Interbeef in Practice: Example of a Joint Genetic Evaluation between France, Ireland and United Kingdom for Pure Bred Limousine Weaning Weights

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Abstract

The first international joint genetic evaluation between France, Ireland and United Kingdom for pure bred Limousin weaning weights offers the opportunity to review the Interbeef story and detail the different steps to achieve before implementing a common genetic evaluation for beef cattle. This study along with the previous EUBEEVAL works reveals the crucial need of identification of foreign animals in the different national databases, differences between countries with regards to data amount and structure, and also a lack of information to estimate maternal (co)variance components. Nevertheless, this objective approach taking into account country specificities provides a new powerful tool for the breeders to enlarge their breeding animal choice.

I- Interbeef: the story so far

The Interbeef story began in 2001 with the initiative of the Irish Cattle Breeder Federation (ICBF) to develop a European joint genetic evaluation of beef breeds in order to enlarge their choice of breeding animals based on objective method. The EUropean BEef EVALuation (EUBEEVAL) project has then been conducted through a collaboration between ICBF, the French National Institut for Agronomic research (INRA) and the Institut de l'Elevage (IE), the British Meat and Livestock Commission (MLC), the Australian University of New England (AGBU) and ICAR: Quintanilla *et al.* (2002) and Renand et al. (2003) from INRA showed the feasibility and the potential benefit of a common genetic evaluation between France, Ireland and United Kingdom but also pointed out the need of a better genetic link identification between the participating countries. Phocas *et al.* (2005) from INRA but on secondment to AGBU determined that the best results in case of beef cattle data are obtained with an animal model with maternal effects applied on rough data and allowing heteroscedasticity for genetic, maternal and residual variances along with associated genetic correlations between countries.

On the basis of these results and new datasets provided in 2005 by ICBF to INRA, Venot *et al.* (2006) estimated new genetic parameters between France and Ireland for Charolais and Limousin breeds: these works have shown different data structure and quality between countries, a lack of information to precisely estimate maternal (co)variance components, but also confirmed the feasibility of common beef cattle genetic evaluation with rather high genetic correlations between countries. Another practical outcome from these first studies is the standardisation of the file exchanges between countries (performances, pedigree and fixed effects files), leading to general guidelines for international exchanges of beef cattle data (Pabiou *et al.*, 2007).

In 2005, the International Committee for Animal Recording (ICAR) identified, through a general survey, a need of international beef genetic evaluation: several countries expressed their interest and France, Ireland, United Kingdom, Denmark, Norway, Finland and Sweden even agreed to a financial contribution in the development of this evaluation. ICAR therefore decided in 2006 to establish a new Interbull service dedicated to beef cattle genetic evaluation, called Interbeef (Journaux *et al.*, 2006).

After several steps of international identification validation to optimize the genetic links between France, Ireland and United Kingdom, new sets of performances associated with pedigree and fixed effects information for Limousin pure bred animals have been send to INRA in 2006 by ICBF (Ireland) and the Scottish Agricultural College (SAC UK). This article presents the different Interbeef steps that have been achieved to implement the first joint genetic evaluation between France (FRA), Ireland (IRL) and United Kingdom (UK) for pure bred Limousin weaning weight and the key lesson learnt.

II- Interbeef in practice

A- Specific trait definition per country

The trait considered in this study consists in adjusted weaning weight with specific definition per country: the French 210 days adjusted weaning weight is calculated by intra-extrapolation for each animal with at least 2 weights, with two conditions on these weights:

- the interval between the target age (210 days) and the closest weighing date must be less than 2 months,
- the interval between the two weighing dates must be less than 300 days.

The UK weaning weight is adjusted to 200 days and is derived using a linear regression on at least two weights between 170 and 300 days. To make the joint genetic evaluation as close as possible to the Irish evaluation, the Irish growth trait is defined as the average of the animal weights measured between 150 and 300 days.

B- Different data structures

This study concerned only adjusted weaning weights of pure bred Limousin animals born between 1986 and 2005 in France, Ireland and United Kingdom. INRA received 8002 Irish and 118406 British performances. However, animals obtained from embryo transfer and twins could not be considered in the model and have been discarded. In the same way, animals with no complete fixed effects information or contemporary group with less than 2 animals were also deleted. Eventually, 6160 Irish and 28345 UK AWW remained. The French data used in this analysis (n=1428050) has been extracted from the national database and is validated for the national evaluation. A description of the data structure is given in table 1.

Although adjusted ten days later, French AWW are in average lighter than the UK ones: these differences are even larger when considering male and female separately (the lower proportion of male in the UK data can be explained by the data selection with regards to the herd and pedigree information). The Irish animals are also heavier than the French ones but this can be explained by the later average age at weaning (225 days).

