

Use of full sibs families to estimate the 'a' coefficients of conversion formulas between countries*

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INTRODUCTION

Genetical links between countries are needed to estimate the conversion factors used to predict the value of an animal in an importing country, given its estimated breeding value in the exporting country. Direct connections due to bulls evaluated both in the importing and exporting countries are generally used. These bulls are usually proven in the exporting country and have some recorded daughters in the importing country, where they are not officially progeny tested with a preplanned design. Some problems may arise with such connections, particularly if the daughters issued from imported semen receive preferential treatments. Moreover, estimates of the 'a' and 'b' factors against the gene flow may be biased by selection and are not recommended (BANOS, 1993). A better connection is obtained when bulls are simultaneously progeny tested in both countries. Unfortunately, too few bulls have been proven in more than one country to provide reliable coefficients of conversion.

As the European countries have widely used North American bull sires and bull dams, families of full sibs are now available, with at least two sons progeny tested in two different countries in each family. These connections can be used to estimate the 'a' coefficients between both countries. This paper describes the method through the example of the conversions between France and USA.

I MATERIALS AND METHODS

Data were issued from the French proofs file of April 1993 (French rolling bases 1992) and from the US proofs file of January 1993 in Holstein breed. Daughter Yield Deviations, identification number of bull, sire and dam were necessary.

Sire and dam of full sibs bulls were North American (US or Canadian). In each family, there were at least one son progeny tested in France and another one in the USA. 163 such families were detected, including 239 bulls in France and 231 bulls in USA. These bulls had at least 35 recorded daughters in 20 herds. When the sample was restricted to the bulls born since 1981, there were 130 families with 199 bulls progeny tested in France and 190 in the USA (each family may have more than one son in each country). In this case, it was noticed that the youngest bull of one family was born at most 3 years after the oldest. This fact shows that the French bulls have been chosen before their US full sibs received their first proof.

As the expected genetic value is the same for all the bulls within family, the 'a' coefficients can be estimated comparing the DYD of the bulls progeny tested in USA to the DYD of the bulls progeny tested in France.

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Theoretical 'b' coefficients were estimated before the full sibs analysis, assuming a genetic correlation of 0.9 between countries. For that purpose, the sire standard deviation in each country was estimated as the square root of the product of the standard deviations of sire estimated transmitting ability and DYD (see BANOS, 1992). Standard deviations were calculated within year of birth and then pooled across years. In each country, the whole set of progeny tested bulls, born from 1981 to 1987, having a US sire and a US dam, and having at least 35 recorded daughters in at least 20 herds was considered.

The full sibs analysis was done twice, considering firstly USA and secondly France as the exporting country. In each case, the Daughter Yield Deviations (DYD) of the bulls progeny tested in the exporting country were multiplied by the 'b' coefficient of the conversions from the exporting country to the importing country, in order to adjust these DYD to the variability of the importing country.

Gene effects were assumed to be strictly additive. The adjusted DYD were analysed using the following model:

$$y = X_1 f + X_2 c + e$$

with y = vector of adjusted DYD of the full sibs
 f = vector of fixed family effects
 c = vector of fixed effects of the country of proof (USA or France)
 e = random vector of residual effects with mean equal to zero and variance-covariance matrix $I\sigma_e^2$
 X_1, X_2 = design matrices

Differences between country effects gave an estimation of the 'a' coefficients, when proofs are expressed in ETA in both countries.

II RESULTS AND DISCUSSION

The table 1 gives the estimated sire standard deviations for French and US bulls.

Table 1: Estimated sire standard deviations*

	Nr of bulls	Milk yield	Fat yield	Prot. yield	Fat content	Prot. content
France	1624	316	12.2	8.6	1.66	0.69
USA	5182	629	22.2	17.2	0.109	0.056

* Note: - French and US proofs are expressed in ETA
 - French yields are expressed in kg, US yields in lbs
 - French contents are expressed in ‰, US contents in %

The table 2 gives the differences between country effects and their standard errors obtained with the full sibs comparison. These standard errors range from 6% to 10% of the DYD standard deviation of the importing country. They are lower than the minimum standard error of 'a' which

would be obtained by a regression and with a sample of bulls corresponding to the minimum requirements of INTERBULL. (INTERBULL,1990).

