table 3.

Table 3. Effects included in national evaluation models and pre-adjustment factors (references as in Table 2).

Trait	Country	Effects in model[1]	Pre-adjustments
SCC	CAN	Herd×test day, age×calving season, DIM, PE w/in lact, animal[2]	None
	DEU	Herd×test day, region, calving age, stage of lact., calving season, PE, animal	None
	DNK	Herd×year, region×season×year, calving age, sire[3]	None
	FIN	Herd×year×parity of group, herd×5-year period×parity of group, calving age×parity, calving season×year, PE, animal	Stage of lact., #lact.
	FRA	Herd×year, parity×region×year, calving month×parity×year, calving age×parity×region×year, preceeding dry period length×parity×region×year, PE, animal	DIM, heterogeneous var. among parities
	GBR	HYS, age×parity, parity, calving month, herd×sire, PE, animal	None
	NLD	Herd×parity×year×season, year×calving month, PE, animal	Stage of lact. ×parity (on test-day records)
	SWE	HYS, calving month, calving age, breed of dam, sire	None
	USA	Management group, animal	DIM, calving age, calving month
Mastitis	DNK	Herd×year, region×season×year, calving age, sire[3]	None
	FIN	Herd×year, calving year×month, parity, sire	None
	SWE	HYS, calving month, calving age, breed of dam, sire	None

1) Phantom groups are also included in all evaluations; 2) multivariate breeding value estimation with milk, fat and protein yield; 3) In Denmark SCC and mastitis are normally analysed simultaneously, but not for this study; DIM = Days In Milk; PE = Permanent Environment; HYS = Herd-year-season effect.

Much variation exists in the environmental effects considered in evaluation models and in pre-adjustments. In all countries, except Canada and Denmark, the trait of interest is analysed independently of other traits. In Canada correlations between SCC and yield traits are within the range of -.15 to 0, and yield traits therefore influence SCC relatively little. In Denmark, SCC is normally analysed with mastitis, but for this study the two traits were analysed separately. In Finland and Sweden similar procedures are used for the genetic evaluations of mastitis and SCC for Ayrshires as for Holsteins.

4.2 Genetic ties

Table 4 shows the average number of common Holstein bulls with at least 50 daughters in two countries for each country trait combination.

Table 4. Average number of common bulls for Holstein data

	SCC									Mastitis		
	CAN	DEU	DNK	FIN	FRA	GBR	NLD	SWE	USA	DNK	FIN	SWE
Avg	158	199	78	17	169	134	175	79	226	72	17	79

Finland generally had weak genetic ties with other Holstein populations (3-25 common bulls available). Sufficient genetic ties existed among the other Holstein populations in this study (70-517 common bulls available). For Ayrshires, there were 36-41 common bulls evaluated in both Finland and Sweden.

4.3 Estimated genetic correlations

Genetic correlations among SCC and mastitis in different Holstein populations estimated with Interbull-REML and REML for R-Mace are given in Table 5.

Table 5. Genetic correlations for Holsteins estimated with multivariate REML for R-Mace (above diagonal) and bivariate Interbull-REML (below diagonal)

		SCC									**Mastitis**		
		CAN	DEU	DNK	FIN	FRA	GBR	NLD	SWE	USA	DNK	FIN	SWE
SCC	CAN		.90[A]	.80[A] .79[C]	.94[A] .98[C]	.93[A]	.96[A]	.93[A]	.82[A] .81[C]	.93[A] .93[C]	.50[C]	.57[C]	.55[C]
	DEU	.88		.85[A]	.88[A]	.95[A] .95[B]	.94[A] .94[B]	.97[A] .97[B]	.81[A]	.87[A] .87[B]	.43[B]	.07[B]	.62[B]
	DNK	.74	.79		.79[A] .84[C]	.89[A]	.89[A]	.88[A]	.98[A] .93[C]	.88[A] .86[C]	.65[C]	.81[C]	.52[C]
	FIN	.50	.51	.85		.94[A]	.96[A]	.94[A]	.83[A] .84[C]	.91[A] .91[C]	.41[C]	.59[C]	.47[C]
	FRA	.92	.93	.81	.48		.98[A] .98[B]	.96[A] .96[B]	.89[A]	.92[A] .92[B]	.36[B]	.31[B]	.58[B]
	GBR	.95	.91	.86	.71	.96		.97[A] .98[B]	.91[A]	.93[A] .93[B]	.40[B]	.29[B]	.65[B]
	NLD	.91	.94	.80	.63	.93	.97		.87[A]	.90[A] .90[B]	.40[B]	.23[B]	.63[B]
	SWE	.77	.81	.86	.81	.81	.80	.80		.91[A] .89[C]	.69[C]	.66[C]	.63[C]
	USA	.92	.84	.80	.67	.90	.91	.87	.87		.53[B] .63[C]	.33[B] .61[C]	.63[B] .57[C]
Mastitis	DNK	.29	.45	.66	.30	.29	.29	.27	.44	.46		.18[B] .71[C]	.86[B] .91[C]
	FIN	.38	-.10	.60	.57	.29	.68	.34	.40	.42	.40		.20[B] .55[C]
	SWE	.53	.50	.38	.31	.41	.48	.49	.61	.50	.65	.49	

