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First Steps Towards a European Joint Genetic Evaluation of the Limousine Breed

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Abstract

Weaning weights of Limousine calves recorded in France (n=1439088), Luxemburg (n=13175) and Ireland (n=7041) were analyzed. First, the connectedness level across these three countries was shown to be satisfactory. Within and across-country genetic parameter REML estimations were ran with a multivariate animal model. Direct heritabilities vary from 0.12 (Ireland) to 0.33 (France). Maternal heritabilities vary from 0.01 (Ireland) to 0.10 (Luxemburg). Genetic correlations between France and Ireland are not different from 1. Direct genetic correlation between France and Luxemburg is also high (0.78) but the maternal one is much lower (0.12). These results are analyzed in the light of the data structure. Their implications for the coming next Limousine European genetic evaluation are discussed.

1. Introduction

The Limousine breed, among others, has been developing in several European countries for the last four decades. Increasingly, breeders are seeking to compare domestic and foreign seed stock in order to enlarge their choice of breeding animals that best fit their own selection objectives. In collaboration with the Irish Cattle Breeding Federation (Ireland), the Institut de l'Élevage (France), and INTERBULL subcommittee of ICAR, a research program was conducted by INRA (France) and AGBU (Australia) with the purpose of developing a European genetic evaluation.

Several joint genetic evaluations already exist between countries with supposed similar farming systems and conditions. The models used in these evaluations assume no Genotype by Country interactions, i.e. the ranking of the bulls is identical in each country. Moreover, larger differences can be expected between countries and more technical issues have to be considered when implementing an across-country genetic evaluation. The two preliminary steps consist in checking (and optimizing) the connectedness between the populations and estimating the within and across country genetic parameters (genetic and

maternal correlations). Depending on these estimations, the model for implementing the international genetic evaluation can be defined and a specific ranking of the bulls for each participating country can be obtained.

Phocas *et al.* (2005) compared 3 strategies for an international genetic evaluation of beef cattle and showed that the best one was an animal model taking into account across-country interactions. According to the genetic parameters, this model should include non-unity genetic correlation and heterogeneous residual and genetic variances across countries. Quintanilla *et al.* (2002) and Renand *et al.* (2003) showed the feasibility of such an approach and ran the first European genetic evaluation in the Charolais breed for the weaning weight, based on a multitrait model (one trait per country).

This paper presents the results of these two steps in the development of an European genetic evaluation of the pure Limousine breed population in Ireland, Luxemburg and France: a) the connectedness level across countries; b) the genetic parameters of weaning weight within countries (heritabilities) and across countries (genetic correlations). Meanwhile, the particularities of the beef cattle data will be discussed.

Table 1. Descriptive statistics of the three Limousine populations.

	Ireland	Luxemburg	France
Number of adjusted weaning weights (AWW)*	7040	13175	1439088
Average AWW * (kg) (std)	260 (42)	256 (42)	255 (38)
AWW * (kg) (std) for males	272 (42)	270 (36)	268 (39)
AWW * (kg) (std) for females	245 (38)	243 (36)	242 (32)
Male proportion	55,6	51,2	51,3
Number of herds	346	76	5620
Median, min and max number of			
birth year per herd	2 [1;18]	5 [1;17]	7 [1;33]
AWW per herd	6 [1;440]	29 [1;1750]	110 [1;3317]
herd-year of birth	3 [1;46]	14 [1;140]	21 [1;245]
Median number of calves per dam	1	3	3

* weaning weight is adjusted at 210 days for Luxemburg and France, and 200 days for Ireland.

2. Data description

2.1 Initial population data

This study considered only the pure Limousine breed animals. A total of 8707 age adjusted weaning weights (AWW), recorded between the mid 70's and 2005 in Ireland, was provided to INRA for the study, associated with the potential influencing factors (sex, birth date, herd, dam age at calving). Animals originating from Luxemburg are routinely evaluated in the French genetic evaluation, IBOVAL. Luxemburg animals were therefore extracted from the database used in IBOVAL. Only the years of birth from 1986 and 2005 were selected in order to have enough information in each population.

