Impact of Second Country Proofs on Genetic Evaluations

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Introduction

Due to the increasing globalisation of the dairy cattle breeding industry, producers around the world have access to semen from proven bulls, which were not used as a young sire domestically. This evolution has strong advantages since it allows for increased rates of genetic progress while better controlling the level of inbreeding, compared to a within country testing and selection strategy alone.

Countries which combine an important domestic young sire testing program with significant levels of importation of semen from bulls first proven in another country must have genetic evaluation systems which account for the inconsistency in the randomness of the semen usage. Research in France (1) indicated that the existing national genetic evaluation system could not accurately account for the non-random use of imported semen for bulls first proven elsewhere. As a consequence the resulting EBV for bulls with such second country proofs in France have not been officially published nor included in the MACE international bull evaluations published by Interbull.

In Canada, semen from bulls in the United States, both young and proven sires, has been imported for decades while semen importation for bulls first proven in Europe started in the early 1990s. The main objective of this project was therefore to examine the accuracy of domestic evaluations for bulls first proven in Canada compared to bulls with second country proofs in Canada.

Mendelian Sampling

The estimated breeding value of an animal is equal to the parent average plus the mendelian sampling (MS). Thus MS is a deviation of the animal's proof from its parent average. All the main computations occurring within MACE (estimation of sire SD, correlations among countries and regressions) are based on MS.

A consolidated file, which includes all national evaluation protein proofs from February 2000 was analysed. Only data from cows with both parents known, daughters of bulls with at least 20 daughters in Canada, were included. An approximate mendelian sampling was computed for each cow as following:

$$MS = EBV - PA$$

where EBV was the 305 day proof of the cow for first lactation and PA was the 305 day first lactation parent average (½ EBV1 of the sire + ½ EBV1 of the dam). Mendelian sampling was computed for each cow and data were split in three groups based on sire information:

1. Daughters of any sire progeny tested in Canada that only has his first crop (**MS11**)
2. Daughters of any sire progeny tested in Canada that now has his second crop (**MS12**)
3. Daughters of any sire progeny tested abroad (**MS21**)

Results

Descriptive statistics for MS by group of cows are reported in the following table:

	MS11	MS12	MS21
N	257083	759592	84059
Mean	-0.1	0.01	0.1
SD	7.09	7.26	7.57
Min	-38.6	-36.72	-32.59
Max	33.17	43.43	38.57

Overall, the mean MS is close to zero for all 3 groups. More significant are the differences in SD of MS, indicating the highest variability in treatment of daughters from 2nd crop foreign bulls, and lowest in 1st crop bulls.

Results are expressed for the three bull groups in three ways: a) SD of MS by year of first calving (Figure 1); b) SD of MS by age of sire at daughter's first calving (Figure 2); and SD of MS by birth year of the sire (Figure 3). The first analysis allows a comparison of variability of MS among groups of same age daughters. The second analysis shows the variability of MS among groups of daughters at the same time of the sire's career. Finally, in the last analysis, variability of MS among groups of daughters is plotted over time.

All trends show that variability is consistently higher in 2nd crop daughters from foreign bulls and lower in 1st crop daughters, with larger differences for daughters born in the early '90s (Figure 1), suggesting a highest variability in treatment of daughters from bulls progeny tested abroad, and lowest in 1st crop daughters of bulls progeny tested in Canada. Figure 3 also demonstrates the overall decreased variability of MS over time, dropping 13% in the last 10 years.

Conclusions

This study has shown a larger variability of Mendelian sampling in daughters of bulls progeny tested abroad and a lower variability of Mendelian sampling in daughters of first crop bulls in Canada. A future study will investigate if heterogeneous variance of MS is present also in 2nd and 3rd lactation indexes of cows, and if it is possible to account for this heterogeneity within the Canadian Test Day Model.

A continuous decreasing trend of variability of MS over time has been observed. This trend may have an impact on national and international genetic evaluations.

References

1 Mattalia S., Boichard, D. & Mathevon, M. 1999. Effect of including within herd-year heterogeneity of variances on French genetic evaluation of foreign Holstein bulls. *Interbull Bulletin No. 22*, 136-140.

