Genetic Correlations Among Somatic Cell Scores, Productive Life, and Type Traits from the United States and Udder Health Measures from Denmark and Sweden

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Introduction

Genetic relationships among somatic cell counts (SCC), udder traits, and mastitis have an impact on the value of these traits for breeding programs. To properly utilize these traits for breeding programs, detailed information is needed about their interrelationships. In addition, these genetic relationships are needed to facilitate international genetic evaluations. In the future, multiple trait across country evaluations (both multi-trait and multi-country) might be feasible where mastitis sire evaluations would be available on all bulls even though direct recording of mastitis takes place in only a few countries. For example, clinical mastitis, SCC, and possibly some udder type traits from Scandinavian countries could be combined with SCC and some udder type traits from other countries to get multi-trait and multi-country evaluations for clinical mastitis. The major benefits of this approach would be the availability of genetic evaluations for clinical mastitis (from correlated traits and direct information on relatives) on newly proven bulls in countries where clinical mastitis is not recorded. Genetic correlations among SCC, udder type traits and mastitis would be required to calculate the most accurate sire evaluations possible from the most commonly recorded data.

The objectives of this paper are to estimate genetic relationships among somatic cell scores (SCS), productive life (PL), and type traits from the United States (US) and udder health measures from Denmark (DK) and Sweden (SW).

Materials and Methods

Official sire evaluations from the US (July 1995) for production traits, PL, SCS, and type traits (from USDA and Holstein Association) were used in the analyses, along with official sire evaluations from DK and from SW (July 1995). In addition, unofficial single trait clinical mastitis (MST) evaluations from DK were used; these evaluations were calculated from the exact data used in calculating the official sire evaluations for DK, however only a single trait model including only clinical mastitis data was used. The official sire evaluations from DK (designated MMT) are calculated from a multiple trait model that includes SCC and clinical mastitis. The SCC data are included to increase the accuracy of the sire evaluations for clinical mastitis. Genetic evaluations from SW (MST) are from single trait analyses using a sire model with relationships. Heritabilities in SW assumed for MST and SCC are .02 and .08, respectively. Denmark also uses a sire model with relationships; heritabilities in DK for clinical mastitis and SCC are .04 and .11, respectively. For the official multiple trait model the genetic correlation between clinical mastitis and SCC in DK was .63. INTERBULL presents details of the evaluation procedures and data (2).

Sire genetic evaluations from the US were merged with sire genetic evaluations from DK to establish a file which included bulls with evaluations and daughters in both countries. The same procedure was used to establish a file which included bulls with evaluations and daughters in SW and the US. Genetic correlations were estimated by adjusting

product moment correlations among sire evaluations for reliabilities (1). Genetic evaluations from the US and from DK or SW would be from independent daughter groups so only genetic covariance should be responsible for the correlations among progeny group performance. Edits were made to include only sires with 50 daughter equivalents in DK or SW and reliability for SCS from the US of .60 or greater or, in the case of matches with type, reliability for linear type of .70 or greater. Edits were also made at 125 daughter equivalents in DK or SW and final results were similar to those reported here.

The methods described by Sigurdsson and Banos (3) were also applied to data used in this study. Meaningful results from these analyses were not obtained because deregressed proofs from the methods were not stable due to low heritabilities and other data characteristics.

Results and Discussion

Means, standard deviations, and descriptions for the sire evaluations used in the study are in Table 1. For the Danish and Swedish traits, higher sire evaluations are more desirable. Mean reliabilities for the US traits were all .95 or above. Mean reliabilities for the Danish traits were from .72 to .88 depending on the trait and data subset (match with US production data or type data). Mean reliabilities for the Swedish traits were .52 for mastitis and .77 for SCC.