Weaning weight (WW) was adjusted to 200 days in Ireland (IRL), and 210 days in France (FRA) and Luxemburg (LUX). Table 1 provides the adjusted weaning weights statistics for the three initial populations and the three population samples considered for the genetic parameters estimation. Although adjusted ten days older, AWW of the French and Luxemburg animals are lightly smaller than the Irish ones.

2.2 Data structure

A description of the data structure for each population is given by Table 1. The major differences are found between the Irish population and the two others: it can be first noticed that a greater proportion of males are weighted in Ireland. The herd size and the number of birth year per herd-year of birth are also reduced in Ireland compared to the ones in the two other countries, leading to a small number of performances par herd-birth year. Moreover, more than fifty percents of the Irish dam have only one calf.

A data selection is needed to use these data in the genetic parameters estimation.

3. Connectedness level across countries

Connectedness between countries is also a critical point for a reliable international evaluation. Weak genetic links between countries can affect predicted genetic values and ranking of the animals. As shown by Fouilloux *et al.* (2006), the crucial issue of disconnectedness was a bias in predicting potential differences in the genetic levels of the different countries.

Table 2. Proportion of weight-recorded animals sired by common used bulls

	France	Luxemburg	Ireland
France	100 %	13 %	10 %
Luxemburg	32%	100 %	5%
Ireland	37%	25%	100 %

Gene flow from France to Luxemburg and Ireland was important: 79 % (resp. 63%) of weight-recorded animals in Luxemburg (resp. Ireland) had a French-born sire. It was more important than for Irish Charolais cattle, where only 32% of calves had at least one French parent (Renand *et al.*, 2003). Because of this important gene flow, the genetic levels of the three countries are likely to be similar.

Moreover, direct connections between countries were established through bulls siring calves in different countries. In Table 2 are reported proportions of calves sired by bulls used at least in two countries. These proportions were rather high in Ireland, where 37% (resp. 25%) of calves are sired from bulls that are also used in France (resp. Luxemburg), but also 25% of the calves are sired from bulls that are also used in Luxemburg. As a conclusion, the connectedness level among the three countries appears to be satisfying.

4. Data sampling

Genetic parameters estimation is very time consuming and can not include too many animals. Nevertheless, the data sampling must insure that there will be a) enough data to estimate the fixed effects (especially in the Irish case) and b) enough genetic links between the countries to estimate the genetic correlations. Thus, this data selection consists in keeping a maximum of informative Irish and Luxemburg animals while limiting the number of French data.

In case of the Irish data, we only considered herds with at least 7 birth years with more than one performance and a consistent sex ratio. Eventually, 2902 performances from 26 herds were selected.

In Luxemburg, 9595 AWW from 34 herds were kept after the same selection method.

On the other hand, the French data sampling has been based on the connection between the selected Irish data and initial French one: we considered the French herds using breeding bulls with more than 2 offsprings in Ireland. Within this pool of French herds, we then only selected the ones that used the largest panel of common bulls. This process led to the choice of 27 French herds corresponding to 18360 performances.

5. Model of analysis

Following the conclusion of Phocas *et al.* (2005), the model used to estimate the genetic parameters (within and across countries) is a single-trait Animal Model accounting for Across-Country Interactions (AMACI). This model is equivalent to the multiple trait model used by Renand *et al.* (2003) 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).

6. Within and across country estimates of genetic parameters estimation

Within country genetic parameters were first estimated for each country separately (Table 3). Estimates of variance components were quite heterogeneous across countries, with Luxemburg estimates intermediate between French and Irish ones. The estimate of direct genetic variance in France was larger than the two others. On the opposite, the environmental (maternal and residual) variances are lower in France.

