

# Interbeef, the story so far.

Eric VENOT, Research Engineer, INRA-SGQA (UR337), F-78352 Jouy-en-Josas, FRANCE  
[eric.venot@jouy.inra.fr](mailto:eric.venot@jouy.inra.fr)

Thanks to the increasing use of artificial insemination these last four decades, beef cattle breeds have been developing outside their historical breed cradles. Breeders can now make their choice in an international panel and are seeking to compare domestic to foreign breeding animals. However, genetic evaluation of seed stock is usually performed within country. Genetic links between countries created through these exchanges can be used to compare seed stock between countries.

## **I. Several common genetic evaluations already in place**

Since the 90's, several countries have developed common genetic evaluation for their beef cattle breeds. This is usually made of a leader country with a large population and associated countries with smaller populations. These countries generally use the same rules for performance recording and have similar environment conditions and farming systems. Examples can be found in Oceania (Australia and New Zealand) with Breedplan (Reverter et al., 2002), North America (United States and Canada) (Benyscheck, 1998; Bullock et al., 2003), and in Europe (France, Italy and Luxemburg) with the IBOVAL system (Laloë and Menissier, 1990; Menissier et al 1996). These joint genetic evaluations suppose nevertheless no interaction between Genotype and Country, which means that all breeding animals are considered as coming from the same country and the animals ranking is the same in each participating country.

This simplifying assumption should be verified by preliminary studies: several works have shown for instance that weaning weights can be evaluated as one character for Angus Breed in Australia and New Zealand (Meyer, 1995), for Hereford breed in USA, Canada and Uruguay (de Mattos et al., 2000 and Lee and Bertrand, 2002) or for Charolais breed in Australia, New Zealand and USA (Donoghue, 2004) (if heteroscedasticity between countries is taking into account in the model). On the other hand, Genotype by Country interaction has been detected for these countries for birth weight or after weaning growth. In this case, genetic evaluation should be run with more sophisticated models.

## **II- The European project for international BEef EVALuation (EUBEEVAL project)**

### **A- A collaborative project**

In 1999, Irish Cattle Breeding Federation (ICBF) in association with the Meat Livestock Commission (MLC) from the United Kingdom (UK) and the Institut de l'Élevage (IE) from France took the initiative in establishing a research project with a double objective:

- 1) develop prototype software to compute breeding values with data from different European countries taking into account the heterogeneity of production systems,  
and
- 2) study the best way for comparing breeding values obtained in different systems.

The first item was developed by the Institut National de la Recherche Agronomique team (INRA) from France on the Charolais breed and the second by the Animal Genetics and Breeding Unit (AGBU) based at the University of New England in Armidale (Australia) on

the Limousin breed. These were funded by the Irish, French and UK participants in the collaboration.

## **B- Scientific results**

### **1- It is feasible!**

At the term of the project in 2004, INRA showed:

- the feasibility of a joint genetic evaluation for beef cattle taking into account this heterogeneity,
- the heterogeneity of the environment effects on weaning weight,
- the potential benefit for the selection intensity.

This preliminary study provided a specific ranking of the French, UK and Irish bulls in each country for Charolais pure bred weaning weights. But it also pointed out data quality problems: better genetic links were needed to compute more reliable genetic parameters in the following studies (see practical results).

### **2- The model of choice**

The AGBU team, with the support of Florence Phocas from INRA, compared different models to apply on beef cattle data:

- a single trait animal model with heterogeneous variances between countries,
- a sire model on deregressed EBVs such as for the international dairy cattle genetic evaluation of Interbull,
- an animal model using raw data and accounting for across country interactions.

The last one was the model of choice to compare beef cattle seed stock from different countries (Phocas and Donoghue, 2004, Phocas *et al.*, 2004). This model presented more precisely below can take into account each country's farming specificities through different fixed effects models but also the different variances heterogeneities and genetic correlations between countries.

## **C- Practical results**

### **1- Cross reference file: key point to trace back the genetic links between the countries**

Associated with these scientific results, this study underlined the necessity of a clean and complete cross-reference table which establish the correspondence between a unique international identification number, a national number (both at the Interbull format) and a national number (at the national format) for every exchanged animals (Quintanilla *et al.*, 2002 ; Renand 2004): this file is the key point of the joint genetic evaluation and allows the organism responsible for the international genetic evaluation to trace back all the genetic links between the countries. The accuracy of the genetic evaluation depends dramatically on the quality of the genetic links between the countries. Therefore, a country importing an animal from another country should keep the original identification number of this animal in its database.

Following this idea, international identifications of many Charolais and Limousin animals that had not been previously identified as coming from a foreign country were corrected in the Irish and UK databases (worked out by Antunes (2004a, 2004b), Pabiou and Journaux thereafter): the quality of the cross reference table between Ireland, United Kingdom and France have been considerably improved for the two breeds. Based on these new links, the

INRA team computed a new set of genetic parameters between France and Ireland for Limousin breed (Venot, 2005a 2005b). Estimation of the genetic parameters between France and UK is presented in details in the last part of this paper (Part IV).

