

Beef without Borders: Genetic Parameters for Charolais and Limousine Interbeef Genetic Evaluation of Weaning Weights

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Abstract

Following the setting up of the new Interbeef service at the Interbull Centre and the entry of Denmark and Sweden into the project, the complete Interbeef process has been rerun in 2008-2009. This new analysis of weaning weights from Denmark, France, Ireland, United Kingdom and Sweden pointed out large difference in data amount, data structure and low connection level between countries.

A multiple country model with direct genetic effects and only permanent environment maternal effect has been chosen and corresponding genetic parameters have been estimated to provide all the tools necessary to run a new joint genetic evaluation.

Keywords: interbeef, genetic parameters, weaning weight

1. Introduction

The previous works realized in the frame of the EUropean BEef EVALuation (EUBEEVAL) and thereafter the Interbeef project consisted in building up the different components of the international beef evaluation engineering: French Livestock Institute (IE) and INRA have developed a software dedicated to multi-country evaluation with maternal effects and specific fixed (covariable or categorical) effect models for each country. It has been used to run a first joint genetic evaluation in 2007 between France (FRA), Ireland (IRL) and United Kingdom (GBR) for pure bred Limousine weaning weights (Venot *et al.*, 2007).

In 2008, connectedness and reliability were assessed to complete the whole Interbeef process:

- connectedness between countries has been assessed following Fouilloux and Laloë method (Fouilloux *et al.*, 2006) using a software developed by IE and INRA for dairy and beef Interbull evaluations,

- reliabilities were estimated using Sullivan's MTEDC software (Sullivan, 2007). In its 2008 version, this software allows to derive approximated reliability from Effective Daughter Contribution (EDC).

Since 2007, Denmark (DNK) and Sweden (SWE) have joined Interbeef and the new Interbeef service has taken place at the Interbull Centre to manage data exchange between countries. A new Interbeef run, from data preparation to genetic evaluation, was performed in 2008-2009.

This article presents the preparation of the different ingredients needed for Interbeef evaluation.

2. Data description

Only pure bred Charolais and Limousine calf weaning weights (WW) were considered in this study. For this new run, Denmark, France, Ireland and Sweden sent raw data for both breeds, while United Kingdom sent only Limousine data.

Raw performance and complete pedigree data were gathered by Interbeef service for initial editing before being sent to INRA for

data preparation and further editing, genetic parameter estimation and breeding values prediction.

Table 1. Descriptive statistics of the populations.

	DNK		FRA		GBR	IRL		SWE	
Breed	CHA	LIM	CHA	LIM	LIM	CHA	LIM	CHA	LIM
Number of AWW	10 863	29 046	2 533 253	1 531 675	79 300	10 826	7 170	78 341	15 085
Number of animals in pedigree	125 537	270 151	3 473 468	1 985 826	129 067	39 337	23 878	103 104	19 126
Number of herds	430	918	7 181	5 236	781	2 015	886	1 392	286
AWW mean* (in kg) (std)	294 (47)	269 (40)	276 (47)	259 (38)	267 (41)	280 (51)	258 (42)	234 (43)	212 (36)
- for males	311 (47)	285 (40)	292 (49)	273 (39)	284 (41)	293 (52)	270 (42)	253 (43)	225 (37)
- for females	278 (40)	257 (34)	261 (38)	247 (32)	249 (34)	246 (46)	243 (35)	224 (35)	202 (30)
Male proportion in herd	60 %	57 %	49 %	49 %	53 %	67 %	60 %	49 %	50 %
Median [min, max] number of year per herd	2 [1,21]	3 [1,21]	8 [1,21]	7 [1,21]	4 [1,20]	1 [1,18]	1 [1,18]	4 [1,14]	4 [1,14]
Median [min, max] number of AWW per herd-year	4 [1,96]	5 [1,125]	37 [1,330]	27 [1,248]	11 [2,290]	1 [1,69]	2 [1,66]	7 [1,204]	6 [1,95]
Proportion of females with only one calf in the dataset	44 %	38 %	30 %	24 %	53 %	75 %	73%	29 %	30 %
<i>for genetic param. estimation</i>									
number of selected AWW	7 012	22 693	58 771	76 866	75 284	7 207	4 875	7 211	13 561

(* AWW is adjusted to 210d in FRA, to 200d in DNK, IRL and GBR. AWW is weight gain between birth and 200 days in SWE)

2.1 Trait definition

The computation of WW differs according to the countries. Details concerning the national genetic evaluations of WW are available on the Interbull website (<http://www-interbull.slu.se/Interbeef>).

