

A First Attempt of an International Genetic Evaluation of Beef Breeds in Europe

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Abstract

Weaning weights from 1,608,739 Charolais calves performance recorded in France (FRA), Great Britain (GBR) and Ireland (IRL) were analysed to produce the first international genetic evaluation for the breed. An animal model with maternal genetic and permanent environment effects was used to estimate 2,065,626 breeding values for each genetic effect. A preliminary analysis showed significantly heterogeneous residual variances across countries. Estimates of the genetic correlations between weaning weights measured in different countries ranged from 0.55 (SE = 0.25) to 0.90 (SE = 0.30). Weaning weights of calves recorded in different countries were therefore considered as different traits, despite the low precision of the genetic correlation estimates. Complementary analyses within country or two by two countries confirmed these conclusions and provided for the genetic parameters used in the evaluation model. About 14 % of calves were genetically linked directly by the common use of 822 sires or maternal grand sires. Genetic links between countries were also provided by common ancestors in the back pedigree.

The correlations between estimated breeding values (EBVs) of connecting bulls used in the three countries were 0.98 for FRA/GBR, 0.92 for FRA/IRL and 0.98 for GBR/IRL. Consequent re-ranking of sires between IRL and FRA was observed however for some highly connecting bulls. The main benefit of the joint evaluation was the increased choice of best seed stock provided by the comparability of EBVs between foreign and domestic bulls.

1. Introduction

Although most of beef cattle populations in Europe are country specific, the Charolais and Limousin breeds have been developing in several countries for the last four decades. The genetic evaluation of seed stock is usually performed within country although some foreign cattle are simultaneously evaluated with the French animals (Italy, Luxembourg, Hungary). The largest Charolais and Limousin populations outside the origin country are found in United Kingdom and Ireland. In these countries, breeders may seek for comparability of their domestic to overseas seed stocks in order to enlarge the choice of animals that better fit their own selection objectives. The method of choice for a fair comparison is a simultaneous analysis of data from the different countries with an adequate animal model.

In collaboration with the Irish Cattle Breeding Federation (Ireland), the Meat and Livestock Commission (UK), the Institut de l'Elevage (France) and INTERBULL sub-committee of ICAR, a research program was conducted at INRA (France) with the purpose of developing an international genetic evaluation in British, French and Irish Charolais and Limousin breeds. Preliminary results were presented by Quintanilla *et al.* (2002a,b).

The different steps required in developing an international genetic evaluation will be illustrated with the Charolais weaning weights.

2. Population data

A total of 1,608,739 age adjusted weaning weights, recorded between the mid 70's and 2001, were provided for the study (Table 1).

Weaning weight (WW) was adjustment to 200 days in Great Britain (GBR) and Ireland (IRL) and 210 days in France (FRA). Although adjusted ten days older, WW of FRA calves were lighter. WW in IRL were markedly more variable.

Table 1. Weaning weight statistics.

	n	mean	s.d.
FRA	1,541,131	274 kg	49 kg
GBR	49,387	302 kg	51 kg
IRL	18,221	286 kg	55 kg

In GBR, the number of WW records was stable over most of the period, at approximately 3,000 per year. In FRA and IRL, a marked increase in performance recording was observed during the study period, in the last years reaching approximately 3,400 calves per year in IRL and 110,000 in FRA. This increase was mainly obtained through the integration of new herds to performance recording. An increase of herd size was also observed in FRA. Herd size differed markedly across countries: from an average of 4 calves per year in IRL, to 10 in GBR and 28 in FRA.

Imported gene flow was shown to contribute a large proportion of germ plasm in IRL where 32% of calves had at least one FRA parent and 3% a GBR parent. In GBR, 12% of the calves had at least a FRA parent. As a consequence, connections could be found in the back pedigree of animals with WW records. For example, for the 1996-2000 GBR and IRL calf crops, 6 and 11 out the 16 ancestors of the 4th generation originated from FRA respectively.

Direct connections between countries were established through bulls siring calves in different countries (Table 2). Characteristically of beef breeding where natural mating is prevailing, a large number of sires, 61,880, were used. As a consequence, only a moderate number of artificial insemination sires (164) provided direct connections across countries. However, these bulls sired a large number of calves (776 each on average) *i.e.* 8% of the total. International trade in replacement heifers also significantly contributed to genetic links between the participating countries and the number of connecting maternal grand sires was 758. As a whole, 822 bulls were found to provide for direct connection as sires or maternal grand sires accounting for 14 % of the recorded calves.

Table 2. Domestic and international sires.