## **2- A software prototype**

To perform the joint genetic evaluation, IE and INRA have developed a software prototype adapted to the beef cattle data: lots of traits considered for beef cattle are indeed influenced by maternal effects. This software can run multi-traits models with direct and maternal genetic effects and also permanent maternal effects, with specific fixed effects models for each trait.

## **3- Standardised exchanged files format**

Another practical outcome of these different works is the standardisation of the files exchanges (performances, pedigree or fixed effects files). Files formats were tested and further improved during the following studies in collaboration between ICBF, IE and INRA, leading to a general guideline for international exchanges of beef cattle data.

## **III- The development of a new Interbull service: Interbeef**

These results were presented at the ICAR general assembly in 2004. After discussions in the ICAR board and Interbull Steering committee, a task force was to assess the potential need for an international beef genetic evaluation service to be offered by Interbull. The result of this general survey demonstrated a clear interest in beef international genetic evaluations: for each major international breed (Angus, Charolais and Limousin), Schild et al (2005) identified about 20 countries with beef performance recording. For each breed, 65 to 75% of the countries expressed an interest in getting a service from Interbull and about half of them, including countries with the biggest recorded populations, agreed to a financial contribution to the cost of such a service. This new service would consist in managing the cross-reference file (through a possible interactive internet interface) and computing an international joint genetic evaluation.

In November 2005, ICAR decided to proceed with the next step in establishing this new service, called **Interbeef**. Interbull estimated that the investment required is one man-year of work for the Uppsala center spread on 3 years. Ireland, France, United Kingdom, Denmark, Norway, Sweden, Finland, ICAR and Interbull have agreed to contribute to the initial investment required to establish the service at the Interbull Centre.

#### **IV- Estimation of genetic parameters between France and UK for pure bred Limousin weaning weight (Preliminary results).**

Following the launch of the BASCO (Beef and Sheep Company) database system and the uploading of the historical data from the MLC's database in mid 2006, adjusted weaning weights of the Limousin pure bred animals recorded in UK have been made available to prepare a joint genetic evaluation for the Limousin breed between UK and France.

The preliminary analysis before implementing the joint genetic evaluation consists in estimating the genetic parameters within countries (heritabilities) and between countries (genetic correlations) in order to check the existence of Genotype by Country interaction.

##### **A- Data description**

This study considered adjusted weaning weights (AWW) of pure bred Limousin animals born between 1986 and 2005 in France and in UK. Weaning weight was adjusted to 200 days in UK and 210 days in France. A total of 81706 UK adjusted weaning weights associated with their corresponding fixed effects (contemporary group, sex, month of birth, dam age at calving) were provided for this study: 5588 of them corresponded to twins or embryo transfers and could not be included in the analysis. The same occurred for 27025 AWW that didn't have herd number and 20748 animals that didn't have enough pedigree information or with less than 2 animals per contemporary group. Eventually, 28345 UK AWW remained, associated with a complete set of pedigree information.

A description of the data structure is given in the following table 1.

**Table 1.** Descriptive statistics of the two Limousin populations.

	United Kingdom	France
Number of adjusted weaning weights (AWW)*	28345	1428050
Average AWW * (kg) (std)	260 (39)	255 (38)
AWW * (kg) (std) for males	278 (42)	268 (39)
AWW * (kg) (std) for females	249 (34)	242 (32)
Male proportion	37 %	49 %
Number of herds	1189	5260
Median, min and max number of:		
birth campaign per herd	2 [1;20]	9 [1;20]
AWW per herd	4 [2;684]	126 [1;3270]
AWW per herd-year of birth	3 [1;91]	22 [1;245]
Average number of calves per dam (std)	2 (1,3)	3.6 (2.7)

\* weaning weight is adjusted at 210 days for France, and 200 days for UK.

Although adjusted ten days later, French AWW are lighter than the UK ones. The low proportion of male in the UK data can be explained by the data selection with regards to the herd and pedigree information. The herd size and the number of birth campaign per herd are also reduced compared to the French ones, leading to a small number of performances per herd-birth campaign. The small averaged number of calves per dam in UK brings less information for maternal genetic parameters estimation compared to France.

## B- Connection between France and UK.

Connectedness between countries is a critical point for a reliable international evaluation. The quality of the joint genetic evaluation depends greatly on the genetic links between countries to estimate potential difference between genetic levels.

In practice, direct connections between countries are established mainly through bulls siring calves in both countries. Table 2 describes the different kinds of sires that have progenies in France and/or in UK: with a total of 430 common sires (table 2), the connectedness level between France and UK appears to be satisfying.