A, B and C indicate which Batch of traits the estimate is obtained from. Batch A incl. SCC in all nine countries. Batch B incl. SCC in DEU, FRA, GBR, NLD, USA and mastitis in DNK, FIN, SWE. Batch C incl. SCC in CAN, DNK, FIN, SWE, USA and mastitis in DNK, FIN, SWE.

Estimated genetic correlations among SCC in different countries were high, and consistent results were obtained from different batches with REML for R-Mace. Estimated genetic correlations between mastitis in Denmark and in Sweden were also high and consistent. Estimated genetic correlations between mastitis in Finland and mastitis in either Denmark or Sweden appeared to be lower, and consistent results were not obtained from different batches. The differences between estimates for the same correlations obtained from different batches can probably be explained by sampling since only 17 and 20 bulls were evaluated and had at least 50 daughters in both Finland and in Denmark and Sweden respectively. Genetic correlations between mastitis in Finland and in either Denmark or Sweden are expected to be lower since three parities are included in the Finnish evaluation for mastitis and only first parity in Denmark and Sweden. Genetic correlations between SCC and mastitis measured in different countries were moderate and on average slightly lower than within country estimates, as expected.

The estimation of genetic correlations between traits measured on the same animals (within countries) with the methods used in this study may be biased (Larroque & Ducrocq, 1999) since they assume zero residual correlations. An AI-REML for Mace (Madsen *et al.*, 2000) was therefore developed to account for non-zero residual correlations.

Estimated genetic correlations obtained with Interbull-REML were typically lower than those obtained with REML for R-Mace, especially in situations with few genetic ties between countries. This was the case even though a well connected subset was used to estimate genetic correlations with both methods. Multivariate analysis were also carried out for Interbull-REML (results not shown), but estimates decreased compared to the bivariate results in all cases, especially in cases with weak genetic ties between populations. Estimates obtained with Interbull-REML are suspected to be underestimated (Sigurdsson *et al.*, 1996). This problem may be more severe for traits with low heritability, since the information about the genetic component in the deregressed national evaluations are lower compared with situations of higher heritabilities.

Estimated genetic correlations for SCC and mastitis for Ayrshires are presented in Table 6.

Table 6. Genetic correlations estimated multivariately[1] with REML for R-Mace (above diagonal) and bivariately with Interbull-REML (below diagonal)

	SCC in Finland	SCC in Sweden	Mastitis in Finland	Mastitis in Sweden
SCC in Finland		.52	.57	.27
SCC in Sweden	.54		.36	.69
Mastitis in Finland	.58	.28		.75
Mastitis in Sweden	.42	.61	.31	

1) All four traits were analysed simultaneously for REML for R-Mace. 5108 bulls, 804 ancestors, 25 phantom groups.

The estimated correlations for Ayrshires were lower compared to those found for Holsteins in most cases. For Ayrshires, estimation of reliable genetic correlations between traits in different countries is difficult because relatively few genetic ties exist between the populations. Estimates using a minimum progeny group size of 10 daughters instead of 50 daughters yielded higher estimates for Ayrshires, but slightly lower estimates for Holsteins on average (results not shown).

5. Main Conclusions and Implications

- SCC is recorded consistently across countries, but inconsistencies in data included in and methods used in different national genetic evaluations were found. High and consistent estimated genetic correlations of the order .9 and more were found between SCC in most countries.