Genetic correlations among SCS, PL, and protein yield (PY) from the US and udder health measures from DK and SW are in Table 2. Genetic correlations between PY and the udder health measures from DK and SW were unfavorable and ranged from -.09 to -.28. Correlations with milk and fat yield are not reported but were similar to the correlations with PY. Genetic correlations between PL and the udder health measures were favorable, especially between PL and clinical mastitis. Correlations between PL and MST in SW were higher than between PL and MST in DK. The differing results could be due to sampling. Of the 80 and 85 bulls in the US-DK and US-SW data files, only 37 were common to both the US-DK and US-SW files. Note that PL evaluations from the US had very high reliabilities (mean >.95) so essentially all the information in the PL evaluations would have been direct information on daughter productive life. Correlations between PL on bulls with early first crop progeny and mastitis might not be as favorable as those reported here because PL evaluations on bulls with early first crop progeny are impacted by traits other than actual productive life on relatives.

Genetic correlations between SCC from DK and SCS from the US and between SCC from SW and SCS from the US were -.87 and -.99, respectively. The negative sign only reflects the scaling of Danish and Swedish sire evaluations (higher values represent lower SCC). Clearly, genetic correlations between US SCS and SCC in DK and SW are very large.

Genetic correlations between MST from DK and SCS from the US and between MST from SW and SCS from the US were -.66 and -.49, respectively. The correlation between US SCS and Danish MST is in close agreement with the within Denmark estimates between these two traits (2). The genetic correlation between the US SCS and MST from SW is lower than the within SW estimates of around .65-.70 (Mats Gundel, personal communication). The correlation is also lower than the estimate between US and DK. This could partly be due to sampling. The correlation between Swedish SCC and MST sire evaluations in the matching 80 bulls was .40 which is slightly lower than expected based the reliability of the proofs and the estimated within population genetic correlation. The results could also indicate that the true genetic correlation is lower between the US and SW versus the US and DK. Clinical mastitis may be slightly different traits in DK and SW. The frequency of recorded clinical mastitis in first lactation (0/1 trait with 1 representing 1 or more episodes) differs between DK and SW by around 15%.

The genetic correlation between US SCS and Danish MST was lower in magnitude

than the genetic correlation between US SCS and Danish MMT (-.66 versus -.75). This result seems reasonable because the genetic correlation between US SCS and Danish SCC was larger in magnitude than the genetic correlation between US SCS and Danish MST. Similar trends were found for the US SCS and the Swedish index of SCC and MST.

Genetic correlations between selected type traits from the US and the measures of udder health from DK and SW are in Table 3. Genetic correlations between final score (FS) and SCC and between FS and MST were all positive and ranged from .07 to .32. These positive correlations are likely due to the impact of udder conformation on FS. Genetic correlations between US udder composite (UCOMP) and SCC and between UCOMP and MST ranged from .26 to .47. Higher values for UCOMP were genetically associated with less mastitis. Selection for higher UCOMP will likely improve mastitis resistance.

The genetic correlations between udder cleft (UC) and the Danish measures of udder health were small, however, higher UC scores tended to be associated with reduced mastitis and SCC in the US-SW matching file. The rear udder traits (height and width) had very small correlations with the measures of udder health.

The genetic correlations between teat placement (TP) and the measures of udder health were all positive with the exception of between TP and MST from DK. Selection for closer TP may have a small desirable impact on udder health. The genetic correlations between teat length (TL) and the measures of udder health were all negative, but small.

The genetic correlations between udder depth (UD) and SCC were moderate and positive (range .37 to .52). Likewise the genetic correlations between UD and MST were positive (from .45 to .52). These genetic correlations indicate that higher udders are genetically associated with reduced mastitis. The genetic correlations between UD and clinical mastitis approach the size of the correlations between SCS and clinical mastitis. The correlation between UD and MST in the US-SW file is larger in magnitude than the correlation between SCS and MST. The results indicate that UD may be very useful for selection to improve udder health, especially where clinical mastitis is not routinely recorded. The genetic correlations between fore udder attachment (FUA) and the measures of udder health were, in general, slightly smaller than the genetic correlations between UD and the measures of udder health (FUA and UD are highly correlated).

Conclusions

Sire evaluations for SCS from the US are a very good indicator of expected sire evaluations for clinical mastitis and for SCC in DK and SW. In addition, bulls that sire higher, more tightly attached udders have daughters with lower rates of clinical mastitis. Individual type traits other than UD and FUA have only low or negligible genetic correlations with measures of udder health.