**Table 2.** Description of the different kinds of sires with offspring in France or/and in UK

Sires with offspring as:	in FRANCE	in UK	in France and UK
Sires	12018	1030	38
Maternal grand sires	2249	837	330
Sires and Maternal grand sires	24253	1382	62
Total	38520	3249	430

## C- Model of analysis.

As presented previously, the model of choice is equivalent to a multiple trait model (AMACI) which decomposed the performances  $y$  into specific fixed effects for each country ( $b$ ), direct ( $u_d$ ) and maternal ( $u_m$ ) genetic effects, and also permanent environment provided by the dam ( $e_m$ ), as follows:

$$y = Xb + Z_d u_d + Z_m u_m + W_m e_m + e$$

It enables to consider heterogeneous genetic, maternal permanent environment and residual variances, along with genetic correlations between countries. The complete set of parameters can be described for two countries as:

$$\begin{aligned} \text{Var}(e) &= \begin{bmatrix} e_1 & 0 \\ 0 & e_2 \end{bmatrix} & \text{Var}(e_m) &= \begin{bmatrix} e_{m1} & 0 \\ 0 & e_{m2} \end{bmatrix} \\ \text{Var} \begin{bmatrix} u_{d1} \\ u_{m1} \\ u_{d2} \\ u_{m2} \end{bmatrix} &= G \otimes A = \begin{bmatrix} \sigma_{d1}^2 & \sigma_{d1m1} & \sigma_{d1d2} & \sigma_{d1m2} \\ \sigma_{d1m1} & \sigma_{m1}^2 & \sigma_{m1d2} & \sigma_{m1m2} \\ \sigma_{d1d2} & \sigma_{d2m1} & \sigma_{d2}^2 & \sigma_{d2m2} \\ \sigma_{d1m2} & \sigma_{m1m2} & \sigma_{d2m2} & \sigma_{m2}^2 \end{bmatrix} \otimes A \end{aligned}$$

, with  $G$  the genetic variance matrix between countries, and  $A$  the relationship matrix between animals.

These elements were estimated by REML using the software ASREML (Gilmour et al., 2000).

## D- Genetic parameters estimation

### 1- Within country estimation

Within country genetic parameters were first estimated for each country separately (two first columns in Table 1). The genetic parameters estimates for both countries are similar with close heritabilities values. The larger UK phenotypic variance corresponds to a larger residual variance. The repartition of the maternal variance between direct and permanent maternal effects is slightly different compared to the French one. However, these values are associated with larger standard deviations.

**Table 3: Within and across country genetic parameters estimates** (standard error in brackets).

	Within Country estimation		Across Country estimation	
	France	United Kingdom	France	United Kingdom
<i>Phenotypic variance <math>\sigma_p^2</math></i>	734 (6)	794 (14)	733 (6)	797 (15)
<i>Direct genetic variance <math>\sigma_d^2</math></i>	214 (15)	194 (21)	210 (15)	212 (32)
<i>Maternal genetic variance <math>\sigma_m^2</math></i>	71 (8)	57 (15)	73 (8)	
<i>Maternal permanent variance <math>\sigma_c^2</math></i>	66 (5)	83 (15)	66 (5)	
<i>Residual variance <math>\sigma_e^2</math></i>	409 (8)	480 (22)	410 (8)	473 (20)
<i>direct-maternal correlation <math>r_{dm}</math></i>	-0,20 (0,06)	-0.19 (0,16)	-0,21 (0,05)	-0.22 (0,06)
<i>direct heritability <math>h^2_d</math></i>	0,29 (0,02)	0,24 (0,04)	0,29 (0,02)	0,27 (0,04)
<i>maternal heritability <math>h^2_m</math></i>	0,10 (0,01)	0,07 (0,03)	0,10 (0,01)	0,09 (0,01)
<i>proportion of maternal permanent effect in the phenotypic variance <math>c^2</math></i>	0,09 (0,01)	0,11 (0,02)	0,09 (0,01)	0,08 (0,01)
<i>direct genetic correlation <math>r_{dFra-dGBR}</math></i>			0.8 (0.15)	
<i>maternal genetic correlation <math>r_{mFra-mGBR}</math></i>			1 *	
<i>correlation between French direct genetic effect and UK maternal effect <math>r_{dFra-mGBR}</math></i>			-0.21 (0.01)	
<i>correlation between UK direct genetic effect and French maternal effect <math>r_{mFra-dGBR}</math></i>			-0.22 (0.1)	

(\*: fixed value)

### 2- Across country estimation

Subsequently, bi-traits AMACI model between France and UK was fitted to estimate genetic correlation across countries (last two columns in Table 1).

