55th Annual Meeting of the European Association for Animal Production
Bled, Slovenia September 5-9th, 2004

Commission on Animal Genetics, Session 30, paper HG5.4

Use of foreign EBVs in genetic evaluation : example of French EBVs conversion in the Canadian Swine Improvement Program

Laurence MAIGNEL[1], Pramod MATHUR[1], Isabelle DELAUNAY[2], Brian SULLIVAN[1]

[1]Canadian Centre for Swine Improvement, Central Experimental Farm, Building #54, Maple Drive
Ottawa, K1A 0C6 Ontario, CANADA
[2] Institut Technique du Porc, La Motte au Vicomte, BP35104
35651 LE RHEU Cedex, FRANCE

Abstract

International evaluations and comparisons have been widely used in cattle breeding schemes for many years. In swine breeding programs, the use of foreign genes is less common, and few examples of international comparisons exist. Imports of animals and semen, and more recently, embryo transfers, allowed the use of French Large White and Landrace genes in Canada. At the same time, A major issue was that the imported boars or semen didn't have Canadian breeding values before having progeny tested in Canada, which could take a long time, especially for sow productivity traits. To address this problem, an agreement was made between the French Pig Technical Institute and the Canadian Centre for Swine Improvement, to exchange EBVs for animals with evaluation results in both countries. Several methods, among those used for dairy cattle, were investigated in order to develop a suitable method to convert French EBVs into Canadian equivalents useful in the Canadian genetic evaluation system. The analysis included 136 boars with progeny in France and in Canada. Conversion formulas were computed regarding EBVs for number of piglets born per litter, age and backfat thickness at 100 kg. There is evidence for a growing interest in this kind of study, in order to improve the reliability and accuracy of swine genetic evaluations, in the context of growing international exchange of genetic material.

1. Introduction

Around the world, swine breeding involves many different pig breeds, but most of the programs use the same major breeds: Yorkshire, Large White and Landrace as dam lines, and Duroc, Hampshire and Piétrain as sire lines. These populations are selected in a great variety of genetic evaluation systems, differing on general structure, performance testing and breeding objectives, as shown by Goetz (2002). However, several classical traits such as litter size, growth rate and backfat thickness are measured and selected in all systems. In the last ten years, genetic links have significantly increased between populations of the same breed selected in different countries. Because of the relatively low efficiency of frozen semen in swine, the use of boars is limited in time and space, compared to what's used in cattle for instance. Nevertheless, more and more examples of genetic material exchanges, involving semen, live animals or embryos, are reported. The use of German Piétrain and French hyperprolific Large White and Landrace boars in many other countries are good examples. Despite this, genetic evaluation of swine seed stocks is usually performed within countries. However, in some cases pigs from different countries are evaluated simultaneously when high levels of connectedness exist, for instance pigs from Luxembourg and Spain evaluated in the French genetic evaluation program. But in most cases, foreign animals are assigned to genetic groups and do not receive EBV until they have progeny with records, by which time they are usually out of usage.

Because of competition issues both at domestic and international levels, collaborations are rarely created between national programs regarding genetic evaluation of swine. Nevertheless, breeders should consider ways to enlarge populations under selection, and be able to find in other countries animals that would better fit their breeding objectives. To make that possible, they should be able to compare foreign breeding values with their own animals' indices. This situation is even aggravated by the fact that breeding values from different countries usually look similar but are not comparable (Goetz, 2002).

This paper deals with an example of the use of foreign EBVs, more specifically French breeding values in the Canadian Swine Improvement Program. Different methods were investigated in order to provide accurate conversion formulas for litter size, age and backfat thickness at 100kg. The analysis was performed in 2000, 2001 and 2003, with more and more boars having progeny tested in France and in Canada.

2. Material and methods

2.1. Data available

In Canada, the use of French genes in the breeding nucleus started in the middle of the nineties, with imports of semen from Yorkshire (YO) and Landrace (LA) hyperprolific boars. Since then, imports have been continuous, and live animals have also been imported from France. In the last two years, several successful trials were carried out to implant embryos collected from French purebred sows into Canadian sows.