Compared to France, the herd size and number of birth campaign per herd in Ireland and United Kingdom are reduced, leading to a small number of performances per herd-birth campaign. The small number of calves per dam in Ireland and UK brings less information for maternal genetic parameters estimation compared to France.

Table 1. Descriptive statistics of the three Limousin populations.

	France	Ireland	United Kingdom
Number of adjusted weaning weights (AWW)*	1 428 050	6 160	28 345
Number of herds	5 260	346	1 189
Average AWW * (kg) (std)	255 (38)	260 (40)	260 (39)
AWW * (kg) (std) for males	268 (39)	272 (42)	278 (42)
AWW * (kg) (std) for females	242 (32)	245 (38)	249 (34)
Male proportion	49 %	56 %	37 %
Median, min and max number of AWW per herd-year of birth	22 [1;245]	3 [1;46]	3 [1;91]
Average number of calves per dam (std)	3.6 (2.7)	1 (1,2)	2 (1,3)

** weaning weight is adjusted to 210 days in France, to 200 days in UK and to around 225 days in Ireland*

C- <u>Connectedness between countries</u>

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 differences between genetic levels. The major work to be done by a country willing to participate to a common genetic evaluation is therefore the recognition of all the foreign animals with their country of origin and their original identifications (in the right format), in its national database. It has been the most time-consuming step in the setting up of this common evaluation between France, Ireland and UK, more particularly because the whole pedigree file had to be covered. However, once the cleaning of the historical pedigree has been done, the construction of the cross reference file is thereafter simplified through the different Interbeef procedures presented by Pabiou *et al.* (2007).

Since the beginning of the project, the quality of the cross-reference file between these three countries has been dramatically improved with the correction of many French Charolais and Limousin animal identifications in the Irish and UK database (started by Antunes in 2004 in Ireland and continued by Pabiou and Journaux thereafter (Journaux *et al.,* 2006)). The key lesson learnt from this preliminary step is the crucial need for a country importing a foreign animals to store the original identification in its national database.

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 and/or Ireland.

There are a consequent number of common sires and maternal grand sires between these three countries. These identified connecting bulls are all originating from France. However, counting the number of common bulls is a rough and not very precise method to assess the connection between the participating countries. A new method has been developed by Laloë and Fouilloux (2006) in the frame of international genetic evaluation of dairy cattle and will be adapted to the Interbeef evaluation in 2007.

D- <u>Model description</u>

The model used in the genetic parameter estimation is the one described by Phocas *et al.* (2005) and consists in a multiple trait animal model with direct and maternal genetic effects and also permanent environment effect provided by the dam. It allows heterogeneous genetic, maternal permanent environment and residual variances, along with direct and maternal genetic correlations between countries.

Fixed effect models were specific to each country and defined by each country itself. The following definitions were used in the genetic parameter estimation and the associated evaluation:

- France: herd*management group*birth campaign*sex, dam age at calving (13 classes) and month at calving (10 classes)
- Ireland: herd*birth campaign*season, sex, linear, quadratic and cubic regression on mean weighing age in interaction with sex.
- United Kingdom: contemporary group obtained from the Crump method, month at calving (12 classes), sex, linear and quadratic regression on dam age at calving.

Table 2. Description of the number of sires with offspring in France or/and in Ireland and/or in UK.

Country		Number of bulls with progenies					
	Type of bull	Only Sires		Sires and MGS*		Only MGS*	
	Min. of progenies	1	6	1	6	1	6
FRA		12 018	9 651	24 252	17 578	2 249	2 752
IRL		155	88	223	108	345	111
UK		1 029	446	1 382	581	848	334
FRA-IRL		31	21	38	25	140	31
FRA-UK		38	28	62	17	329	38
IRL-UK		21	12	29	11	37	7
FRA-IRL-UK		17	7	24	13	23	1

* MGS ⇔ Maternal Grand Sire

E- **Genetic parameters estimations**

The genetic parameter estimation has been performed with the ASREML software (Gilmour *et al.*, 2000) in 3 steps: within country genetic parameters were first estimated for each country separately and these estimates were then used as initial values for the 2x2 estimations (Table 3). Eventually, genetic parameter estimates were obtained for the three countries together.

Table 3. Within and 2 by 2 country genetic parameters estimates (standard error in brackets).