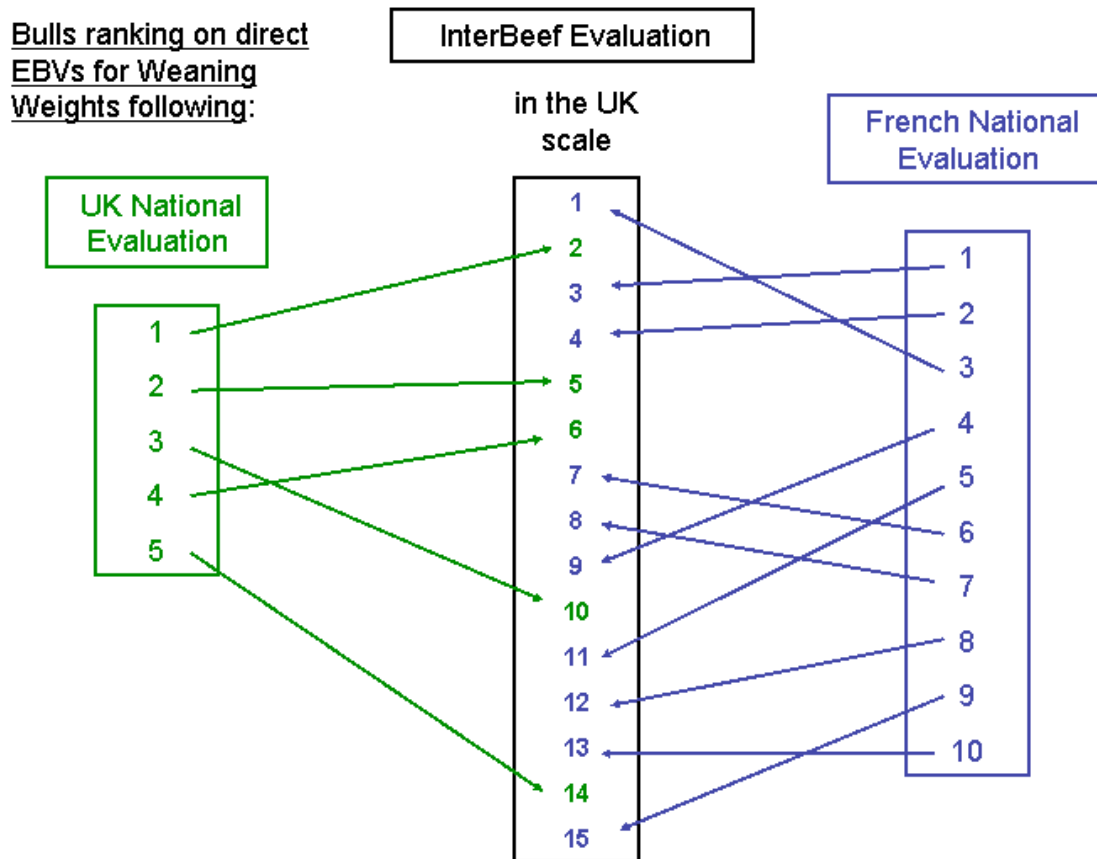
Preliminary work showed that maternal genetic correlation between France and UK was very high and close to the limit 1: therefore, it has been fixed to 1 to improve model convergence.

In the same way, the same distribution of the maternal variance between maternal genetic and permanent effects has been considered. The direct genetic correlation between France and UK equals 0.8.

Practically, this means that a Genotype by Country interaction exists for the direct genetic effect: reranking of bulls with regards to the direct EBVs for weaning weights is expected

between France and UK: graphic 1 gives examples of the possible reranking of bulls between French, UK and Interbeef Evaluations.  
 On the other hand, the bulls ranking will be the same for the maternal genetic effects.

Graphic 1: Examples of possible reranking between the different genetic evaluations.



The different ingredients necessary to run the joint genetic evaluation between France and UK for the Limousin breed are now gathered and this genetic evaluation will take place very soon.

The part on the joint genetic evaluation below was not included in the British Cattle Conference paper.

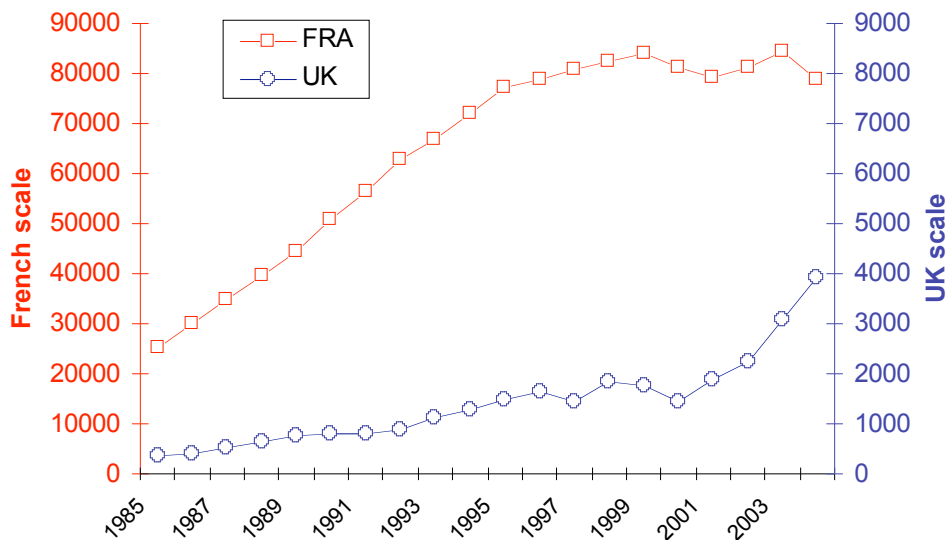
## E- Joint genetic evaluation

Based on the genetic parameter estimates presented before, a joint genetic evaluation between France and UK has been run in January. A data description is first given followed by genetic trends presentation and EBVs distributions.