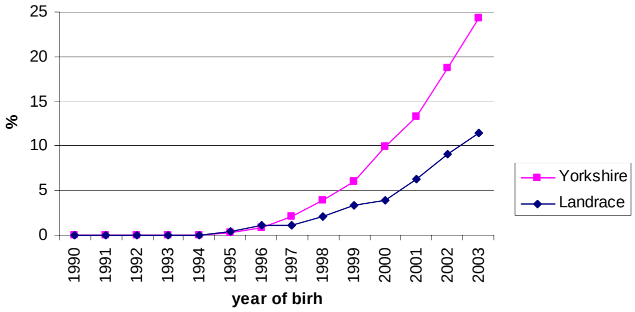

Figure 1. Evolution of the average % of French blood in Canadian tested pigs

Figure 1 shows the evolution of the average percentage of French blood in the Canadian Yorkshire and Landrace breeding populations, between 1990 and 2003.

During several years, no information was available on the imported French boars. They had Canadian EBVs computed only when their first progeny was tested, which could be at least 10 months after their first use in selection for production traits, and 18 months for reproduction traits. Moreover, since the price of swine semen is based on the boar EBVs, the semen of those imported boars was very cheap for a long time, which encouraged their use by Canadian breeders.

In 1999, an agreement was signed between the French Swine Breeders Association (Livres Généalogiques Porcins Collectifs) and the Canadian Centre for Swine Improvement (CCSI) to exchange EBVs for imported animals. CCSI started to work on methods to convert French EBVs into Canadian equivalents, in order to make them useful for Canadian breeders. The study involved EBVs for litter size (LS), age at 100kg (A100) and backfat thickness at 100kg (BF100), because these three traits are routinely measured and evaluated in both countries. Table 1 shows a summary of data available for the analysis in terms of numbers of boars involved and average numbers of progeny with records both in France and Canada. Many French boars imported as young animals and with progeny only in Canada were not included. Compared to similar studies performed in 2000 and 2001 by CCSI, the number of boars involved has increased a lot, which should improve the accuracy of the analysis. All the boars used in 2000 and 2001 analyses are also in 2003 data set.

Table 1. Animals used in the conversion analysis

Trait	Breed	Number of boars Analysis performed in			Average number of progeny tested (2003 study)	
		2000	2001	**2003**	France	Canada
Litter size (LS)	YO	19	38	**68**	284	81
	LA	5	22	**44**	183	88
Age at 100kg (A100)	YO	40	65	**78**	376	141
	LA	20	41	**58**	206	101
Backfat at 100kg (BFT100)	YO	40	65	**78**	376	141
	LA	20	41	**58**	206	101

2.2. Methods

Different methods to provide conversion formulas for breeding values were already studied and many of them have been widely detailed in the INTERBULL network. Depending on the data available, the traits involved and the amount of genetic links, several methods can be used in order to define suitable conversion formulas. Most of them are derived from Goddard (1985) and Wilmink et al (1986) methods. These methods and their variants were reviewed by Powell and Sieber (1992) and more recently by Jorjani and Fikse (2004) who also performed a comparison with multiple across country evaluation (MACE) methodology.

The method developed by Goddard (1985) has several advantages: it takes into account mean and variance differences between countries, sire×country interactions, and provides a method for calculating reliability of converted values. The method suggested by Wilmimk (1986) gives three different methods to derive conversion formulas, in a situation where the genetic correlation between traits is supposed to be equal to unity.

Two simple models using single-trait analysis are presented in the following sections, derived from Wilmink and Goddard methods.

2.2.1. Model 1

The conversion formula was: Canadian EBV = French EBV + μ

It is assumed a 1 unit increase in Canadian breeding value for each 1 unit increase in French breeding value, and the only thing to be estimated is the difference in genetic mean between both countries.

The model used was :

$\mathbf{Y} = \mu + \mathbf{e}$

where **Y** is the observed difference between the Canadian and French EBV, μ is the conversion factor, and **e** is a random residual with heterogeneous variance.

