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# Relationships between evaluations of Canadian and USA Holstein bulls for longevity and somatic cell score

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**Abstract**

Canadian and United States evaluations of Holstein bulls were compared for longevity and somatic cell score. A total of 13 236 bulls was evaluated for longevity with 462 bulls having evaluations in both countries, and 10 945 bulls evaluated for somatic cell score with 564 bulls having evaluations in both countries. Multiple across country evaluation procedures were used to estimate the genetic correlations between countries, and to evaluate all bulls on each country's scale of expression. The genetic correlation for longevity (calculated and expressed differently in each country) was 0.91, and for somatic cell score was 0.93, which were as high as correlation estimates for production traits between many countries. The correlation between the international evaluation and the original Canadian evaluations were 0.971 for functional herdlife and 0.981 for somatic cell score, and for the United States were 0.999 and 0.997, respectively. International comparisons of bulls for traits other than production and conformation are feasible. 

*Keywords:* International comparisons; Longevity; Somatic cell score

## 1. Introduction

International comparisons of dairy bulls for production traits have been computed by Interbull for nearly five years including over 20 countries. Recently, international comparisons for conformation traits have been the subject of a trial run by Interbull through the Holstein Association of America. There are traits other than production and conformation which are also of economic importance. Two of these are longevity and somatic cell score (SCS). Longevity evaluations give information about involuntary culling of bulls' daughters, and SCS evaluations are indirect indicators of potential mastitis problems.

The United States began national evaluation systems for these traits in January 1994. SCS evaluations, (USCS), are based on the mean of all test day measures within a lactation, which are adjusted for lactation length within parities (Schutz, 1994).

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Evaluations are expressed as predicted transmitting abilities with the mean SCS of first lactation cows born during 1985 added. Productive life (PL), is defined as a measure of lactation length (10 months per lactation) and limited to the first 7 years of life. Evaluations are expressed as deviations from an average cow born in 1985 (VanRaden and Wiggans, 1995). PL reflects the time from first calving to disposal and is not adjusted for the production level of the cow, but does include a contribution from linear type traits. Details about how the type traits were incorporated into the PL evaluations were not available.

Canada began evaluations for these two traits in January 1996. SCS evaluations, (CSCS), are based on a three lactation test day model, and the resulting evaluations for each lactation are combined and expressed relative to a mean of 3.00 (Reents et al., 1995) as estimated transmitting abilities. A three lactation multiple trait model for functional herd life that includes adjustments for fat and protein production levels of the cow is used (Jairath et al., 1998) to give a direct measure of herd life, and an indirect measure of herd life is predicted from conformation traits. The official herd life (HL) evaluation is the combination of the direct and indirect measures which are weighted depending on the amount of information in each. Note that HL includes an adjustment for production level while PL does not, and both evaluations include some contribution from type traits in that country. There are advantages and disadvantages of each kind of evaluation as discussed by Powell et al. (1997).

The simplest way to compare Canadian and US bulls for these traits is to compute a conversion formula such as Powell et al. (1997). They used bulls that were born since 1975, had daughter information in 20 or more herds (in both countries) and a reliability greater than 50% to derive the conversion formulas. For longevity, 433 bulls had evaluations in both Canada and the US and these gave a correlation between HL and PL of 0.60. For SCS, 354 bulls with evaluations in both countries gave a correlation between USCS and CSCS of 0.82. For bulls initially proven in Canada, the correlations were 0.64 for longevity (based on 258 bulls) and 0.77 for SCS (based on 182 bulls). This methodology, however, does not consider the hundreds of half-sibs and other relatives that have proofs in just one country. The multiple across country evaluation model (MACE) of Schaeffer (1994) can accommodate all bulls that are related in different countries through common sires and grandsires.

The objectives of this study were to apply the MACE methodology to evaluations of Holstein bulls for longevity and SCS from Canada and the US, to re-estimate the genetic correlation between countries, and to derive conversion formulas for animals not included in the MACE analysis.

## 2. Materials and methods

The official evaluations for longevity and SCS from Canada and the US were obtained from July 1996. The evaluation systems have been described above. Bulls were required to have a minimum reliability of 50% within a country, daughters records from 20 or more herds, and 20 or more daughters per bull. Some details on the bulls included in the study are shown in Table 1. Note that the bulls in each country have similar average number of daughters and herds for longevity evaluations, but SCS evaluations showed slightly more information from US bull evaluations. The assumed heritabilities for the within country evaluations were 0.030 and 0.085 for HL and PL, respectively, and were 0.09 and 0.10 for CSCS and USCS, respectively.