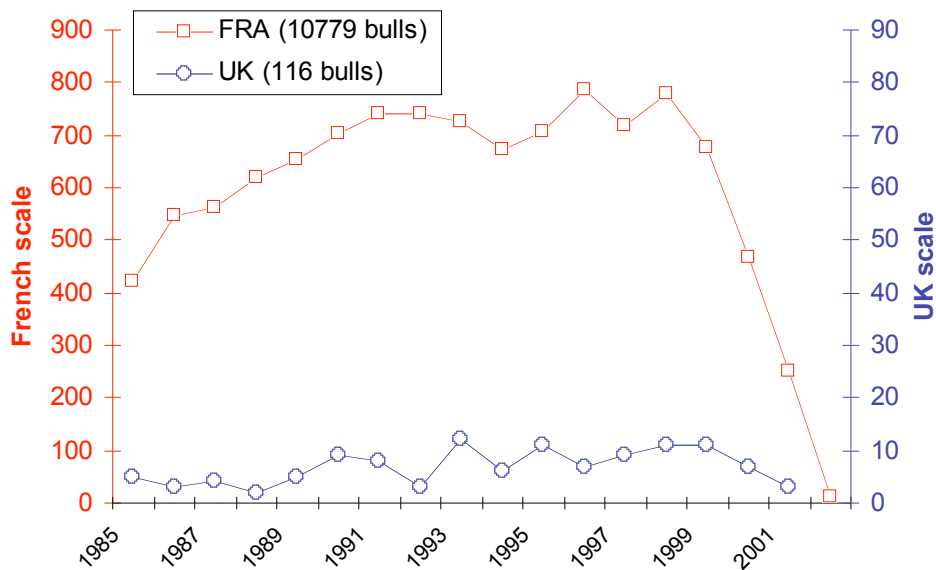
### **1- General description of the data**

The total number of animal with performance evaluated in each birth campaign is presented in the next graph, followed by the same presentation for the sires with at least 25 offspring with performance.

#### **Number of animals evaluated per birth campaign**



#### **Number of bulls with at least 25 offsprings with performances**





The following tables give a general description of the evaluated population and more particularly the distribution of the progenies between the countries.

**Table 1: Description of the number of animals evaluated**

Country of origin of the animals	Number of animals evaluated	Number of animals with performances	Number of sires
France	1 582 487	1 428 065	35 545
UK	39 477	28 330	1 682
Total	1 621 964	1 456 395	37 227

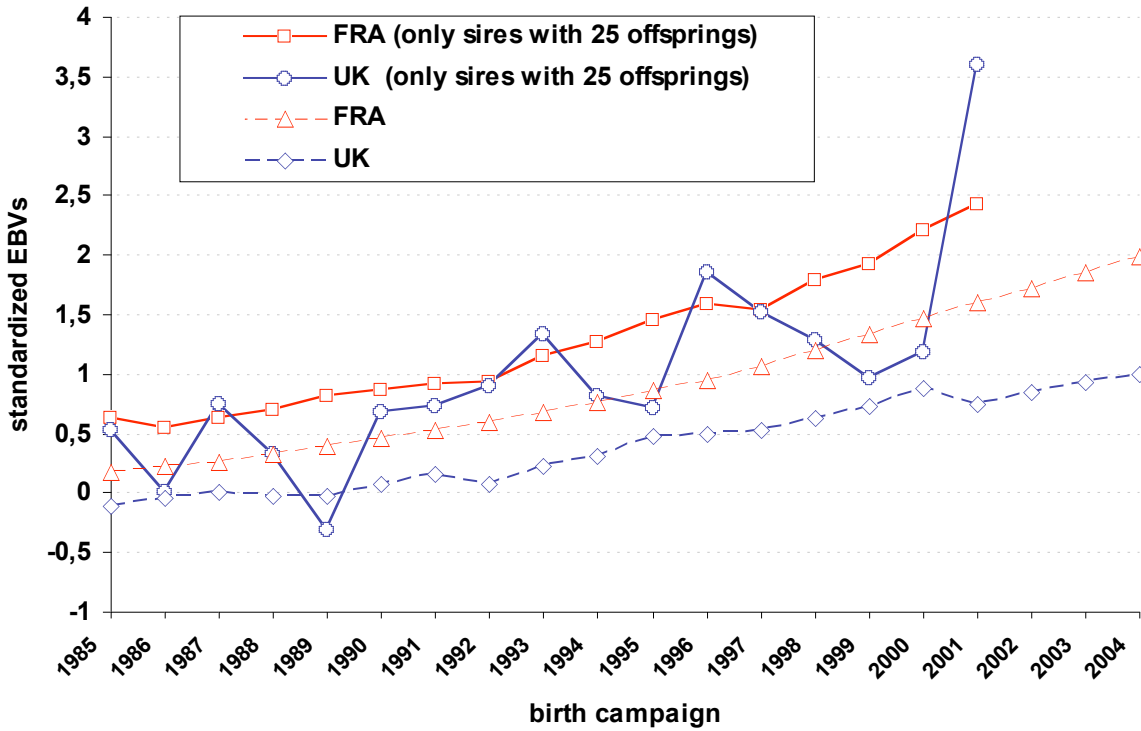
**Table 2: Description of the sire progenies distribution in France and UK.**