The variance of each residual was : $R_{CA}^2.\sigma_a^2(1 - R_{FR}^2.R_{CA}^2)$

where R_{FR}^2 is the repeatability of the French EBV, R_{CA}^2 is the repeatability of the Canadian EBV,and σ_a^2 is the genetic variance of the trait.

Generalized least-squares estimates of μ and its standard error were computed.

With this model, the repeatability of each converted EBV is given by :

$$\mathrm{convR}^2 = \mathrm{R}^2_{\mathrm{FR}} - \mathrm{SE}^2/\sigma^2_{\mathrm{a}}$$

where R^2_{FR} is the repeatability of the French EBV, SE^2 is the square of the standard error of the estimate of μ, and σ^2_a is the genetic variance of the trait

2.2.2. Model 2

This model does not assume that the French and Canadian scales are equal, and estimates the increase in Canadian breeding values associated with each unit of increase in French breeding values.The model fitted was :

$$\mathbf{C = \mu + b.F + e}$$

where C is the deregressed Canadian EBV : $C = (EBV - \bar{x}) / R^2_{CA}$, $\bar{x}$ is the sample mean, F is the French EBV, b is a scale conversion factor, μ is an intercept, and e is a random residual with heterogeneous variance equal to $\sigma^2_a (1 - R^2_{FR}.R^2_{CA}) / R^2_{CA}$, where σ^2_a is the genetic variance of the trait specific to Canada.

The conversion formula is : $Canadian\ EBV = \bar{x} + \mu + b.(French\ EBV)$

With this model, the repeatability of each converted EBV is then given by :

$$\mathrm{convR}^2 = R^2_{FR} - \frac{1}{\sigma^2_a}[c_{11} + (2c_{12} \times F) + (c_{22} \times F^2)]$$

where $\begin{pmatrix} c_{11} & c_{12} \\ c_{12} & c_{22} \end{pmatrix} = V\begin{pmatrix} \hat{\mu} \\ \hat{b} \end{pmatrix}$, ie the cij are the sampling (co)variances of the estimates of μ and b.

3. Results and Discussion

3.1. General statistics

Table 2 shows means and standard deviations of EBVs for each trait studied in Yorkshire and Landrace breeds.

Table 2. Statistics on within-country EBVs for boars used in the conversion analysis

Trait	Breed	Number of boars	EBV mean		Standard deviation of EBV	
			France	Canada	France	Canada
Litter size (LS)	YO	68	-0.30	+1.46	0.85	0.81
	LA	44	-0.21	+0.78	0.88	0.62
Age at 100kg (A100)	YO	78	+0.20	-0.82	3.65	5.32
	LA	58	-2.54	+0.47	4.60	4.89
Backfat at 100kg (BF100)	YO	78	+0.08	+0.58	0.68	1.09
	LA	58	-0.36	+2.18	0.65	1.35

There are differences in EBV means and standard deviations between the two countries. Several factors can explain those differences, for instance differences in trait definition or adjustments, differences in genetic parameters, in models used or in base-adjustment methods for EBVs, but also differences in genetic merit between both countries, and different levels of EBV accuracy for the boars in the sample. Figure 2 shows the distribution of French and Canadian EBVs for litter size, age and backfat in both breeds. These graphs show a relationship between both EBVs for each breed and trait, but there appears to be quite a variation. As a first approach, it is important to notice that all the points don't have the same importance in the graph, since they were calculated on a variable amount of data. Thus, the repeatability of each EBV in each country should be taken into account in the analysis. To address that, table 3 shows across-country correlations adjusted for repeatabilities.