Number of sires used by country	Number of countries with progeny of the sires		
	One	Two	Three
FRA	58,023	97	42
GBR	2,549	59	42
IRL	1,144	88	42
Total	61,716	122	42

2. Within and across country estimates of genetic parameters

The within and across-country estimation of genetic parameters were performed on different set of records. In order to have comparative results on the effect of including heteroskedasticity across subclasses, FRA data was subdivided in four sub-samples according to the regional activity of the AI cooperatives.

Table 3. Estimated genetic parameters within countries and regions.

	FRA 1 n = 69,532	FRA 2 n = 71,523	FRA 3 n = 73,306	FRA 4 n = 55,084	GBR n = 44,054	IRL n = 9,392
σ_d^2	251 ± 19	185 ± 14	205 ± 14	219 ± 17	221 ± 25	203 ± 54
σ_{dm}	-76 ± 12	-49 ± 10	-51 ± 9	-61 ± 11	-82 ± 17.5	-47 ± 40
σ_m^2	141 ± 13	132 ± 12	127 ± 11	131 ± 13	143 ± 18	146 ± 46
σ_{ep}^2	141 ± 8	130 ± 8	109 ± 7	113 ± 8	139 ± 11	152 ± 30
σ_e^2	818 ± 12	862 ± 10	783 ± 9	794 ± 11	939 ± 16	1230 ± 38
h_d^2	0.20	0.15	0.18	0.18	0.18	0.13
h_m^2	0.11	0.11	0.11	0.11	0.12	0.09
rg_{dm}	-0.40	-0.31	-0.32	-0.36	-0.46	-0.27

In a first step, the within-country analysis was performed on large records sets consisting of data recorded between 1981 and 2001 in herds with at least 15 records per year for FRA, 10 for GBR and 7-8 for IRL, where herd sizes were considerably smaller. The model included fixed effects (b : herd*year, season, sex and age of dam), direct (u_d) and maternal (u_m) genetic effects and permanent environment provided by the dam (e_m) :

$$[1] \quad y = Xb + Z_d u_d + Z_m u_m + W_m e_m + e$$

The second moments of the random effects,

$$\text{var} \begin{bmatrix} u_d \\ u_m \end{bmatrix} = G_0 \otimes A, \quad \text{with}$$

$$G_0 = \begin{bmatrix} \sigma_d^2 & \sigma_{dm} \\ \sigma_{dm} & \sigma_m^2 \end{bmatrix}, \text{ and } \text{var}[e_m] = I \cdot \sigma_{em}^2 \text{ and } \text{var}[e] = I \cdot \sigma_e^2 \text{ were estimated by REML using ASREML (Gilmour } et al., 2000).$$

The estimates in the four FRA regions, GBR and IRL are reported in Table 3. The GBR and IRL genetic variances were within the range of the four FRA region estimates. However their residual variance estimate was higher, especially in IRL.

In a second step, a joint analysis of the six regions/countries was performed on a sub-set of data pertaining to connected herds, *i.e.* herds that used at least one of the 822 connecting bulls. For FRA regions, a further random sampling had to be done for reducing the amount of data. For computation constraints, a sire (s), maternal grand sire (t) model was used

$$[2] \quad y = Xb + Zs + Wt + e$$

In order to test the heterogeneity of the sire and residual variances across the six sub-classes and to estimate the genetic correlations between sire effects, a heteroskedastic model was used where $\text{Var}(e) = \bigoplus_{i=1}^6 I_{n_i} \sigma_{ei}^2$, being n_i the number of records in the i^{th} sub-class and $\text{Var}(s) = D \Delta D' \otimes A$, being $D = \text{diag}\{\sigma_{si}^2\}_{i=1,6}$ and Δ a correlation matrix whose non-diagonal elements (δ_{ij} , $i \neq j$) were the correlation coefficients between sire effects in the i^{th} and j^{th} sub-classes.

As shown in previous analyses, with other data samples (Quintanilla *et al.*, 2002 *a,b*), the model with heterogeneous variances was highly significant as compared to a model with homogeneous (co)variances. The model with a genetic correlation differing from unity was also found significantly more likely as compared with a model without genetic*region interaction. The final model, with different correlations across countries and homogeneous ones across the four FRA regions, showed even higher likelihood.

The estimated genetic parameters are reported in Table 4. The residual variances still appeared higher in GBR and IRL samples. The estimates of the correlations between the sire effects across country ranged from 0.55 to 0.90, apparently revealing some genetic*country interactions. However, the accuracy of these estimates was low and their consistency to predict genetic correlations could be questioned since they were obtained with reduced samples and a simplified model that gave inflated estimates of direct heritability as compared to the within country animal models [1] above. Two by two regions/countries analyses, using larger samples, gave similar correlations between countries and supported the homogeneous correlation around 0.9 across the four FRA regions (results not shown).