Country of origin of the sires	Number of sires with progenies in both countries	Number of sires with progenies only in UK	Number of sires with progenies only in France
France	100	252	35 193
UK	0	1682	0
Total	100	1934	35 193

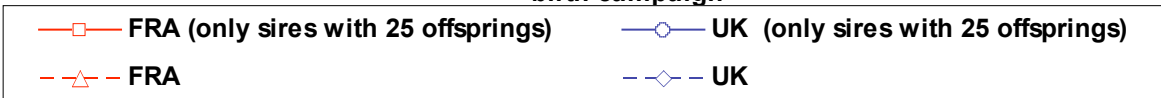
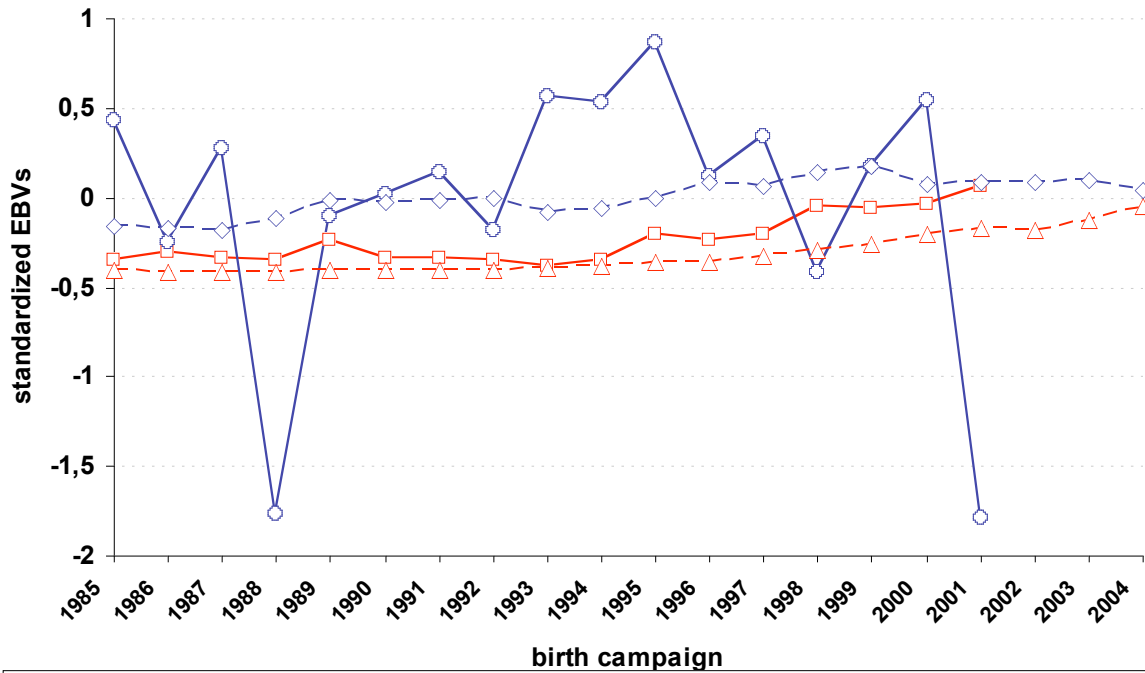
## 2- Genetic trends

The two following graphs present the genetic trends relative to direct and maternal genetic effects for France and UK: for each country, the genetic trend of a specific birth campaign is the mean of the breeding values of the evaluated animals with performances, born within the birth campaign and within the country. In these two graphs, the same genetic trends are also given for sires with more than 25 offspring. The number of sires is reduced compared to the number of evaluated animals leading to more variable UK genetic trends but EBVs are in this case more reliable.