The small amount of information available in Ireland to separate direct and maternal genetic effects made difficult the estimation of the maternal variance components (σ_m^2 , σ_c^2 , r_{dm}) in this country. It leads to a very low maternal heritability (0.01). This may be explained by the Irish data structure (number of birth years per herd, number of weighted females...) and a lack of depth in the pedigree. Due to the high standard error of the direct-maternal genetic correlation, a likelihood ratio test showed that a model with direct-maternal correlation fixed to 0 was as good as the complete model for Irish data.

Table 3. Independent estimates of within country genetic parameters for each country (standard error in brackets).

	France	Irlande	Luxemburg
σ_p^2	754 (11)	1062 (32)	906 (14)
σ_d^2	245 (25)	130 (60)	187 (30)
σ_m^2	71 (13)	15 (36)	87 (21)
σ_c^2	46 (8)	123 (35)	82 (13)
σ_e^2	421 (14)	788 (44)	605 (19)
r_{dm}	-0,22 (0,09)	0,14 (1,01)	-0,43 (0,11)
h^2_d	0,33 (0,03)	0,12 (0,06)	0,21 (0,03)
h^2_m	0,09 (0,02)	0,01 (0,03)	0,10 (0,02)
c^2	0,06 (0,01)	0,12 (0,03)	0,09 (0,01)

Subsequently, bi-trait models between France-Ireland and between France-Luxemburg were fitted to estimate genetic correlation across countries (Table 4).

A preliminary analysis of French and Irish data, under a model with maternal genetic effects assumed to be correlated with the direct effects within and across countries, showed

low convergence due to the uncertainty on Irish maternal effects and to the extremely high correlation estimates for both direct and maternal genetic effects across countries. Since all the direct-maternal covariances (within and across countries) seemed to be close to 0 and the maternal genetic correlation between the two countries being close to one, a model assuming no correlation between direct and maternal genetic effects and a maternal genetic correlation fixed to 0.98 was fitted to get a proper convergence. With these constraints, the direct genetic correlation between these two countries is unity.

A high direct genetic correlation (0.78) was estimated between France and Luxemburg while the maternal correlation value was very low (0.12).

Table 4. Within and across country estimates of genetic parameters (standard error in brackets).

	FRA	IRL	FRA	LUX
<i>Nb perf.</i>	18360	2902	9975	9595
σ_p^2	754 (11)	1101 (34)	779 (14)	891 (16)
σ_d^2	218 (19)	158 (54)	206 (30)	200 (35)
σ_m^2	58 (10)	37 (31)	89 (22)	73 (24)
σ_c^2	43 (8)	126 (34)	67 (13)	71 (15)
σ_e^2	435 (12)	780 (42)	474 (19)	591 (22)
r_{dm}	0*	0*	-0.41 (0.11)	-0.36 (0.14)
h^2_d	0,29 (0,02)	0,14 (0,04)	0,26 (0,04)	0,22 (0,04)
h^2_m	0,08 (0,01)	0,03 (0,03)	0,11 (0,03)	0,08 (0,03)
c^2	0,06 (0,01)	0,11 (0,03)	0,09 (0,02)	0,08 (0,02)
$r_{dFra-d2}$	1 (0.15)		0,78 (0,18)	
$r_{mFra-m2}$	0,98*		0,12 (0,43)	
$r_{dFra-m2}$	0*		- 0,09 (0,31)	
$r_{mFra-d2}$	0*		0,05 (0,31)	

(* fixed value)

7. Implications

This preliminary analysis before implementing the first European genetic evaluation of the Limousine breed showed enough connections between France, Ireland and Luxemburg and provided within and across country genetic parameters.

The two high direct genetic correlations between France-Ireland and France-Luxemburg mean practically that no Genotype x Country interaction is to be considered in the joint genetic evaluation model: there would be no reranking of bulls depending on the country where they are used with regards to their direct genetic values. Reranking is however expected between France and Luxemburg for the maternal genetic values. Further investigations are needed to improve the estimation of the maternal effects and the associated variance components in Ireland and Luxemburg.

All the elements needed to start the European genetic evaluation of the Limousine breed are now at our disposal.

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