	Within country estimations			Across country estimations			
(* ⇔ fixed value)	FRA	IRL	UK	FRA-IRL		FRA-UK	
Phenotypic variance σ^2_p	734 (6)	1252 (28)	794 (14)	755 (11)	1255 (29)	733 (6)	797 (15)
Direct genetic variance σ^2_d	214 (15)	206 (59)	194 (21)	213 (19)	172 (45)	210 (15)	212 (32)
Maternal genetic variance σ^2_m	71 (8)	56 (37)	57 (15)	64 (11)	26 (24)	73 (8)	
Maternal permanent variance σ^2_c	66 (5)	182 (31)	83 (15)	48 (8)	200 (32)	66 (5)	
Residual variance σ^2_e	409 (8)	849 (41)	480 (22)	430 (12)	857 (37)	410 (8)	473 (20)
Direct heritability h^2_d	0,29 (0,02)	0.17 (0.05)	0,24 (0,04)	0,28 (0,02)	0,14 (0,04)	0,29 (0,02)	0,27 (0,04)
Maternal heritability h^2_m	0,10 (0,01)	0.05 (0.03)	0,07 (0,03)	0,08 (0,01)	0,02 (0,02)	0,10 (0,01)	0,09 (0,01)
Direct-maternal correlation r_{dm}	-0,20 (0,06)	-0.39 (0.24)	-0.19 (0,16)	0*	0*	-0,21 (0,05)	-0.22 (0,06)
Proportion of maternal permanent effect in the phenotypic variance c^2	0,09 (0,01)	0.15 (0.02)	0,11 (0,02)	0.06 (0.01)	0,16 (0,02)	0,09 (0,01)	0,08 (0,01)
Direct genetic correlation r_{d1-d2}				0.93 (0.14)		0.8 (0.15)	
Maternal genetic correlation r_{m1-m2}				1*		1*	
Corr. between country1 direct genetic effect and country2 maternal effect r_{d1-m2}				0*		-0.21 (0.01)	
Corr. between country2 direct genetic effect and country1 maternal effect r_{m1-d2}				0*		-0.22 (0.1)	

Estimates of variance components were homogeneous between France and United Kingdom with nevertheless a larger direct genetic variance and a lower environmental (residual and maternal) variance for France. On the opposite, Irish estimates differ from the two others, more particularly with much larger phenotypic and residual variances.

The 2 by 2 analysis has been marked by convergence problems, mainly due to large uncertainty on the Irish maternal effects and very high maternal genetic correlation estimates between countries. Maternal genetic correlation was therefore fixed to 1, in both FRA–UK and FRA–IRL estimations. And for the latest, no correlation between direct and maternal effects was assumed to get proper convergence. With these constraints, the direct genetic correlations between FRA–UK and FRA–IRL were respectively 0.8 and 0.93. No convergence has been reached for the IRL–UK genetic parameter estimation.

With regards to these convergence problems encountered in the 2 by 2 country estimations, it has been chosen not to take into account any maternal genetic effect in the model but only a common maternal effect to correct for a general maternal permanent environment effect. In these conditions, the results presented in Table 4 were obtained.

Table 4. Across country genetic parameters estimates (standard error in brackets).

	FRA	IRL	UK
Direct genetic(co)variances and correlations (below diagonal)			
France	233 (13)	250	148
Ireland	**1***	272 (49)	181
UK	**0.67**	**0.76**	208 (23)
Residual variance	393 (8)	884 (39)	483 (18)
Maternal variance	96 (4)		
Phenotypic variance	722 (7)	1252 (29)	788 (14)
Direct heritability	0.32 (0.02)	0.22 (0.03)	0.26 (0.03)

(: fixed value)*

Very high direct genetic correlation between France and Ireland has been found and needed to be fixed to 1 to obtain convergence. The two others direct genetic correlations were lower with 0.67 and 0.76 for FRA-IRL, and IRL-UK, respectively. Practically, this means that a Genotype by Country interaction exists for the direct genetic effect in these two last cases: reranking of bulls with regards to the direct EBV's for weaning weights is then expected. On the other hand, the bulls ranking will be the same between France and Ireland.

F- Joint genetic evaluation

The IE and INRA software

To perform the joint genetic evaluation, Fouilloux and Laloë from IE and INRA have developed a software adapted to the beef cattle data: this software has been used in its first version in the EUBEEVAL project but has been greatly improved these last years with its extension to an "infinite" number of correlated traits or the introduction of covariables as fixed effects. Eventually, this software can run multi-traits models with direct and maternal genetic effects and also permanent maternal effects, with specific fixed (covariable or categorical) effect models for each trait and taken into heteroscedasticity between countries. The next development steps will consist in adding genetic groups, accuracy measure and heteroscedasticity within trait.

Evaluation results

Based on the genetic parameter estimation results, a joint genetic evaluation has been run in March 2007 between France, Ireland and United Kingdom using an animal model with a common maternal effect. Only the results for the sires with more than 10 progenies altogether whatever the country will be considered below as an example of results that can be expected from the international beef evaluation.

A specific set of genetic values was obtained for each country. However, the direct genetic correlation between France and Ireland equals unity and very few reranking are expected between these two countries.