The Canadian evaluation system for longevity was

Table 1
Details about bulls included in the study

| Trait | Canada | USA |
|---|---|---|
| *Longevity* | | |
| No. of bulls | 3747 | 9489 |
| Mean reliability | 85 | 66 |
| Average No. herds | 149 | 143 |
| Birth years | 1955–1990 | 1980–1991 |
| Average No. daughters | 324 | 326 |
| *Somatic cell scores* | | |
| No. of bulls | 2980 | 7965 |
| Mean reliability | 77 | 71 |
| Average No. herds | 114 | 140 |
| Birth years | 1958–1992 | 1980–1991 |
| Average No. daughters | 203 | 323 |

based on the production data files that date back to 1957, and hence bulls date back to 1955. The evaluation system for SCS was based on test day records from 1987, but a few old bulls managed to meet the daughter and herd restrictions for inclusion in this study. The HL and SCS bull proof files from the US were limited to bulls born from 1980 onwards regardless of the data included in their evaluation systems. A routine international comparison analysis may need to put restrictions on birthdates of bulls, but none were imposed on this study.

The mean reliabilities for longevity were higher in Canada than in the US although the average number of daughters and herds was the same and the heritability was lower in Canada. For US bulls, the maximum and standard deviation of number of herds per bull were much greater than in Canada which apparently contributed to the lower mean reliability of bulls in the US. There could also be differences between countries in the approximation methods used to compute reliabilities. Details on these approximations were not compared.

The model for the MACE methodology has been described by Schaeffer (1994) as

$$\mathrm{y}_{\boldsymbol{i}} = \mu_i 1 + Z_i Q \mathrm{g}_{\boldsymbol{i}} + Z_i \mathrm{s}_{\boldsymbol{i}} + e_i$$

where

$\mathbf{y}_{\boldsymbol{i}}$ is a vector of deregressed sire evaluations from country $i$

$\mu_i$ is the average evaluation for country $i$ for the bulls included in the analysis

$\mathbf{g}_{\boldsymbol{i}}$ is a vector of unknown parent genetic groups

$\mathbf{s}_{\boldsymbol{i}}$ is a vector of sire genetic values (either breeding values or transmitting abilities), $Var(\boldsymbol{s}_{\boldsymbol{i}}) = \boldsymbol{A}\sigma^2_{\mathrm{s}_i}$

and

$$\mathrm{Var}(\mathrm{s}_{\boldsymbol{i}}) = \mathrm{A}\sigma^2_{\mathrm{s}_{\boldsymbol{i}}}$$

and

$$\mathrm{Var}(e_i) = \mathrm{D}_{\boldsymbol{i}}\sigma^2_{e_i}$$

If

$$\mathbf{s}' = \left(\mathbf{s}'_1 \quad \mathbf{s}'_2 \quad \cdots \quad \mathrm{s}'_{\boldsymbol{m}}\right)$$

the vector of sire effects for $m$ countries, then

$$\mathrm{Var}(\mathbf{s}) = \mathbf{A} \otimes \mathbf{G}$$

where $\mathbf{G}$ is an $m$ by $m$ matrix of sire variances on the diagonals and sire covariances between countries on the off-diagonals. The matrix $\mathbf{D}_{\boldsymbol{i}}$ is diagonal and contains information related to the reliability of each bulls' evaluation within country $i$, such as number of effective progeny. Each country provides values for $\mathbf{s}_{\boldsymbol{i}}$, for $\mathbf{D}_{\boldsymbol{i}}$, and the assumed heritability of the trait.

Deregressed evaluations, $\mathbf{y}_{\boldsymbol{i}}$, were calculated separately for each country as described by Rozzi and Schaeffer (1996). At the same time sire and residual variances were estimated as described by Schaeffer (1994) assuming that heritability was constant. Genetic correlations between countries were estimated as given by Schaeffer (1994) which used the method of Calo et al. (1973). That is, the actual correlation between evaluations for sires with sons in both countries was divided by the expected correlation based on the reliabilities.

Genetic evaluations were computed using MACE methodology for all bulls in the data. Hence evaluations were obtained for all US and Canadian bulls expressed on each country's scale. That is, all bulls in the analysis of longevity, for example, had both an HL and a PL evaluation. From these evaluations, conversion formulas could be computed which would allow the conversion of evaluations on cows from one country to another, if necessary.

