Genetic Evaluation of Carcass Traits in Dairy Cattle

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Abstract

Two new genetic evaluations on carcass data, extracted from the Normabev database, have been developed by the UMT 3G (Gestion Génétique et Génomique des populations bovines). The first (VC) is a multi-breed evaluation of sires on their ability to produce veal calves. It evaluates sires of dual-purpose breeds Montbeliarde (MON) or Normande (NOR) and sires of beef breeds mated with dairy cows. The second (YB) evaluates sires of the MON, NOR and Simmental (SIM) breeds on their ability to produce young bulls for slaughter. The YB evaluation considers three traits simultaneously (carcass weight, age at slaughter and carcass conformation), the VC four (the same three, plus meat color). Heritability estimates are moderate to quite high for carcass weight and conformation (0.12 to 0.37, depending on the breed and the evaluation), lower for age at slaughter and meat color (0.05 to 0.27). Genetic correlations between carcass weight and conformation and between carcass weight and age at slaughter are favorable. Genetic correlations between YB traits on the one hand and VC, milk production and female type traits on the other hand were also estimated. These correlations are low to moderate (favorable) between YB and milk production. Hence, meat production traits can be improved without compromising genetic trends on milk production traits too much. YB traits are favorably correlated with VC (0.32 to 0.70) and female type traits. VC polygenic evaluations became official in 2015. YB polygenic evaluations will be official in 2017. YB and VC genomic evaluations are currently developed in MON and NOR, following the methodology applied in other dairy cattle genomic evaluations.

Key words: carcass traits, dairy cattle, France, veal calves, young bulls

Introduction

In France, a large part of the production of veal calves (VC) and young bulls (YB) comes from dairy cattle: between 2006 and 2013, 25% of slaughtered YB were purebred dairy breeds and 86% of VC were purebred dairy breeds or crossbred with dairy breeds (Institut de l'Elevage, INRA, 2015). However, genetic selection for meat traits has been very limited in dairy breeds until now. The only records available were cow type traits and, in Montbéliarde (MON) and Normande (NOR) breeds, measures of growth and muscularity of candidates to progeny testing (selection step abandoned several years ago) during their selection. For the production of VC for industrial crossbreeding, bull testing was used to control birth ease and meat performance of their offspring, but its management was difficult both locally and nationally.

The development of a genetic evaluation for carcass performances of YB in beef breeds since 2010 was possible due to the access to the NORMABEV (Interprofessionnal technical association for cattle and meat) database, which regroups the slaughter information of all cattle slaughtered in France. The UMT 3G (that associates INRA, Institut de l'Élevage and Allice) conducts studies since 2012 in order to use this database for dairy cattle. The objectives of these studies are:

i) To provide dairy breeders with keys to characterize dairy or beef bulls on their ability to produce offspring for VC production
ii) To give dual-purpose breeds new tools for the selection of bulls on YB carcass performances.

The main results of these studies and ongoing studies are presented in this article.

Materials and Methods

1.1 DATA IN THE NORMABEV DATABASE

The NORMABEV database contains, for each slaughtered animal, the following information : slaughter date (from which the Age at Slaughter AS can be calculated), carcass weight (CW), in kg, carcass conformation (CC) score, on the EUROP scale, each class divided into 3 subclasses, carcass fatness (CF) score, meat color (MC) score (for VC only), noted from 0 (white) to 4 (red). A preliminary study showed a too small variability of CF; hence only AS, CC, CW and MC (for VC) were used. For the analysis, CC scores were converted to numerical notes, from 1 (poor, P-) to 15 (excellent, E+).

1.2 DATA SELECTION FOR GENETIC PARAMETER ESTIMATION AND GENETIC EVALUATION

1.2.1 Evaluation of veal calves

Veal calves considered for genetic evaluation were either purebred MON or NOR (to evaluate MON and NOR bulls) or crossbred between MON, NOR or Holstein (HOL) dams and Charolais (CHA), Blonde d'Aquitaine (BLA), INRA 95 (I95), Limousine (LIM) or Blanc Bleu Belge (BBB) sires.

Data quality filters were then applied: VC were selected only if they were born after 2007, if they had both parents and last owner known, if they were slaughtered between 70 and 250 days of age and if they had a consistent CW (50 to 250kg).

Number of records and average performances available in June 2016 for VC genetic evaluations are presented in tables 1 and 2. The dams of VC crossbred with beef sires were mostly HOL except for VC with CHA sires, for which the dams were mostly MON (table 1). Only these breeds were used as maternal breeds to evaluate beef sires on VC traits.