Table 5 summarises the results of this evaluation with the number of progenies per sire and country depending on the origin of the sires and the direct EBV's means on each country specific scale. French AI bulls EBV's mean is greater than the Irish and then the UK ones in each scale. Graph 1 and 2 present also the distributions of the direct EBV's of pure bred Limousin sires according to the country of origin in the Irish and British scale respectively (with country EBV's means represented by the vertical lines).

Focus on best bulls

If we only consider the 10% best pure bred Limousin bulls in the UK scale for example, 2200 are originating from France (2196 common and 104 AI French bulls), 4 from Ireland and 63 from United Kingdom. When considering the top 15 bulls of this common ranking, 11 are UK bulls and 4 are French AI bulls but the details of the number of progenies in each country indicates that only two of these AI French bulls are actually in use in United Kingdom. The first Irish bull takes the 102nd place in this ranking. On the French scale, 4 UK and 1 Irish bulls also appear in the top 100 bulls.

Table 5. Joint genetic evaluation results.

		Average number of progenies per sire in:			EBV's mean on the:		
Origin of the sires	Number of sires	France	Ireland	UK	French scale	Irish scale	UK scale
French non AI bulls	22 720	50	0.1	0.2	9.8	10.3	5.7
French AI bulls	414	569	4	1	15.3	16.3	9.5
Irish bulls	64	0	24	0	10.3	10.9	6.0
UK bulls	475	0	0	31	7.4	8.2	5.8

Figure 1:

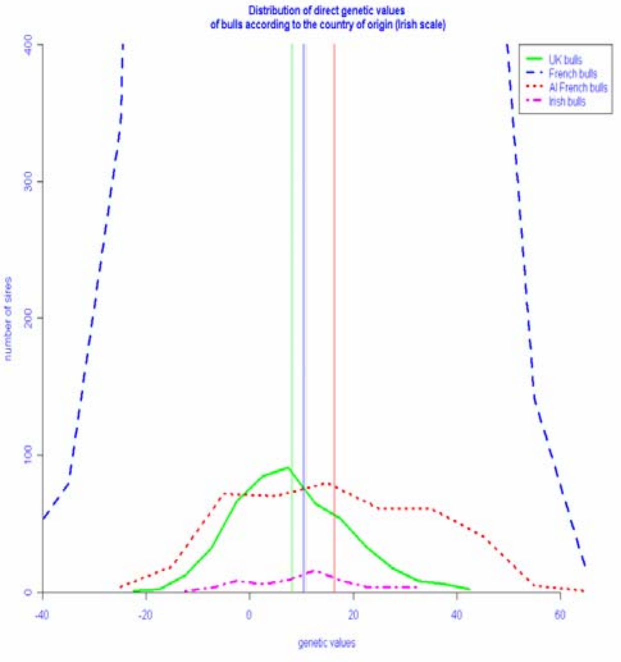
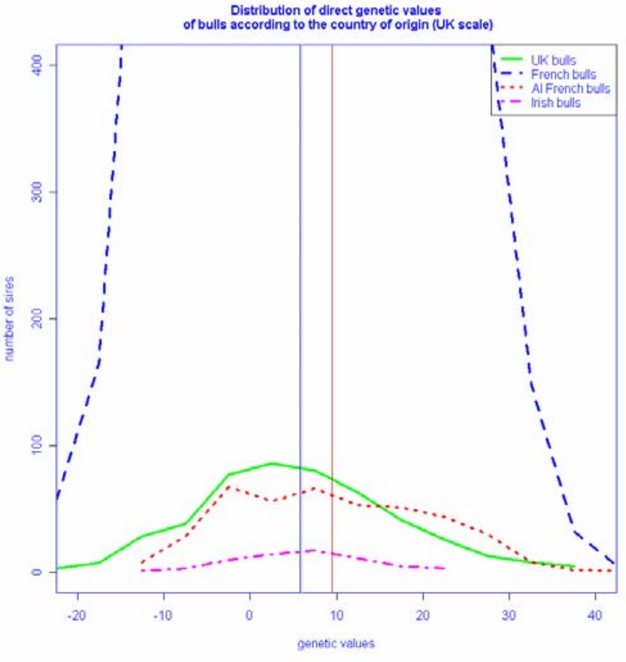


Figure2:



Conclusion

All the different Interbeef steps needed to implement the joint genetic evaluation between France, Ireland and United Kingdom has been covered in this study. It pointed out several practical issues to be taken into account in the future Interbeef developments:

- different data amount and population structure between countries,
- connectedness between countries identified through standardised international identification,
- genetic correlations close to the parameter space limit,
- lack of information to estimate the maternal genetic (co)variances components.

Nonetheless, it also clearly shows the great interest of this new powerful approach for the beef cattle breeders: they will be able to choose their breeding animals adapted to their production system specificities out of an international panel and based on an objective comparison.

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