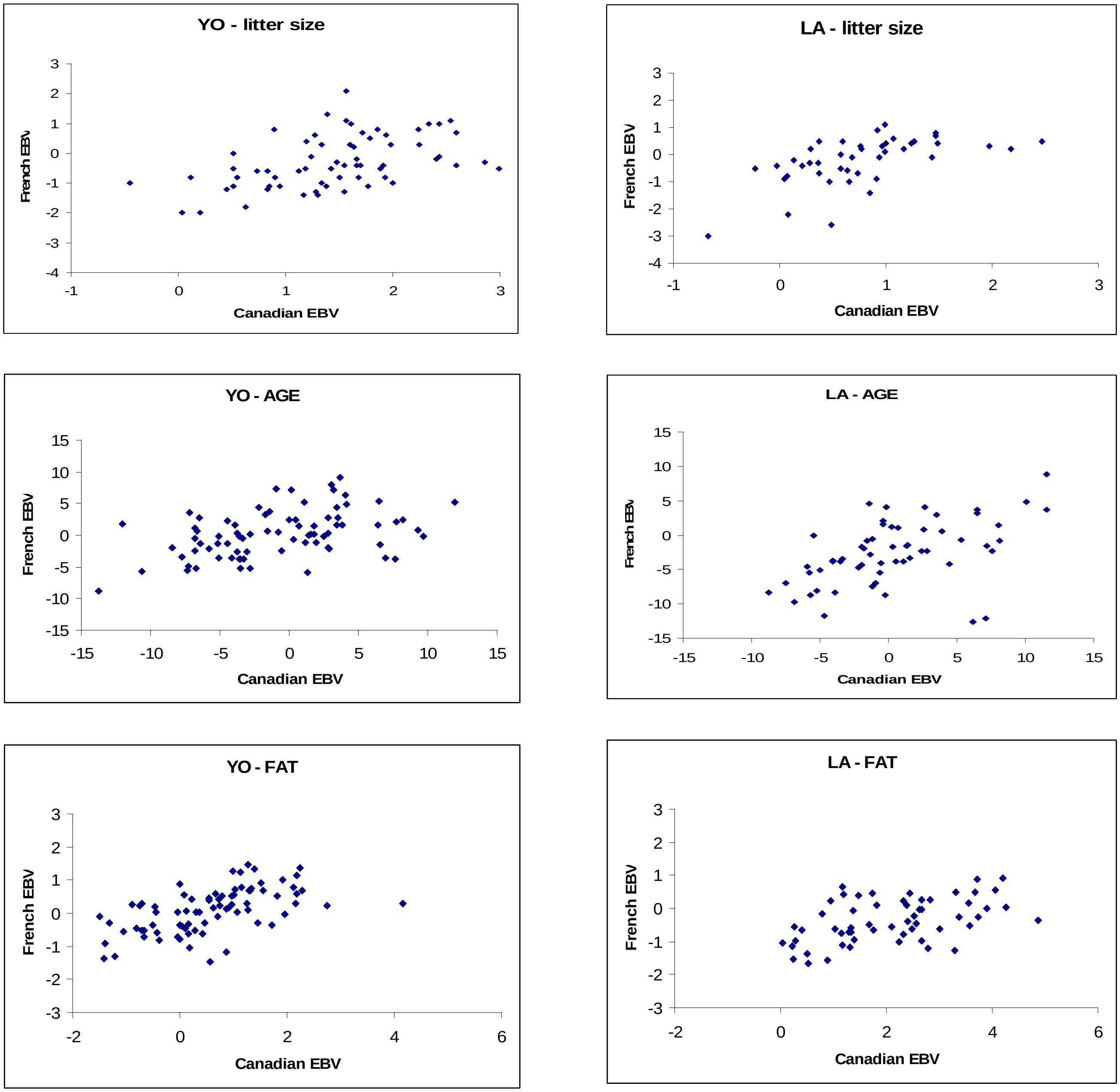

Figure 2. Distribution of French and Canadian EBVs for boars with evaluation results in both countries

Across-countries correlations presented in table 3 were computed using the following formula :

$$E(r) = \frac{r_g \sum_{i=1}^{N} (R_{i,FR}^2 . R_{i,CA}^2)}{\sqrt{\sum_{i=1}^{N} R_{i,FR}^2 \sum_{i=1}^{N} R_{i,CA}^2}} \qquad \text{(Calo et al, 1973)}$$

where r_g is the genetic correlation between the traits evaluated, assumed equal to 1 in this case.