For the estimation of genetic parameters (study done in years 2012 to 2014), only VC of bulls with at least 4 offspring for the NOR evaluation, 5 for the MON evaluation and 20 for the HOL evaluation were kept. For MON or NOR evaluations, only VC from dams with at least 2 offspring were kept, in order to allow proper estimation of maternal permanent environment effects. For HOL evaluation, fattening herds were eliminated if they had less than 30% crossbred VC, due to the large number of purebred HOL VC, in order to ensure proper estimation of crossbreeding genetic parameters.

In the end, dataset contained 48 203 VC records for the evaluation on HOL maternal breed, 17 201 on MON maternal breed and 4 013 on NOR maternal breed.

Table 1. Number of veal calves for the VC genetic evaluation in June 2016, per parent breed.

		Dam breed		
		HOL	MON	NOR
Purebred VC		3 270 660	693 463	284 600
Crossbred VC ; sire breed	BBB	238 028	51 297	15 872
	LIM	144 822	55 930	16 036
	CHA	129 284	223 304	17 254
	BLA	21 993	5 690	3 644
	I95	75 425	14 315	4 918

Table 2. Average (standard errors) VC performances available in June 2016.

Trait	Dam breed		
	HOL	MON	NOR
CW (kg)	133 (19)	136 (24)	131 (21)
CC* (cl)	0 (2scl)	R (2scl)	R- (2scl)
MC* (cl)	2 (1/2 cl)	2 (1/2 cl)	2 (1/2 cl)
AS (j)	175 (16)	166 (22)	167 (22)

* cl = class; scl = subclass

1.2.2 Evaluation of young bulls

The YB study, done in 2015, was carried out on French 3 main dual-purpose breeds (MON, NOR and Simmental (SIM)), willing to add meat traits to the traits currently under selection.

YB were selected if they were purebred males born between 2006 and 2012, if they had both parents known, if they were slaughtered between 12 and 24 months, if last owner was known and CW was consistent. Only YB of sires with at least 5 offspring were considered. In the end, 119 642 MON, 112 843 NOR and 5 456 SIM were selected.

Table 3 presents average performances of selected YB. They were very similar among breeds.

Table 3. Average (standard errors) performances of YB.

Trait	YB breed		
	HOL	MON	NOR
CW (kg)	382.9 (51.4)	381.9 (49.9)	387.7 (54.2)
CW* (cl)	R- (1scl)	0+ (1scl)	R- (1scl)
AS (j)	621.9 (67.5)	633.5 (63.1)	615.2 (78.8)

1.3 GENETIC PARAMETER ESTIMATION

1.3.1 Statistical analysis

Statistical model definition was carried out in specific studies (Promp, 2012, Croué *et al.*, 2016). Only final models are presented here.

Multitrait animal models were used to evaluate all traits simultaneously (3 traits for YB, 4 for VC).

The following model was used for the VC evaluation:

$$Y_{ijklm}=\mu+a_i+cont\_vc_j+agd_k+sex_l+bs_m+\varepsilon_{ijklm} \quad [1]$$

with Y_{ijklm} the veal calf performance (CC, CW, AS or MC), μ the general mean, $cont\_vc_j$ the contemporary group (fattening gerd*year of birth*season of slaughter), agd_k the age of the dam at calving, sex_l the veal calf sex, bs_m the sire breed, a_i the animal random genetic value and ε_{ijklm} the random residual value. A random maternal permanent environment effect was also included for AS on MON and NOR support.

The following model was used for the YB evaluation:

$$Y_{ijk}=\mu+a_i+cont\_yb_j+agdp_k+sb_l+\zeta_{ijkl} \quad [2]$$

with Y_{ijkl} the young bull performance (CW, CC, AS), μ the general mean, $cont\_yb_j$ the contemporary group (fattening herd*year of slaughter*season of slaughter),$agdp_k$ the age of the dam at calving in interaction with its parity, sbl the season of birth, a_i the random animal genetic value and ζ_{ijkl} the random residual value.

For YB, a heterogeneous residual variance was associated to the analysis of CW and CC to account for a higher variability of these performances in older animals. This is due to the fact that YB have to be slaughtered before 2 years old to be considered YB, with no consideration of weight or conformation.

1.3.2 Methods

Variance component estimation was performed using the Restricted Maximum Likelihood Method. Genetic values were estimated using the BLUP methodology using and INRA software, routinely used for the genetic evaluation of cattle.

1.4 ESTIMATION OF GENETIC CORRELATIONS BETWEEN VC AND YB TRAITS AND WITH OTHER TRAITS UNDER SELECTION

During the study on YB traits, genetic correlations with other traits were estimated, especially with VC traits, dairy production traits and cow conformation traits.