**Genetic trends for direct genetic effect in UK scale**

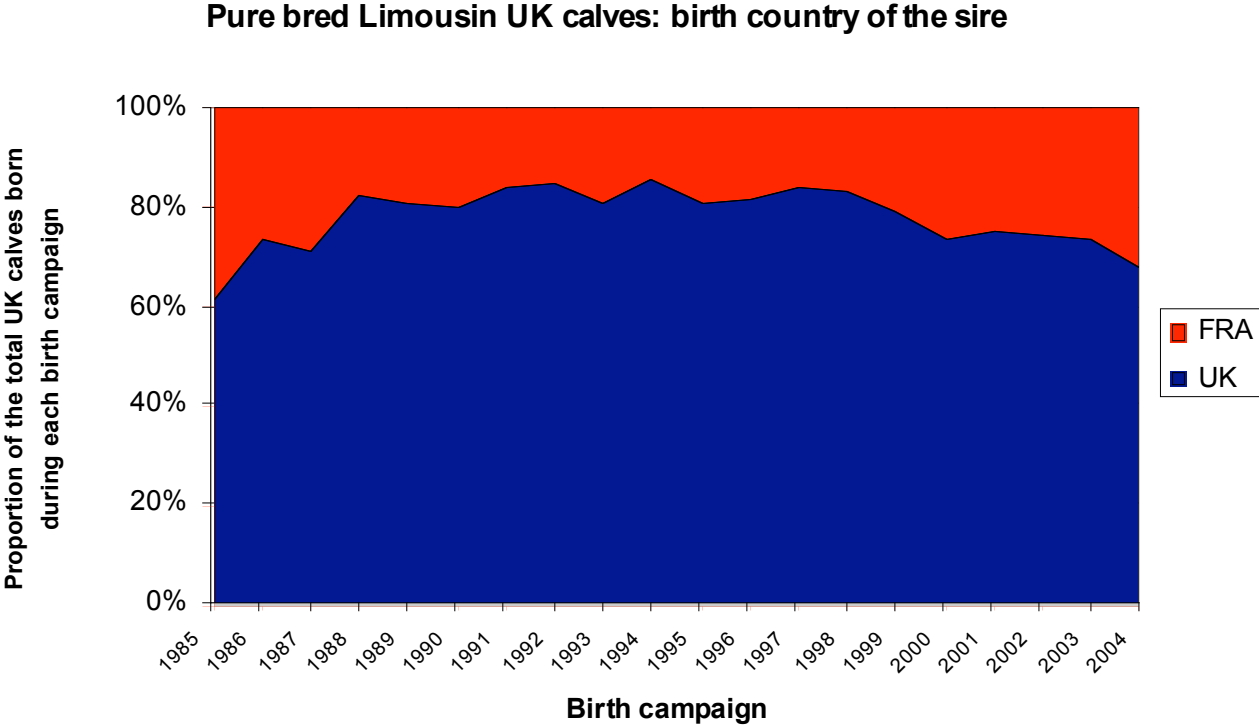


**Genetic trends for maternal genetic effect in UK scale**



### 3- Origin of the sires with progenies in United Kingdom

The next graph shows that more than 15% of the pure bred Limousin calves have a French sire in each birth campaign. This proportion has decreased until 1988, remained stable between 1988 and 1998 (around 16%) but started to increase again since 1998 to reach 32 % in 2004.



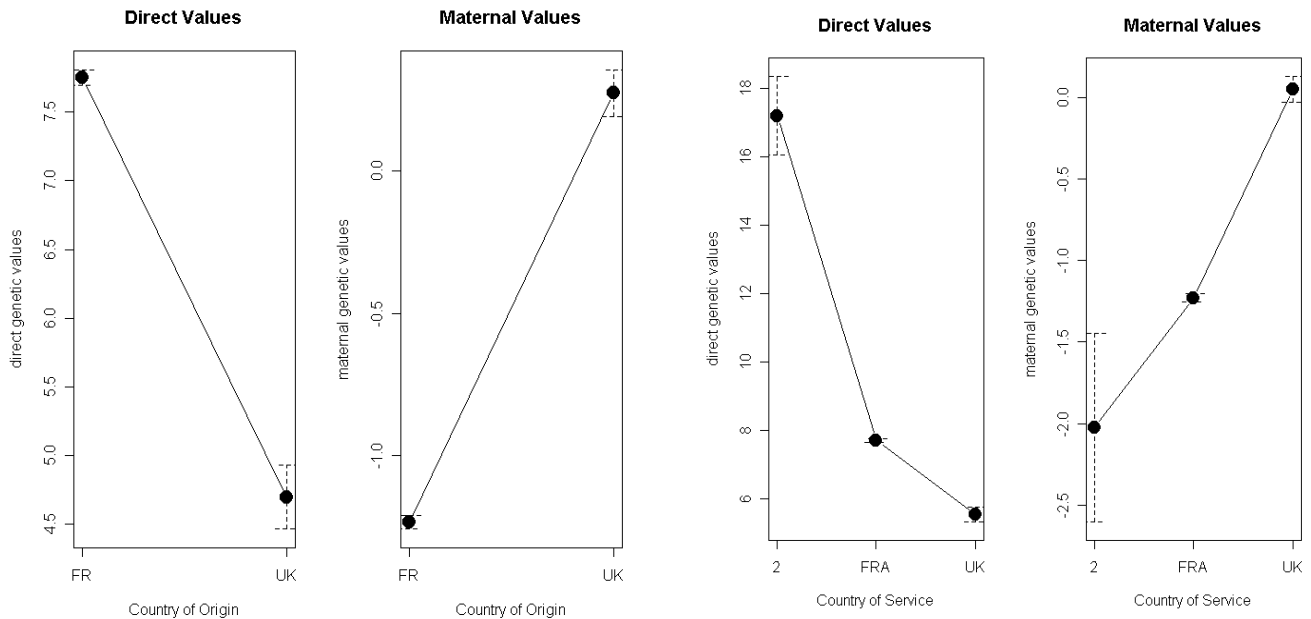
#### 4- Focus on the sire EBVs

The next diagrams present the general statistics on the direct and maternal sires EBVs: the French sire direct EBV mean is higher than the UK one but it is the opposite for the maternal genetic values.