Table 2: Differences between country effects (USA-->France and France--> USA) estimated by the full sibs comparison.* - French male rolling bases 1992

	Milk yield	Fat yield	Prot. yield	Fat content	Prot. content
USA-->France	-134.5 (32)	-10.95 (1.09)	-4.55 (0.9)	-0.75 (1.15)	0.0 (0.06)
France-->USA (unofficial)	+405 (63)	+24.9 (2.1)	+12.9 (1.8)	+0.051 (0.0098)	-0.001 (0.0048)

* Note: - French and US proofs are expressed in ETA
 - French yields are expressed in kg, US yields in lbs
 - French contents are expressed in ‰, US contents in %
 - Standard errors are in parentheses

Finally, the 'a' and 'b' coefficients used to convert US proofs into French proofs were multiplied by 2 to express the converted proofs in EBV instead of ETA. Moreover, as the French proofs are now published with the male rolling bases 1993, the 'a' coefficients were updated by subtracting the mean decrease of the French proofs produced by the change of bases. In the other direction, as the proofs of the exporting country are expressed in EBV, the 'b' coefficients were divided by 2. The 'a' coefficients were updated by adding the mean decrease of the French proofs produced by the change of bases multiplied by 'b'.

The table 3 gives the 'a' and 'b' coefficients of the conversion formulas (French male rolling bases 1993). Only the conversion factors from USA to France are official.

Table 3: 'a' and 'b' coefficients obtained by the full sibs method (French rolling bases 1993)

		Milk yield	Fat yield	Prot. yield	Fat content	Prot. content
USA --> France (official)	b	0.90	0.99	0.90	27.5	22.4
	a	-399	-28.9	-13.1	-1.7	-0.1
France --> USA (unofficial)	b	0.90	0.82	0.90	0.0294	0.0362
	a	+522	+30.6	+16.5	+0.057	+0.003

Comparison with SCHAEFFER's method

SCHAEFFER (1985) proposed to analyse the DYD with a model which takes into account an international genetic value of each bull and a country effect, using all the male relationships between bulls. In the full sibs method, the family effects take the place of the genetic values of the bulls and of the relationships between bulls.

The sample of bulls used in the full sibs comparison is restricted to full sibs and does not account for the whole set of DYD of bulls progeny tested by each country as does Schaeffer's method. The full sibs comparison can only be used when there are enough families having at least one full sib progeny tested in the importing country and one in the exporting country. With the use

method. The full sibs comparison can only be used when there are enough families having at least one full sib progeny tested in the importing country and one in the exporting country. With the use of embryo transfer, this condition is now met in many cases. On the other hand, SCHAEFFER's method takes only the male relationships into account and assumes that dams of bulls progeny tested in each country have the same genetic level within MGS. This hypothesis may not be fulfilled when the selection objective is not the same between countries. This assumption is no more necessary with a full sibs comparison, which is the main advantage of this method.

SCHAEFFER's method provides a simultaneous estimation of the 'a' coefficients used in both directions and for more than two countries. A simultaneous estimation of the 'a' coefficients for more than two countries can be also obtained by the full sibs method, if the genetic correlation between these countries is assumed to be equal to 1 and if there are enough families of full sibs to link all these countries. Then, DYD should be standardized by the sire standard deviations of each country.

CONCLUSION

When there are enough full sibs progeny tested in two different countries, the full sibs method may provide useful information, particularly coherent estimations of the 'a' coefficients of the conversion formulas used in both directions. There is no assumption on the genetic level of the dams. Moreover, only the progeny tested bulls are considered.

Nevertheless, this method does not use the whole set of DYD estimated in each country. It only can be applied when there are enough full sibs families to link the different countries.

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