Correlations among the various measures of udder health and udder related type traits indicate that multi-trait and multi-country evaluations for clinical mastitis would have moderate accuracies for bulls sampled in countries where clinical mastitis data are not available. Procedures to calculate these multi-trait and multi-country evaluations should be pursued.

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Table 1. Means, standard deviations, and descriptions for US, Danish, and Swedish sire genetic evaluations[1]

	Means	SD	Higher values for the trait correspond to:
US traits			
Protein	8.00	22.6	higher yield
Productive life	.62	1.41	longer life
Somatic cell score	3.18	.171	higher cell scores
Final score	.078	.905	higher final scores
Udder composite	-.087	.917	higher composite scores
Udder clef	.099	1.08	deeper cleft
Rear udder height	.218	1.19	higher attachment
Rear udder width	.343	1.10	wider attachment
Udder depth	-.536	1.33	higher udder
Fore udder attachment	-.248	1.18	tighter attachment
Teat placement	.173	1.24	closer teats
Teat length	-.042	1.17	longer teats
Danish traits[2]			
Somatic cell count (single trait analysis)	-.026	.110	lower cell counts
Clinical mastitis (single trait analysis)	-.019	.030	lower rates of clinical mastitis
Clinical mastitis (multiple trait analysis)	-.020	.031	lower rates of clinical mastitis
Swedish traits			
Somatic cell count (single trait analysis)	99.5	6.85	lower cell counts
Clinical mastitis (single trait analysis)	100.3	6.11	lower rates of clinical mastitis
Clinical mastitis index (index of 2 single traits - somatic cell counts and clinical mastitis)	99.8	6.37	lower rates of clinical mastitis

[1] Data on US protein, productive life, somatic cell score and Danish udder health evaluations are from 85 sires and data on US type and Swedish udder health evaluations are from 79 sires.

[2] Danish evaluations are not standardized, but they are normally standardized before publication in Denmark.

Table 2. Genetic correlations among (correlations among sire genetic evaluations adjusted for reliabilities) somatic cell score, productive life, and protein yield from the US and udder health measures from Denmark and Sweden

	Denmark[1]			Sweden[1]		
US trait	SCC[2]	MST	MMT	SCC	MST	INDEX
Protein	-.18	-.28	-.28	-.32	-.09	-.20
Productive life	.06	.28	.26	.30	.59	.65
Somatic cell score	-.87	-.66	-.75	-.99	-.49	-.87

[1] Correlations are based on 85 bulls with US and Danish genetic evaluations and 80 bulls with US and Swedish genetic evaluations. Edits were made to include only bulls with approximate minimum 50 daughter equivalents in somatic cell count and clinical mastitis evaluations and reliabilities for US somatic cell score of .60 or greater.

[2] SCC = somatic cell count from a single trait analysis; MST = clinical mastitis from a single trait analysis; MMT = clinical mastitis from a multiple trait analysis including clinical mastitis and somatic cell count; INDEX = mastitis index from single trait evaluation of clinical mastitis and single trait evaluation for somatic cell count.

Table 3. Genetic correlations among (correlations among sire genetic evaluations adjusted for reliabilities) selected type traits from the US and udder health measures from Denmark and Sweden

	Denmark[1]			Sweden[1]		
US trait	SCC[2]	MST	MMT	SCC	MST	INDEX
Final score	.18	.07	.09	.25	.32	.34
Udder composite	.34	.26	.31	.40	.47	.46
Udder cleft	.09	-.01	.01	.21	.23	.29
Rear udder height	.01	-.02	-.02	.09	.09	.13
Rear udder width	.11	-.06	-.05	.10	-.07	.01
Udder depth	.37	.45	.49	.52	.52	.63
Fore udder attachment	.38	.34	.39	.39	.31	.41
Teat placement	.24	-.01	.04	.18	.19	.21
Teat length	-.05	-.09	-.09	-.02	-.09	-.05

[1] Correlations are based on 77 bulls with US and Danish genetic evaluations and 79 bulls with US and Swedish genetic evaluations. Edits were made to include only bulls with approximate minimum 50 daughter equivalents in somatic cell count and clinical mastitis evaluations and reliabilities for US type of .70 or greater.

[2] See footnote no. 2 in Table 2.