FRA and GBR consider in their national model adjusted weaning weights (AWW) at 210 days and 200 days respectively whereas SWE uses weight gain between birth and WW adjusted to 200 days. These AWW are computed based on several recorded weights. IRL uses the average of weights and ages recorded between 150 and 300 days (mostly only one weight). In DNK a single weight recorded between 140 and 260 days is used. In these two latter countries, weaning weight is regressed on weaning age in the national model. However, the first Interbeef call of data for this study mentioned only AWW. Therefore, these countries sent also WW adjusted to 200 days base on the population.

2.2. Data structure

To have a common study period for all countries, calves born since 1988 were taken into account. The largest population were obviously found in France with more than 80 000 CHA and 50 000 LIM weights per year (ww/y). GBR LIM population follows with more than 3 000 ww/y with a large increase between 2002 and 2006 and a large decrease starting in 2007. On the other side, Sweden has more CHA data than LIM ones (more than 3 000 ww/y for CHA and less than 1 000 ww/y for LIM). DNK and IRL populations are smaller due to country size and non inclusion of the IRL cross bred animals.

Large differences in data structures can be found between countries, as shown in Table 1. Ireland presents the most particular data structure for both breeds, with more than 50% of the herds recorded only one year and about 75% of the dams with only one recorded calf. Moreover, more males than females are

weighted in IRL and DNK, suggesting a non-exhaustive recording in these countries.

2.3 Editing

Only animals with known herd, birth date and dam and with AWW within 3 standard deviations from the mean were retained. Twin and embryo transfer were also discarded from the analysis.

3. Interbeef pedigree and connectedness between countries

3.1 Common pedigree preparation

The major work in Interbeef data preparation consisted in validating the identification of the foreign animals by their country of origin: each country first detected the foreign animals in its database and then sent this list to the different countries of origin with the help of Interbeef service. The validated animals were then added to a central Cross Reference File (CRF) that gives eventually the correspondence between national and international identification for the foreign animals used abroad. In each country, only foreign animals validated in the CRF were considered as real foreign animal.

After this first validation step, all pedigree were merged into a common “Interbeef pedigree” file. A general check of this file permitted to correct two kinds of inconsistency: wrong country of origin and error in pedigree of foreign animals used in national evaluations.

3.2 Origin of the paternal genes

Similarly to Bouquet *et al.* (2009), probability of gene origin was computed using the whole pedigree file up to founders. Proportion of foreign paternal genes has been estimated in the different populations (table 2). All kind of profiles can be found: Ireland with more than 70% of the paternal genes coming from France or France with only trace of foreign genes in the population.

Table 2. Origin of paternal genes per country.

Country	CHA	LIM
DNK	47% (46,6% FRA + 0,4% SWE)	47,6% (46,2% FRA + 0,5% GBR)
FRA	0%	0,02% GBR
IRL	72,4% (FRA)	81,2% (73% FRA + 8,2% GBR)
GBR		43,6% (FRA)
SWE	11,5% (7,1% DNK + 4,1% FRA + 0,3% IRL)	34,7% (19,4% FRA + 15,3%DNK)

3.3 Connectedness measure

The connectedness criterion defined by Fouilloux *et al.* (2006) was computed in each breed. This criterion, the mean rate of bias re-estimation, is obtained by simulation with a sire model and uses the real population structure. Results are presented in table 3 for each country and breed.

Table 3. Connectedness measure: mean rate of bias re-estimation.