## 3. Results and discussion

The estimates of sire and residual variances for longevity and SCS for US and Canada are given in Table 2. The estimates were derived assuming the

Table 2
Estimates of sire and residual variances

| Trait | Canada | USA |
|---|---|---|
| *Longevity* | | |
| Sire variance | 0.067 | 2.293 |
| Residual variance | 8.880 | 105.608 |
| *Somatic cell scores* | | |
| Sire variance | 0.072 | 0.053 |
| Residual variance | 3.119 | 2.079 |

heritabilities from each country were the true values, and were subsequently utilized in MACE evaluation. HL and PL were obviously expressed on different scales while SCS was measured in the same manner in both countries. These variances and the estimated genetic correlations between US and Canada are critical to the MACE evaluations. Much effort has been directed towards the development of better methods to estimate these parameters. The estimated genetic correlation between HL and PL was 0.91, and between USCS and CSCS was 0.93. The genetic correlation estimates from this study were substantially higher than those of Powell et al. (1997). The difference between estimates is due to the difference of information going into each estimate. In Powell et al. (1997), only bulls with highly reliable evaluations in both US and Canada were included. In this study, the correlation was estimated from bulls with sons and grandsons in both countries, which gives more ties between countries. The higher correlation estimates mean that MACE can be used for both longevity and SCS for these two countries, which would be superior to the use of conversion formulas. A conversion formula implies that bulls rank identically in both countries. MACE allows and provides evaluations specific to each country, and bulls do not have to rank identically in each country.

The MACE evaluations for HL were correlated with the original Canadian HL evaluations at 0.971, while for the US the correlation was 0.999. For SCS, the correlation between CSCS and MACE evaluation on the Canadian scale was 0.981, while for the US the correlation was 0.997. There was virtually no difference between the original US evaluations for PL and USCS and the MACE evaluations on the US scale. Canadian MACE evaluations, however, seemed to benefit from the additional information coming from the US.

Looking at the MACE evaluations on the Canadian scale, in the top 100 bulls for CSCS, 90 were bulls of US origin, and for HL 82 were bulls of US origin. In the top 100 of the MACE evaluations on the US scale, 100 were of US origin for USCS and 97 were of US origin for PL. Thus, rankings in Canada and US were not equivalent, but were very similar, which reflects the high, but less than unity genetic correlations for these traits.

Conversion formulas were derived from all bulls in the MACE analyses and are given in Table 3. These formulas only apply to the July 1996 evaluations. From Powell et al. (1997) the formula to convert Canadian CSCS evaluations to the US scale was

$$\text{USCS} = 0.64 + (0.836 \times \text{CSCS})$$

which is very similar to the formula shown in Table 3 from this study.

Table 3
Formulas for converting evaluations expressed in USA (Canada) to an equivalent expression in Canada (USA)

| Trait | Intercept + $b \times$ evaluation |
|---|---|
| *Longevity* | |
| HL | $-0.019 + (0.148 \times \text{PL})$ |
| PL | $0.135 + (6.398 \times \text{HL})$ |
| *Somatic cell scores* | |
| CSCS | $-0.235 + (1.023 \times \text{USCS})$ |
| USCS | $0.676 + (0.830 \times \text{CSCS})$ |

## 4. Conclusions

MACE should be the preferred methodology for combining trait evaluations from different countries. This study demonstrated that MACE could be successfully applied to longevity and SCS. This work would need to be repeated because Canada changed to a multiple lactation, multiple trait, random regression test day model for production traits and somatic cell scores simultaneously, in February 1999. This is not a big difference from the previous fixed regression test day model for SCS alone, but heritability is slightly higher in the random regression test day model because of the positive correlations of SCS with production traits. Canada is also considering changes to evaluations of longevity (Boettcher et al., 1999).

If other countries were to be included with Canada and the US, then genetic correlations between them could be much lower depending on the definition of herd life and the method of analysis in each country. The correlations could also depend on how well reasons for disposal are recorded in each country. There should be fewer problems with SCS, but some countries record and evaluate actual mastitis inci-

dence and the correlations with SCS may be very much lower (Lund et al., 1999). Countries that record and evaluate both mastitis incidence and SCS should be able to provide information on the correlation between these two traits. Perhaps a multiple trait MACE procedure that includes both mastitis and SCS evaluations from one country, merged with either mastitis or SCS evaluations from other countries should be developed.

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