A two-step approach was used (Ducrocq *et al.*, 2001): for each evaluation (YB, VC and other official genetic evaluation - Institut de l’Elevage, INRA, 2016), the phenotypes were first corrected for all environmental effects of the model used. The genetic correlation between YB traits and each other group of traits (VC, production and conformation) were then estimated (with REML) through a multi-trait model using the corrected performances as phenotypes. This model only includes a birth year effect and an animal genetic effect.

Results & Discussion

2.1 ESTIMATED GENETIC PARAMETERS – VC AND YB

Heritabilities obtained for VC and YB traits were consistent between similar traits and among breeds (tab. 4 and 5).

For VC, they were always higher for calves with MON or NOR dams than for calves with HOL dams.

Heritabilities were moderate for CW (0.18 to 0.27 for VC, 0.12 to 0.19 for YB) and CC (0.22 to 0.37 for VC, 0.21 to 0.26 for YB), low to moderate for AS (0.05 to 0.27 for VC, 0.08 to 0.17 for YB). Genetic correlations were moderate to high and positive between CW and CC, low to high and negative (favorable) between CW and AS. Genetic correlations between AS and CC were slightly positive to moderately negative (favorable) for MON and NOR maternal breeds (-0.25 to 0.16). The high standard error observed for SIM did not allow us to conclude anything.

MC appeared to be slightly to moderately correlated with VC conformation.

Tables 4. VC genetic parameters (diagonal: heritabilities, below diagonal: phenotypic correlations, above diagonal: genetic correlations, standard error in brackets).
4a – Holstein maternal breed.

	CW	AS	CC	MC
CW	**0.18 (0.01)**	- 0.18 (0.08)	0.59 (0.04)	0.02 (0.07)
AS	0.16 (0.00)	**0.05 (0.01)**	0.02 (0.08)	-0.18 (0.09)
CC	0.53 (0.00)	-0.05 (0.01)	**0.22 (0.02)**	-0.07 (0.07)
MC	0.01 (0.01)	0.06 (0.00)	-0.07 (0.01)	**0.90 (0.01)**

4b –Montbéliarde maternal breed.

	CW	AS	CC	MC
CW	**0.27 (0.03)**	- 0.14 (0.09)	0.77 (0.04)	-0.34 (0.11)
AS	0.03 (0.01)	**0.27 (0.03)**	0.12 (0.08)	0.16 (0.12)
CC	0.69 (0.01)	0.00 (0.01)	**0.37 (0.04)**	-0.25 (0.10)
MC	-0.12 (0.01)	0.04 (0.01)	-0.18 (0.01)	**0.10 (0.02)**

4c – Normande maternal breed.

	CW	AS	CC	MC
CW	**0.24 (0.01)**	-0.03 (0.00)	0.68 (0.00)	0.05 (0.00)
AS	0.09 (0.02)	**-0.09 (0.00)**	0.16 (0.00)	0.51 (0.00)
CC	0.66 (0.01)	-0.04 (0.02)	**0.34 (0.01)**	-0.42 (0.00)
MC	-0.03 (0.02)	0.05 (0.02)	-0.09 (0.03)	**0.11 (0.00)**

Tables 5. YB genetic parameters
5a – Montbéliarde breed.

	CW	AS	CC
CW	**0.19 (0.01)**	-0.58 (0.05)	0.52 (0.03)
AS	0.16 (0.00)	**0.09 (0.01)**	-0.25 (0.06)
CC	0.54 (0.00)	0.03 (0.00)	**0.23 (0.01)**

5b – Normande breed.

	CW	AS	CC
CW	**0.12 (0.01)**	-0.49 (0.06)	0.47 (0.04)
AS	0.16 (0.00)	**0.17 (0.01)**	-0.02 (0.05)
CC	0.57 (0.00)	0.03 (0.01)	**0.26 (0.02)**

5b – French Simmental breed.

	CW	AS	CC
CW	**0.17 (0.04)**	-0.71 (0.15)	0.30 (0.13)
AS	0.17 (0.02)	**0.08 (0.03)**	0.11 (0.18)
CC	0.48 (0.01)	0.07 (0.02)	**0.21 (0.04)**

2.2 GENETIC CORRELATIONS BETWEEN YB TRAITS, VC TRAITS AND OTHERTRAITS UNDER EVALUATION

See Croué *et al.*, 2016 for all the results.

Table 6. Genetic correlations between VC and YB similar traits.