Country	CHA	LIM
DNK	8,2%	17%
FRA	2,7%	13%
IRL	-3,2%	17%
GBR		6%
SWE	7,2%	10%

(Example: when the same difference of genetic levels is introduced by simulation between SWE and other countries, only 7,2% in average of this difference is fully re-estimated through genetic links between SWE and the other countries, indicating low connection level.)

Connecteness between countries is very low in both breeds, especially in CHA. In comparison, Interbull dairy connectedness values are much larger, above 70% for a majority of countries (Fouilloux *et al.*, 2008). Similarly a high connectedness level, above 50%, was found between French regions for weaning weights in CHA breed (results not shown).

Although this criterion takes into account the probability of paternal gene origin in the whole pedigree, it depends primarily on direct connexion through common sires and poorly on common ancestors in the pedigree. Bouquet *et al.*, (2009) showed that the French pedigree file provided old (4th to 5th generation) genetic links to DNK, IRL, SWE and GBR Limousine pedigree files.

3.4 Common bulls

Numbers of common bulls used in different countries are reported in table 4 and numbers of progeny of these common bulls tested in the different countries are reported in tables 5 and 6.

Table 4. Origin of the connecting bulls and number of countries with progeny of these bulls.

	Number of countries				Total
	2	3	4	5	
Charolais					
DNK	1				1
FRA	111	33	13		157
IRL	4				4
SWE	6	2	1		9
Total	122	35	14		171
Limousine					
DNK	14	1	2	1	18
FRA	248	48	25	7	328
GBR	24	5	1	1	31
IRL	9				9
SWE	4	2		1	7
Total	299	56	28	10	393

The number of connecting bulls is rather small for both breeds: 171 CHA and 393 LIM. They are predominantly originating from France (92% for CHA and 83% for LIM). Most of them (70%) are used in only 2 different countries.

Table 5. Number of CHA common bulls and percentage of their progeny in the performance file of country 1 (between brackets).

Charolais		Country 2			
		DNK	FRA	IRL	SWE
Country 1	DNK	736	68 (16%)	40 (13%)	23 (12%)
	FRA	(10%)	66 287	128 (10%)	32 (7%)
	IRL	(12%)	(4%)	1 402	20 (17%)
	SWE	(1%)	(1%)	(1%)	2 945

Table 6. Number of LIM common bulls and percentage of their progeny in the performance file of country 1 (between brackets).

Limousine		Country 2				
		DNK	FRA	GBR	IRL	SWE
Country 1	DNK	1 657	71 (11%)	50 (9%)	36 (7%)	24 (6%)
	FRA	(12%)	30 788	251 (15%)	113 (13%)	26 (9%)
	GBR	(3%)	(7%)	3 878	128 (14%)	21 (1%)
	IRL	(20%)	(36%)	(48%)	825	15 (1%)
	SWE	(5%)	(4%)	(3%)	(3%)	604

The corresponding populations of progeny sired by these connecting bulls in the different countries are also of limited size.

4. Fixed effect model

Interbeef model should be as close as possible to the national models but several national particularities couldn't be taken into account in the international model, such as multiple breed evaluation characteristics for IRL, different definitions of genetic groups for DNK, IRL and GBR or weight regressed on the age at weighing for DNK and IRL.

Country specific fixed effects definitions are given in table 7.

Table 7. Fixed effects definition (number of levels between brackets).

DNK	Sex (2), Season of calving (7), Age of Dam x Parity (19)
FRA	Sex (2), Season of calving (11), Age of Dam x Parity (24)
IRL	Sex (2)
GBR	Sex (2), Calving month (12), age of dam and (age of dam) ² as covariables
SWE	Sex (2), Season (5), Age of dam (3).

5. Genetic parameter estimation

For each breed, genetic parameter estimation has been first run for each country separately. It has not been possible to run the genetic parameter estimation with the complete set of countries for both breeds. The matrices of genetic parameters have been therefore constructed with successive 2 by 2 or 3 by 3 estimations.

5.1 Data sampling

Data sampling mainly concerned France. Only French herds using breeding bulls with progeny in other countries and the largest panel of common bulls were retained.

