

Genetic Evaluation of calving ease traits for French beef bulls used for crossbreeding with dairy cows

Govignon-Gion A., Boulesteix P., Brunet J.L., Delpéuch A., Miller S.,
Venot E., Mattalia S.



The Project

◆ Today, 2 separate genetic evaluations of beef bulls for calving ease traits :

- Farm records of pure-breed calves (IBOVAL evaluation)
 - Bulls progeny tested for crossbreeding with dairy cows
 - Information specially recorded during progeny test
- => limited number of bulls and progeny

◆ Strong development of crossbreeding



Large-scale genetic evaluation of calving ease for crossbred calves, using on-farm records?

- Enough data with good quality in the national DB?
- Add records of crossbred calves in IBOVAL, or a new genetic evaluation ?

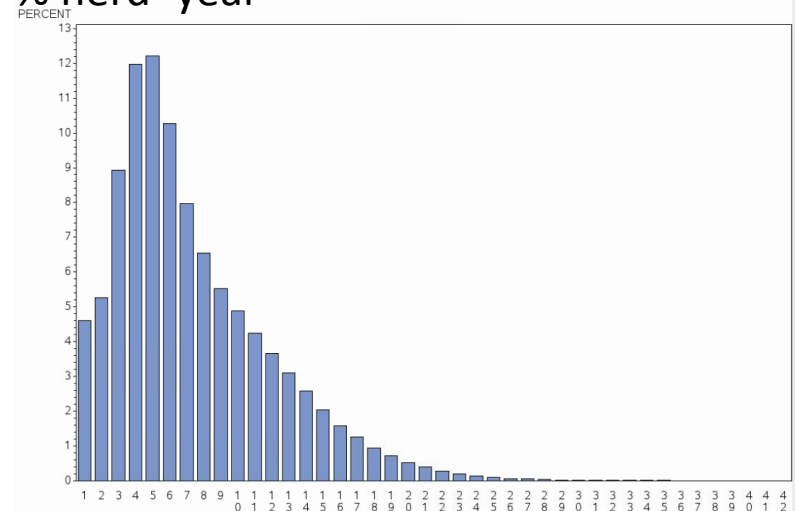


Data analysis

Sire	LIM, BLA , INRA95, BBF	CHA
	x	x
Dam	HOL	MON
Traits	BC : Birth Condition Score (1->5) and BW : Birth Weight (kg)	
Calves	crossbred calves born since 2000	

- ◆ Quality of data :
Enough variability of BC and **BW** within contemporary group (CG) ?
- ◆ Structure of population :
crossbred calves per sire, per CG,
common bulls with pure breed calves...?

% herd*year

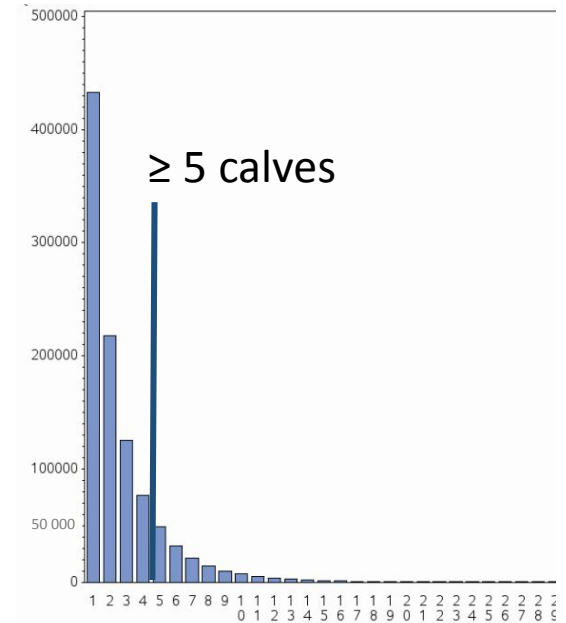


Nb different weights within H-Y in dairy herds (HOL)

Genetic parameters estimation (1)

- ◆ **Selection criteria** : should be adapted to the structure of the crossbred population (small size of CG).
- Selection of crossbreed calves:
 - BC **and** BW for each crossbred calves
 - CG = herd*year*sex ≥ 2 or 5 crossbred calves
 - ≥ 2 different values for each trait per CG
 - ≥ 10 calves per sire
- To estimate rg with pure breed: performances of calves born from “Common sires”

Nb herd*year*sex



Nb crossbred calves
(CHA)

Genetic parameters estimation (2)

◆ After selection data :

	CHA	LIM	INR	BLA	BBB
Crossbred Calves	184 179	112 916	47 197	20 384	153 008
Purebred calves	314 514	384 407	-	228 410	-
CG	25 732	19 455		3 585	22 168
Sires	1 253	2 128	144	662	554
Dams	120 334	99 316	43 148	18 342	114 598
% dam with 1 crossbred calves	67 %	89 %	90 %	91 %	85%