Table 4. Estimated genetic parameters in the joint analysis.

	FRA 1 n = 10,492	FRA 2 n = 10,523	FRA 3 n = 11,594	FRA 4 n = 10,636	GBR n = 11,430	IRL n = 8,678
σ_s^2	97 ± 14	88 ± 11	88 ± 11	113 ± 13	103 ± 16	53 ± 15
δ	FRAi - FRAj 0.89 ± 0.04		FRA - GBR 0.81 ± 0.18	FRA - IRL 0.55 ± 0.25	GBR - IRL 0.90 ± 0.30	
σ_m^2	48 ± 4					
σ_e^2	1184 ± 17	1094 ± 16	1059 ± 15	1030 ± 15	1300 ± 18	1617 ± 27
h_d^2	0.29	0.29	0.30	0.38	0.28	0.12

3. Genetic evaluation across countries

With environment variances shown to differ markedly across countries and the hypothesis of G*E interaction that could not be rejected, an animal model with maternal genetic effects, heterogeneous variances and different genetic correlations between countries was the model of choice. Specific genetic evaluation software was developed in order to evaluate the feasibility and the consistency of a multi-trait genetic evaluation. The within country estimates of the (co)variances (Table 3) were used and combined with the genetic correlation coefficients estimated in the joint analysis (Table 4).

The use of a multi-trait model, generated three country specific estimated breeding value (EBV) distributions that were correlated to 0.99 for FRA/GBR, 0.96 for FRA/IRL and 0.99 for GBR/IRL. For the 822 connecting bulls these correlations were almost identical (0.98, 0.92 and 0.98 respectively) indicating little re-ranking of bulls across countries. However, among the 54 highly connecting bulls (at least 25 progeny in each country), these correlations were lower: 0.91, 0.72 and 0.94 respectively. Consequent re-ranking was actually observed between FRA and IRL EBVs of some of these bulls.

In Table 5 are reported the statistics for each country specific sire EBVs for direct effects. The threshold value of the top 10% sires, used domestically, was given in order to fix the limit when foreign sires, used in other countries, might be usefully compared with the best domestic sires on the basis of the local EBVs.

Table 5. Within country EBVs of sire direct effects on weaning weights.

	Country of recording (kg)		
	FRA	GBR	IRL
Mean	7.8	6.3	4.3
s.d.	11.4	9.3	7.4
Threshold for top 10%	22.9	18.4	13.9

Table 6 shows how the choice of bulls might be expanded as a consequence of the joint evaluation of animals originating from different countries. For example, among the 1,274 sires used in IRL, the top 127 sires could be directly compared to 3,924 FRA and 278 GBR sires whose “Irish” EBV was estimated through genetic ties between countries.

Table 6. Origin of domestic sires and foreign sires with EBV > top 10% threshold.

Origin of domestic sires	Country of recording		
	FRA	GBR	IRL
FRA	58,153	231	250
GBR	7	2,416	57
IRL	0	3	955
others	2	0	12
Total	58,162	2,650	1,274

Origin of foreign sires > threshold	Country of recording		
	FRA	GBR	IRL
FRA	51	6,362	3,924
GBR	28	2	278
IRL	29	52	0

The first benefit that can be drawn from an international genetic evaluation in the Charolais breed would be the tremendous enlargement of the choice of the best seed stock provided by the comparability of foreign-used to domestic-used sires.

4. Conclusion

This first attempt of an international genetic evaluation of a beef breed in Europe clearly showed that the main benefit will be to widen the basis for selecting seed stock fitting the GBR and IRL Charolais populations as a consequence of the ability to compare domestic-used sires with the much larger FRA population.

The model used for this evaluation assumed genetic correlations between countries different from unity. Consequently, the breeders will have to deal with sires that have three breeding values for the same genetic effects. This complexity should be accepted if there were actual significant genetic*country interactions. The evidence was stronger that such interactions existed with IRL. However the accuracy of the estimated correlations was low. Further study is needed to understand the nature and factors involved in the low correlation between IRL and FRA, especially the possibility of preferential mating with the highly connecting bulls. The benefit of using a complex model (which treats WW in each country as correlated trait) *versus* a simpler model (that includes only the heterogeneity of the environment variances) should be questioned and needs more evidence of the existence of genetic*country interactions.

Most of the estimations of these genetic correlations and also the comparability of EBVs, rely on the genetic links across countries. Emphasis should be given to the constitution of a valid cross reference file and to tracing back the pedigree of imported seed stock. The clear identification of imported seed stock is the minimum requisite for integrating an international evaluation system. International identification rules should be clearly defined in order to avoid confusion between animals.

References

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