In this approach, if the repeatability is the same within and across countries, and the genetic correlation is 1, the expected correlation is equal to the repeatability of the EBV.

Table 3. Across country correlations for LS, A100 and BF100 EBVs

Trait	Breed	Number of boars	Correlation between French and Canadian EBVs
Litter size (LS)	YO	68	0.41
	LA	44	0.41
Age at 100kg (A100)	YO	78	0.53
	LA	58	0.51
Backfat at 100kg (BF100)	YO	78	0.65
	LA	58	0.64

Between-countries correlations range from 0.41 to 0.65, but with the relatively low number of boars involved, the wide range of repeatabilities in the data set available, and the possibility of chance effect in the sampling of boars, it is difficult to draw any conclusion from these figures.

3.2. Conversion analysis using Model 1

Table 4 shows the conversion factor estimates, computed in 2000, 2001 and 2003, using model 1.
The conversion formula is : Canadian EBV = French EBV + conversion factor.

Table 4. Results of the conversion analysis using model 1

Trait	Breed	Conversion factor ± std error		
		2000	2001	2003
Litter size (LS)	YO	+1.1 ± 0.08	+1.4 ± 0.05	**+1.6 ± 0.05**
	LA	+1.2 ± 0.14	+0.7 ± 0.07	**+1.2 ± 0.06**
Age at 100kg (A100)	YO	-3.6 ± 0.5	-2.2 ± 0.5	**-0.8 ± 0.4**
	LA	+4.9 ± 0.7	+2.5 ± 0.5	**+3.6 ± 0.5**
Backfat at 100kg (BF100)	YO	+0.52 ± 0.13	+0.47 ± 0.10	**+0.47 ± 0.08**
	LA	+1.37 ± 0.18	+1.82 ± 0.11	**+2.46 ± 0.10**

With the increasing number of boars used in the analysis, the standard errors of estimates tend to be lower in the most recent analysis. Except for BF100 in Yorkshire, the new conversion factors are quite different from those estimated in 2001, but also more accurate. The changes are found to be consistent with genetic trends in both countries, faster on LS in France compared to Canada, very similar on BF100 and a bit lower on A100.

3.3. Conversion analysis using Model 2

Conversion factor estimates, computed in 2000, 2001 and 2003, using model 2, are shown in Table 5. The conversion formula is Canadian EBV = a + b×French EBV

Table 5. Results of the conversion analysis using model 2

Trait	Breed	Analysis	a (Intercept)	b (Slope)
Litter size (LS)	YO	2000	+1.2 ± 0.4	2.02 ± 0.65
		2001	+1.4 ± 0.3	1.69 ± 0.37
		2003	**+1.9 ± 0.3**	**+1.34 ± 0.32**
	LA	2000	+0.9 ± 0.6	1.30 ± 1.38
		2001	+0.9 ± 0.3	0.88 ± 0.31
		2003	**+0.9 ± 0.2**	**+1.39 ± 0.24**
Age at 100kg (A100)	YO	2000	-2.5 ± 1.4	2.0 ± 0.4
		2001	-1.3 ± 1.0	1.6 ± 0.3
		2003	**-1.2 ± 0.9**	**1.3 ± 0.3**
	LA	2000	+7.0 ± 3.1	2.5 ± 0.9
		2001	+1.7 ± 1.0	1.1 ± 0.2
		2003	**+4.1 ± 1.0**	**1.1 ± 0.2**
Backfat at 100kg (BF100)	YO	2000	+0.4 ± 0.2	1.58 ± 0.23
		2001	+0.5 ± 0.1	1.60 ± 0.11
		2003	**+0.5 ± 0.1**	**1.07 ± 0.15**
	LA	2000	+1.5 ± 0.4	0.28 ± 0.58
		2001	+1.4 ± 0.1	1.03 ± 0.16
		2003	**+2.6 ± 0.2**	**1.23 ± 0.26**

Intercept estimates computed in 2003 are either equally or more accurate than what was computed in 2000 and 2001, thanks to more information used. Some values, for example for BF100 and A100 in Landrace, are found to be quite different from previous estimates, which is consistent with results from model 1. Estimates of the slope for litter size conversion are more accurate than in previous analyses in both breeds.