- Mastitis is recorded slightly different in Denmark compared to the two other Nordic countries, and three parities are considered in Finland compared with only first parity in Denmark and Sweden. High estimated genetic correlation between clinical mastitis in Denmark and Sweden were obtained, whereas estimates between clinical mastitis in Finland and the two other Nordic countries were lower.
- Adequate connectedness existed among all Holstein populations included in this study, except for Finland. Connectedness is also problematic for the available Ayrshire data.
- Estimates between SCC in one country and clinical mastitis in another country were typically slightly smaller than within country estimates as expected.
- Estimated correlations were smaller for the two Ayrshire populations compared with similar estimates for the Holstein populations.
- Interbull-REML yielded lower estimates for genetic correlations compared to REML for R-Mace, especially in cases with few genetic ties, even though well connected subsets of bulls were used to estimate genetic parameters with both methods.

The feasibility of estimating genetic correlations to be used in international genetic evaluations for traits related to mastitis resistance (SCC and clinical mastitis) have been demonstrated for nine Holstein and two Ayrshire populations using Mace technology. International genetic evaluations (Mace) of bulls for SCC and clinical mastitis will provide dairy producers around the world with better and more diverse information in deciding which bulls to use. This gives better opportunities in achieving optimal genetic improvement and helps to secure genetic diversity. Furthermore, it may help to gain better public acceptance of the dairy breeding industry as a whole. This project has now reached the stage for Mace pilot runs to be conducted as a basis for discussion at the upcoming Interbull workshop in Verden.

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References

Fikse, W.F. 1995. Genetic correlations between countries for somatic cell count and conformation traits. *Thesis at Wageningen Agricultural University.* 17 pp.

Groen, A.F., Steine, T., Colleau, J.J., Pedersen, J., Pribyl, J. & Reinsch, N. 1997. Economic values in dairy cattle breeding, with special reference to functional traits. Report of an EAAP-working group. *Livest. Prod. Sci. 49*, 1.

Interbull, 1996. Sire evaluation procedures for non-dairy-production and growth & beef production traits practised in various countries. *Interbull Bulletin. 13.* 210 pp.

Jairath, L., Dekkers, J.M.C., Schaeffer, L.R., Liu, Z., Burnside, E.B. & Kolstad, B. 1998. Genetic evaluation for herd life in Canada. *J. Dairy Sci. 81*, 550.

Klei, L. & Weigel, K.A. 1998. A method to estimate correlations among traits in different countries using data on all bulls. Proceedings of the 1998 Interbull meeting in Rotorua, New Zealand. *Interbull Bulletin 17*, 8.

Kolmodin, R. 1999. Predicting Swedish breeding values for Dutch dairy bulls, *Examensarbete 208,* Dep. Animal breeding and genetics, Swedish University of Agricultural Sciences.

Larroque, H. & Ducrocq, V. 1999. An indirect approach for the estimation of genetic correlations between longevity and other traits. *Interbull Bulletin 21*, 128.

Madsen, P., Jensen, J. & Mark T. 2000. Reduced Rank Estimation of (Co)-Variance Components for International Evaluations using AI-REML. *Paper at the 2000 Interbull meeting in Bled,* Slovenia.

Mrode, R.A. & Swanson, G.J.T. 1997. Association between somatic cell count progeny tests in the United States of America (USA), The Netherlands and the United Kingdom (UK). Proc. British Soc. Anim. Sci. 1997.

Nielsen, U.S., Aamand, G.P. & Mark, T. 2000. The national genetic evaluation for udder health and other health traits in Denmark. *Paper at the 2000 Interbull meeting in Bled*, Slovenia.

Reklewski, Z., Philipsson, J., Grochowska, R., Fikse, F. & Dymnicki, E. 1998. Estimates of genotype by environment effects for milk traits and somatic cell counts among daughters of Swedish Friesian sires in Poland and Sweden. *Animal science papers and reports. Polish Academy of sciences, Inst. of Genetics and Animal Breeding, Jastrzebiec 16.4,* 197.

Rogers, G.W., Banos, G., Nielsen, U.S. & Philipsson, J. 1998. Genetic correlations among somatic cell scores, productive life, and type traits from the United States and udder health measures from Denmark and Sweden. *J. Dairy Sci. 81*, 1445.

Schaeffer, L.R. 1994. Multiple-country comparison of dairy sires. *J. Dairy Sci. 77*, 2671.

Sigurdsson, A., Banos, G. & Philipsson, J. 1996. Estimation of genetic (co)variance components for international evaluation of dairy bulls. *Acta Agric. Scand. A. 46,* 129.