Cont. Group = herd*year*sex

Genetic parameters estimation (3)

- ◆ Multitrait Sire Model

BLA, LIM, CHA : BC_Cr, BW_Cr, BC_Pur, BW_Pur

INRA 95, BBF : BC_Cr, BW_Cr

- ◆ Fixed effects

herd * year * sex

birth_season * year

dam_age at birth * parity

- ◆ Random effects

genetic sire effect

for pure data only : permanent maternal environment effect

- ◆ Estimation using Wombat software (K. Meyer)

Genetic parameters (1)

◆ Heritability and *standard genetic deviation*

	CHA	LIM	INRA 95	BLA	BBF
BW_pur	0,43 <i>3,07</i>	0,45 <i>2,52</i>		0,48 <i>3,42</i>	
BC_pur	0,18 <i>0,30</i>	0,09 <i>0,12</i>		0,15 <i>0,23</i>	
	CHA*MON	LIM*HOL	INR*HOL	BLA*HOL	BBF*HOL
BW_cross	0,32 <i>3,03</i>	0,17 <i>1,73</i>	0,20 <i>2,20</i>	0,25 <i>2,32</i>	0,18 <i>2,05</i>
BC_cross	0,13 <i>0,25</i>	0,08 <i>0,19</i>	0,11 <i>0,23</i>	0,15 <i>0,26</i>	0,11 <i>0,24</i>

Pure breed: very consistent results with those used in IBOVAL

Crossbreed:

- Heritability lower for BW than in pure breed
- Difference between CHA*MON and the others

Genetic parameters (2)

- ◆ Genetic correlations between pure and crossbred traits

CHA* MON	BW_ pur	BC_ pur	BW_ cr
BC_pur	0,70		
BW_cr	0,90	0,65	
BC_cr	0,90	0,67	0,96

LIM* HOL	BW_ pur	BC_ pur	BW_ cr
BC_pur	0,60		
BW_cr	0,89	0,45	
BC_cr	0,93	0,55	0,91

BLA* HOL	BW_ pur	BC_ Pur	BW_ cr
BC_pur	0,66		
BW_cr	0,92	0,71	
BC_cr	0,86	0,58	0,83

High correlations for birth weight
Lower for birth condition score

➔ Could not be considered as the same trait

Genetic parameters (3)

- Genetic correlations between the traits in crossbred

CHA* MON	BW_ pur	BC_ pur	BW_ cr
BC_pur	0,70		
BW_cr	0,90	0,65	
BC_cr	0,90	0,67	0,96

LIM* HOL	BW_ pur	BC_ pur	BW_ cr
BC_pur	0,60		
BW_cr	0,89	0,45	
BC_cr	0,93	0,55	0,91

BLA* HOL	BW_ pur	BC_ Pur	BW_ cr
BC_pur	0,66		
BW_cr	0,92	0,71	
BC_cr	0,86	0,58	0,83

INR*HOL	BW_cr
BC_cr	0,97

BBF*HOL	BW_cr
BC_cr	0,95

High correlations between the traits BW and BC for crossbred calves

Genetic evaluation (1)

- BC_cr and BC_pur are not considered as the same trait
- Not possible to include a genetic maternal effect for crossbred calves

➔ **Develop a separate genetic evaluation for calving ease**
 ...but taking into account purebred calves information

◆ Genetic evaluation in 2 steps – Animal model

	LIM, BLA, CHA	BBF, INRA
First step	4 performances	2 performances
Animal model	BC and BW purebred	BC and BW crossbred
UNI-trait	BC and BW crossbred	
Second step	4 preadj	2 preadj
Animal Model	BC and BW purebred	BC and BW crossbred
MULTI-Trait	BC and BW crossbred	

pre_adjusted
data

Genetic evaluation (2)

- ◆ Data selection for evaluation

BC or BW for each crossbred calves

GC = herd*year \geq 2 calves

\geq 2 sires

\geq 2 different values for each trait

Number of calves and of sires included in the pilot run (June 2017)

	CHA*MON	LIM*HOL	INR*HOL	BLA*HOL	BBB*HOL
Crossbred Calves	461 041	392 392	167 617	67 807	469 609
Purebred Calves	3 350 225	2 008 208	-	1 222 990	-
« common » sires	1 728	2 113	-	1 071	-
Sires with cross only	1 937	2 435	121	508	980

Results and publication (1)

- ◆ EBV published and reliability

$$\text{IFNxt} = 0,50 * \text{BC_cross} + 0,50 * \text{WC_cross} \quad (\text{same weight for all breeds})$$

Expressed as a deviation from a standardized reference base :