The regression slope is found to be non-significantly different from 1, except for LS where it is very close to 1 (+1.34 ± 0.32 for YO and +1.39 ± 0.24 for LA**)**. Thus, it was decided to use the results obtained from model 1 to provide conversion formulas, till the next estimation is available.

In addition to the practical usefulness of formulas for breeders, foreign breeding values can also be integrated into Canadian genetic evaluations, as an extension of the genetic groups model, using the following steps :

- assign all foreign boars to the same group
- adjust the foreign EBV to the same evaluation base as Canadian EBV
- “deregress” the base-adjusted foreign EBV using foreign repeatability
- add artificial progeny records for each foreign boar, where each record is equal to the deregressed EBV and the number of records reflects the foreign repeatability.
- run a conventional animal model evaluation with 1 genetic group for all foreign animals, and one or more for Canadian unknown parents
- check the difference between both group solutions, which should be negligible if the foreign EBV was correctly adjusted.

4. Conclusions

Despite the increasing amount of French genes in the Canadian populations, this analysis was based on a limited amount of boars, having progeny tested both in France and Canada. It provided formulas to convert French EBVs into Canadian equivalents. Thus, as soon as an animal is registered at the Canadian Livestock Records Corporation, if its French EBVs are available, they can be converted into Canadian equivalents. These provisional values are made available to breeders, till their first progeny is tested in Canada. Converted repeatabilities are also provided.

The large amount of genetic links existing between French and Canadian purebred populations allowed to reach a reasonable level of accuracy in conversion formulas. This situation is very suitable for a conversion analysis. Nevertheless, regular updates of conversion formulas are required, in order to increase accuracy thanks to new data available, but also to take into account genetic trends and possible changes in evaluation programs. The use of converted breeding values has significantly increased the efficiency of the Canadian Swine Improvement Program in the last years.

Further steps to achieve will be to extend this work to other traits, maybe testing other conversion methods, and to integrate converted values into Canadian genetic evaluations. This kind of study could also give the opportunity to develop joint genetic evaluations and to work on possible genotype×environment interactions existing in pigs. With the current increase of gene exchanges and the growing development of frozen semen in swine, international genetic evaluations could become one of the future challenges in swine breeding.

References

- Calo, L. L., McDowell, R. E., VanVleck, L. D., and Miller,. P. D. 1973. Genetic aspects of beef production among Holstein-Friesians pedigree selected for milk production. J. Anim. Sci. 37:676–682.
- Canadian Centre for Swine Improvement, 2000. Conversion of French EBV to Canadian EBV : summary, 9pp.
- Goddard, M. 1985. A method of comparing sires evaluated in different countries. Livest. Prod. Sci. 13:321.
- Goetz, K. U., 2002. Status of performance testing and genetic evaluation in the participating countries. 3th International Workshop on Genetic Evaluation of Pigs, 17-21 April 2002, Nitra, Slovakia.
- Jorjani, H., Fikse, F., 2004. Conversion equations revisited : single- and multiple-trait conversion equations and comparison with simple-MACE. Interbull Bulletin No 32, 2004. p25-30.
- Powell, R. L.,1988. Comparison of procedures to convert sire evaluations between countries. J. Dairy Sci. 71:1609.
- Powell, R. L., Sieber M., 1992. Direct and indirect conversion of bull evaluation for yield traits between countries. J. Dairy Sci. 75:11-38.
- Schaeffer R. L., 1994. Multiple-Country Comparison of Dairy Sires. J. Dairy Sci. 77:2671.
- Wilmink, J. B. M., Mcijaing A., and Engel B., 1986. Conversion of breeding values for milk from foreign populations. Livest. Prod. Sci. 14223.