	CW	AS	CC
MON	**0.43 (0.05)**	0.40 (0.08)	0.54 (0.04)
NOR	0.44 (0.06)	**0.32 (0.09)**	0.70 (0.03)

Table 7. Genetic correlations between YB conformation and cow type traits.

	CW	MC
	Muscularity at whithers	0.37 (0.04)
MON	Muscularity at thighs	0.45 (0.04)
	Muscularity at top line	0.51 (0.03)
NOR	Muscularity at loin	0.35 (0.04)
	Muscularity at thighs	0.59 (0.03)
SIM	Muscularity	0.36 (0.09)

Table 8. Genetic correlations between milk production and YB traits.

	CW	AS	CC
MON	0.18 (0.04)	-0.21 (0.06)	-0.02 (0.04)
NOR	0.08 (0.05)	-0.21 (0.05)	-0.13 (0.04)
SIM	0.26 (0.09)	-0.36 (0.14)	-0.01 (0.09)

Correlations between VC and YB similar traits (table 6) were high: bulls with a high genetic potential for one kind of production also have a high potential for the other.

In the three breeds, genetic correlations between cow type traits related to muscularity and YB conformation were high (table 7).

Genetic correlations with milk production (table 8) were moderate but positive (0.08 to 0.26) with CW and null to slightly negative (-0.01 to -0.13) with CC.

Discussion

3.1 ESTIMATED GENETIC PARAMETERS

The genetic parameters estimated for VC and YB traits were consistent. They were also consistent with those observed in France on traits recorded at slaughter on beef purebred YB (Fouilloux *et al.*, 2001). Heritability was always moderate for CC and CW and the genetic correlation between these traits was high and positive. These traits can be used for genetic selection on carcass traits for dual-purpose breeds and for selection of beef sires for dairy crossbreeding.

Furthermore, genetic correlations estimated between YB traits and other evaluated traits in dual-purpose breeds were favorable. First, cow type traits are consistent with the phenotypes measured at slaughter on their offspring. Second, there was no genetic opposition between carcass traits and milk production traits. This allows for a selection on carcass traits without a negative impact on dairy production. Moreover, the selection for years on dairy production traits did not strongly degrade carcass traits for these breeds.

3.2 BENEFIT OF USING AS IN GENETIC EVALUATIONS

AS is introduced within genetic evaluations as a genetic trait and not as an environmental effect because AS depends not only on breeder decisions, but also on animals precocity which is a trait of economic interest. This is visible through the heritability of this trait, which is quite significant in some breeds and productions, and its always high genetic correlation with CW.

Furthermore, the genetic correlations and the residual and phenotypic correlations are of opposite signs. This shows the complexity of this trait: if the fastest-growing animals can be slaughtered before others, on the whole population however, VC and YB slaughtered lately are heavier. In this kind of situation where genetic and residual correlations are of opposite signs, Thompson and Meyer (1986) recommend a simultaneous genetic evaluation of both traits.

3.3 CURRENT USE OF RESULS (VC)

Since the beginning of 2015, an official genetic evaluation is performed on VC carcass traits. The publication rules were decided within the France Genetique Elevage (FGE) interprofession.

For beef breeds, the results are published for all LIM, CHA, BLA and I95 bulls having VC proofs precise enough and a published calving ease proof. The published proofs for CHA bulls result from MON evaluation; for other beef breeds, the published proofs result from HOL evaluation. The BBB breed does not have calving ease information, hence BBB proofs are not published.

For dairy breeds, only MON and NOR proofs are published. The Holstein breeding association is not interested in including carcass traits in the Holstein breeding goal.

For the first official publication, 608 beef bulls and 1763 dairy bulls had a published proof.

3.4 TO A GENOMIC EVALUATION OF VC AND YB TRAITS FOR DUAL PURPOSE BREEDS

The genetic selection on carcass traits for dual purpose breeds will become more efficient when the YB evaluation will be added to the already official VC evaluation and even more when genomic evaluations will be developed for these traits.

That is why the UMT 3G is working on these developments. This work will allow provide bulls with genomic proofs for all VC and YB carcass traits. Using the same method as the one already used in official genomic evaluations on other traits, they will rely on a population of genotyped bulls having offspring with VC or YB phenotypes. For YB evaluation, this population will also include the genotyped and phenotyped YB (young males genotyped as candidates for reproduction but not selected by AI companies).

Conclusions

The use of slaughter data for genetic purpose is growing to allow dual-purpose breeders to have new tools for the selection of their sires. One novelty of the study was, for VC, to develop a multi-breed evaluation which is interesting for the selection of both dual-purpose breeds and beef sires for dairy crossbreeding on these traits. These results will help dual-purpose breeds to improve selection on carcass traits.

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