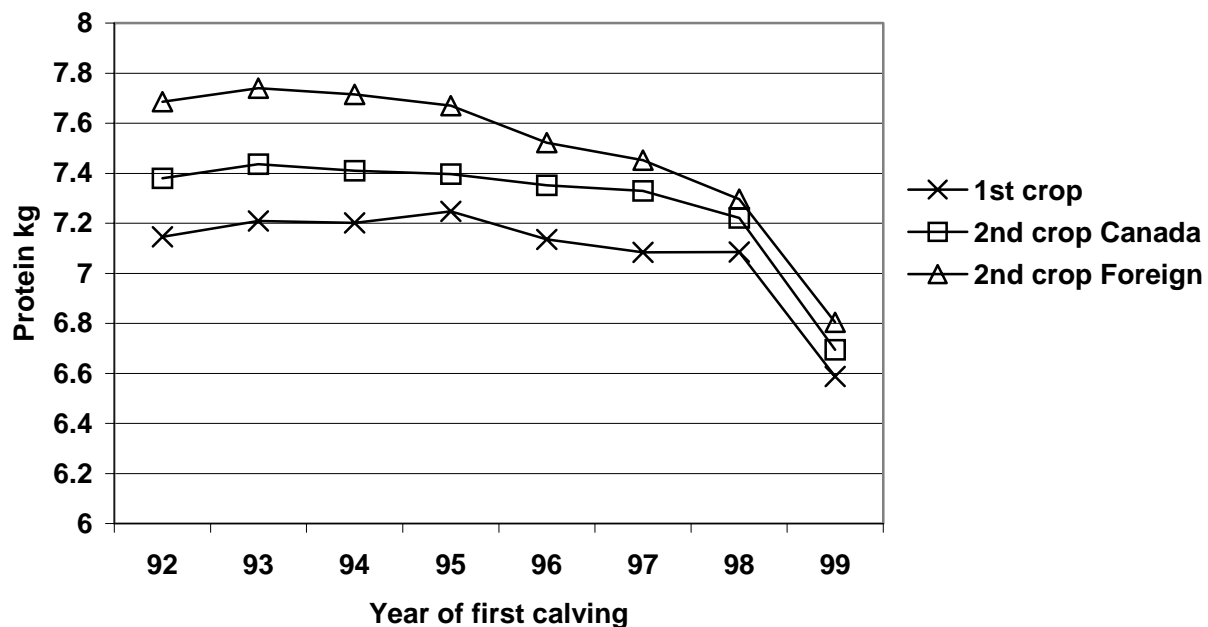## Figure 1. Trend of SD of Mendelian Sampling of cows by year of first calving

Figure 2. Trend of SD of Mendelian Sampling of cows by age of bull at daughter's first calving

Legend:
- 1st crop
- 2nd crop Canada
- 2nd crop Foreign

Y-axis: Protein kg
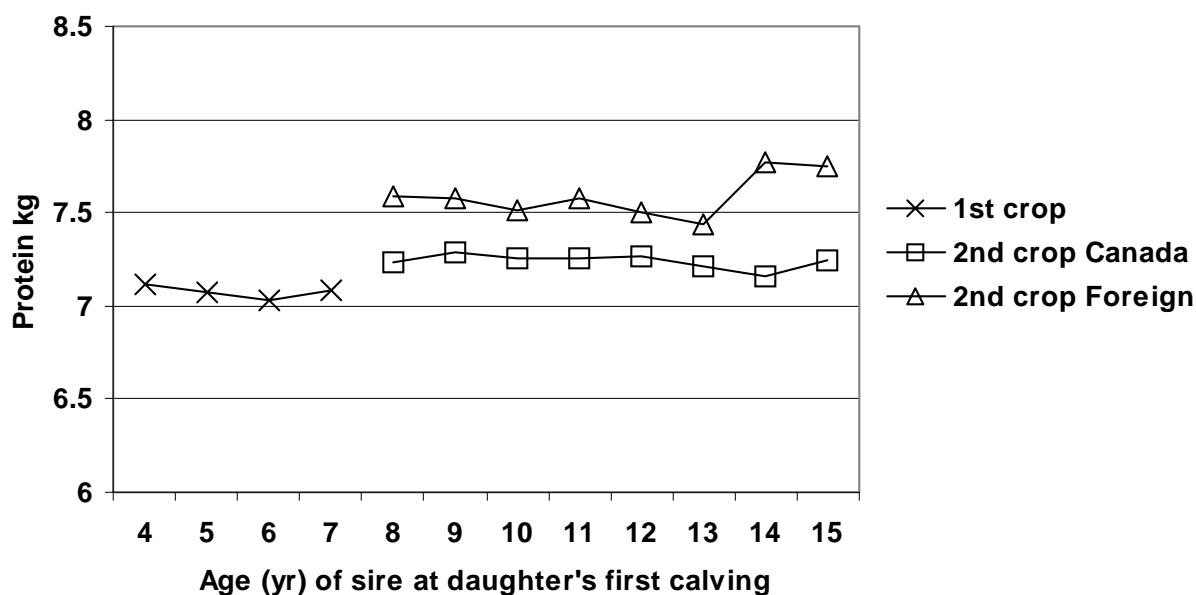X-axis: Age (yr) of sire at daughter's first calving

Figure 3. Trend of SD of mendelian sampling of cows by sire birth year

Legend:
- 1st crop
- 2nd crop Canada
- 2nd crop Foreign
- Overall

Y-axis: Protein kg
X-axis: Birth year of sire