#### Comparison of the direct and maternal sires EBVs in the UK scale

depending on the origin of the sire

depending on the country of service

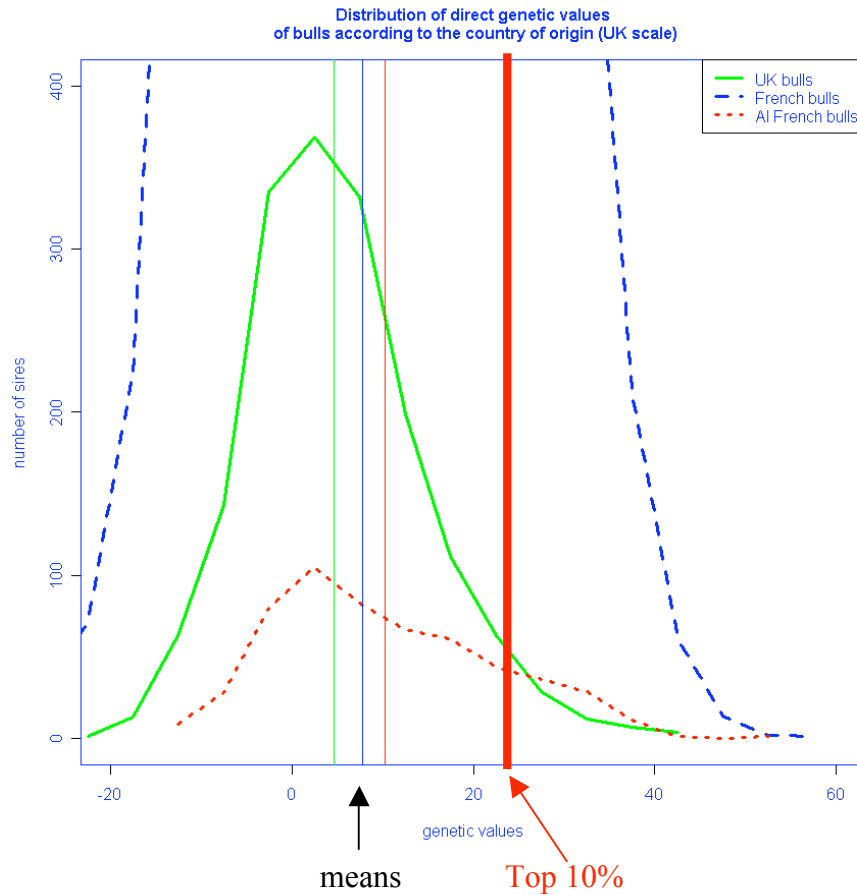


The distributions of the direct EBVs of pure bred Limousin sires according to the country of origin in the UK scale are given in the next graph (with means represented by the vertical lines). If we only consider the 10% best pure bred Limousin bulls, 3638 are originating from France and 83 from United Kingdom.

Table 3 gives the details of the number of progenies in each country for the first 20 UK or French AI bulls: half of these top 20 bulls are French AI bulls and only two of them are already in use in United Kingdom. If we consider the direct ranking in the French scale, 3 UK bulls also appear in the top 50 bulls.

#### CONCLUSION

These results for pure Limousin breed show all the interest of a joint genetic evaluation between France and United Kingdom: breeders will have a larger choice of foreign bulls specifically ranked following their country farming conditions.



**Table 3: Number of progenies in France or in UK for the first 20 French AI or UK bulls**

ranking	Type of bull	direct EBV	Number of progenies	
		(UK scale)	in France	in UK
1	French AI bull	50,1	243	0
2	French AI bull	43,6	53	0
3	UK bull	42,6	0	43
4	UK bull	42,1	0	21
5	UK bull	41,2	0	34
6	UK bull	40,4	0	7
7	French AI bull	39,7	129	0
8	French AI bull	39,5	2266	0
9	UK bull	39,3	0	3
10	French AI bull	38,8	901	0
11	French AI bull	38,5	186	0
12	UK bull	37,9	0	48
13	French AI bull	37,3	22475	33
14	UK bull	37,0	0	9
15	UK bull	36,4	0	45
16	French AI bull	36,3	0	93
17	French AI bull	35,9	89	0
18	French AI bull	35,7	3382	38
19	UK bull	35,7	0	75
20	UK bull	35,6	0	22

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