For all countries, small contemporary groups (<3 WW) and little-used sires (< 3 offspring) were discarded.

Five generations were considered in the pedigree. The results of this selection process are given in table 1.

5.2 Model of analysis

Data amount and structure, as well as the lack of maternal information for some countries didn't allow getting proper maternal genetic parameter. A simplified model including direct genetic effects and a maternal permanent environment effect appears to be the best compromise between feasibility and accuracy. To limit computing time, genetic parameter estimations were performed using a sire model with a non genetic dam effect. The results were then transformed for animal genetic evaluation model. ASREML software (Gilmour *et al.*, 2000) has been used for these estimations.

5.3 Within country estimation

Genetic parameter estimates are in Table 8 and 9. They are quite similar between all countries except for Ireland. IRL shows much larger phenotypic variances for both breeds (1.6 times higher than French CHA variance and 1.4 for LIM). With $h^2 = 0.50$, IRL CHA direct heritability is also higher than the others. This can be due to the fact that only pure bred animals are considered in the study limiting the number of IRL data taken into account but also to the fact that not all the animals in the herds are weighted, leading maybe to selection bias.

5.4 Between country estimation

For several between country estimations, no convergence was reached certainly due to a lack of connection between the countries. It has been the case between Ireland and Sweden or Denmark and Sweden for Charolais breed. For this second case, inclusion of the French data allows to get proper estimates between DNK and SWE.

Besides, lots of the direct genetic correlations were close to the parameter space limit 1 and had to be fixed to 1 (technically to 0.99 in ASREML).

Eventually, the bending method of Jorjani (Jorjani *et al.*, 2003) was applied in order to get definite positive matrices

This method allows taking into account the amount of information available for the estimation. In this case, the number of bulls and common bulls between the countries were used to perform the weighted bending.

The resulting matrices of genetic parameters are in table 8 (CHA) and table 9 (LIM). Direct genetic correlations are high between the different countries, above 0.75 for both breeds and are higher for Limousine than for Charolais breed. However, the accuracy of these estimates is limited with standard errors for a majority of correlation estimates around 0.15. Low connectedness and particular data structures pointed out during data preparation can explain this low accuracy and difficulties in estimating genetic correlations.

6. Conclusion

The new run of international identification validation has permitted to clean up pedigree and detect new connecting bulls. However, connection between the participating countries appeared rather low compared to dairy values or within France values, due to the lack of direct sire connexions. Along with particular data structure in several countries, this low connexion leads to imprecise genetic correlations among countries.

With checked data and pedigree files and a set of genetic parameters at its disposal, Interbeef team can now begin to cook an international genetic evaluation of weaning weight.

7. References

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Table 8. Interbeef genetic parameters for Charolais breed (correlation standard errors between brackets).

(variances above the diagonal, corr. below)		DNK	FRA	IRL	SWE
Direct genetic effect	DNK	310	232	510	214
	FRA	0.77 (0.15)	291	425	256
	IRL	0.99*	0.85 (0.10)	863	396
	SWE	0.79 (0.20)	0.98 (0.06)	0.88*	235
Phenotypical variance		1034	1076	1725	898
Permanent environment variance		124	204	380	225
Residual variance		600	581	483	439
Direct heritability		0.30	0.27	0.50	0.26

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Table 9. Interbeef genetic parameters for Limousine breed (correlation standard errors between brackets).

(var. above the diag., corr. below)		DNK	FRA	GBR	IRL	SWE
Direct genetic effect	DNK	298	245	208	293	247
	FRA	0.95 (0.03)	221	205	247	219
	GBR	0.84 (0.14)	0.96 (0.05)	205	215	202
	IRL	0.99*	0.97*	0.88 (0.11)	291	246
	SWE	0.95*	0.98*	0.94*	0.96*	227
Phenotypical variance		692	670	790	970	629
Permanent env. variance		97	127	158	116	138
Residual variance		297	322	427	563	264
Direct heritability		0.43	0.33	0.26	0.30	0.36

(*: correlation first fixed at the parameter space limit and maybe modified by the bending process)