- mean = 100
- genetic standard deviation=10

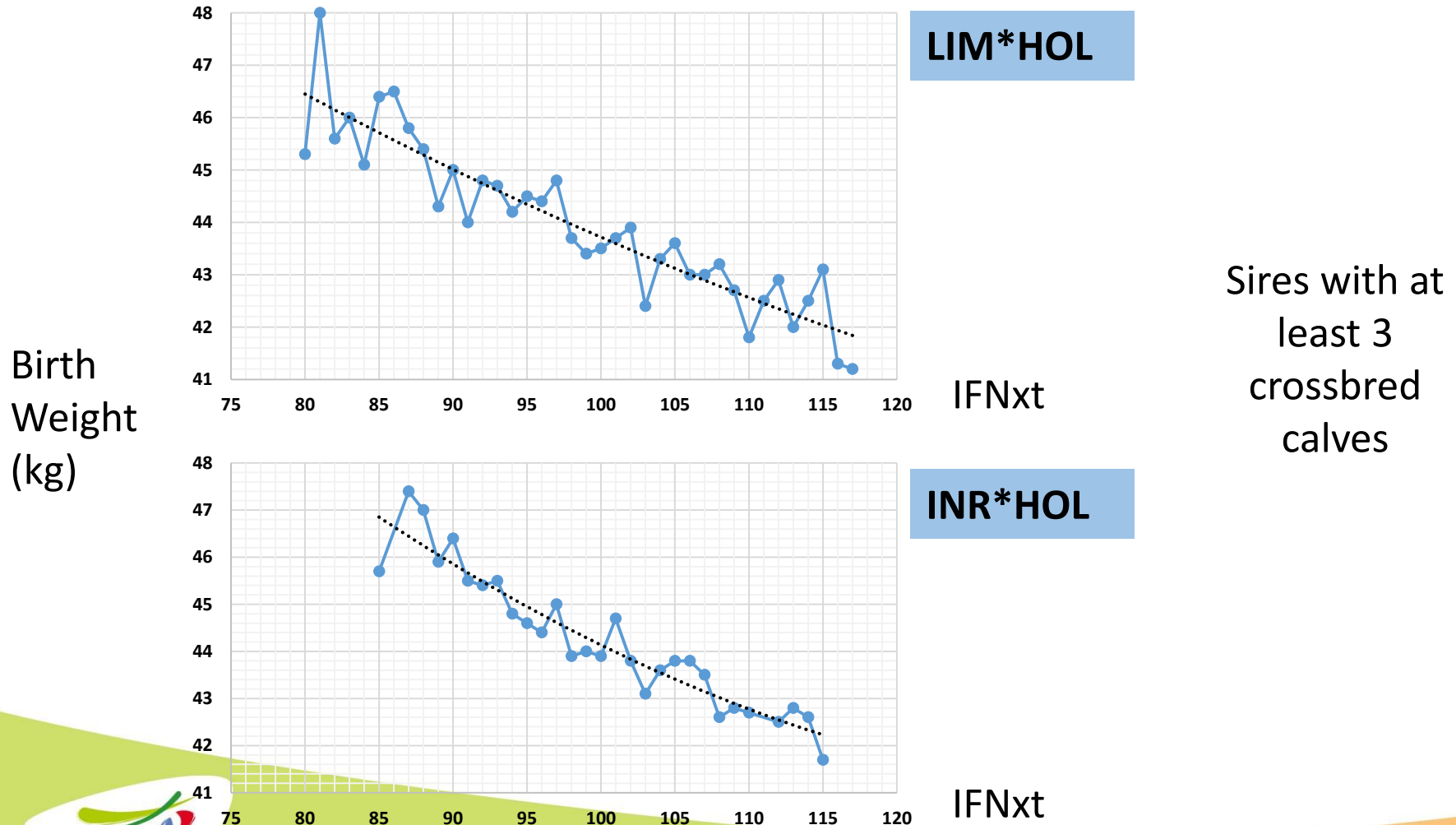
Computation of accuracy using MTEDC software (Sullivan)

- ◆ Official publication Reliability $\geq 0,50$
 ≥ 25 crossbred calves
 ≥ 10 calves for each traits BC and BW

June 2017	CHA*MON	LIM*HOL	INR*HOL	BLA*HOL	BBF*HOL
publishable sires	507	333	86	169	430

Results and publication (2)

- ◆ Relation between EBV and performance (crossbred calves)



Conclusion and perspectives

- ▶ This study showed that:
 - ▶ Birth condition could not be considered as a single trait in pure-breed and crossbreed situations
 - ▶ The performances recorded directly by the breeders at birth of their calves could be used for a large scale evaluation (=> no need for a special progeny test scheme & record of info)
- ▶ A specific evaluation, enhanced with pure-breed information
- ▶ First official evaluation planned in December 2017
- ▶ Perspectives

Evaluation expected for CHA * HOL

Multibreed evaluation (within a same maternal breed)?

Genomics ?

Thank you for your attention

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