



**HAL**  
open science

## Genetic correlations between carcass and meat quality traits of adult cows and similar traits of young Bulls in French Charolais beef cattle

Carlos Aviles, Aurélie Vinet, Romain Saintilan, Brigitte Picard, Jacques Lepetit, Rémi Dumont, Marie-Pierre Oury, Daniel Krauss, David Maupetit, Gilles Renand

### ► To cite this version:

Carlos Aviles, Aurélie Vinet, Romain Saintilan, Brigitte Picard, Jacques Lepetit, et al.. Genetic correlations between carcass and meat quality traits of adult cows and similar traits of young Bulls in French Charolais beef cattle. 10. World Congress on Genetics Applied to Livestock Production (WCGALP), Aug 2014, Vancouver, Canada. , 2014, 10th World Congress on Genetics Applied to Livestock Production. hal-01194136

**HAL Id: hal-01194136**

**<https://hal.science/hal-01194136>**

Submitted on 2 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

**Genetic Correlations Between Carcass and Meat Quality Traits of Adult Cows and Similar Traits of Young Bulls in French Charolais Beef Cattle**

C. Aviles\*, A. Vinet\*, R. Saintilan<sup>†</sup>, B. Picard<sup>‡</sup>, J. Lepetit<sup>§</sup>, R. Dumont<sup>#</sup>, M.P. Oury<sup>#</sup>, D. Krauss<sup>||</sup>, D. Maupetit<sup>||</sup> and G. Renand\*

\*INRA GABI 78352 Jouy en Josas, <sup>†</sup>UNCEIA 78352 Jouy en Josas, <sup>‡</sup>INRA URH St Genès Champanelle,

<sup>§</sup>INRA QuaPA St Genès Champanelle, <sup>#</sup>AgroSupDijon 21009 Dijon,

<sup>||</sup>INRA UE de Bourges 18390 Osmoy, France.

**ABSTRACT:** The present work aims at assessing the genetic determinism of carcass and meat quality of adult cows in relation to similar traits measured on young bulls. In a purebred Charolais herd, 546 cows and 1,386 young bulls, progeny of 72 sires, were slaughtered at 7 years and 17 months of age respectively. Carcass yield (CY), muscularity (CM), internal fat weight (CIF) and 6<sup>th</sup> rib fat content (CRF) were measured on all animals among which 468 cows and 806 young bulls were genotyped with the Illumina BovineSNP50® Beadchip. In addition muscle intramuscular lipid (ML) and collagen (MC) contents were measured on 196 and 734 animals respectively. The close genetic correlation estimated between both genders for CY and CRF was concurrent with a number of common QTL among which a very strong one in the region of *myostatin* gene on chromosome 2.

**Keywords:** beef cows; beef traits; genetics; QTL

### Introduction

Improving carcass and meat quality has been a constant objective for beef producers for providing the meat industry with the desired quality animals. The French beef market is specific since 3/4 of beef meat consumed in France is from females, 2/3 of which originate from beef herds (Institut de l'Élevage, 2013). If the production of young bulls is mostly standardized and largely done in specialized operations, practices and conditions for the adult cow finishing are extremely variable and spread over a large number of farms. Although slaughter and meat quality traits of adult cows are important improvement objectives, all the studies on the genetic determinism of beef traits were conducted with young bulls finished in specialized operation (Bouquet et al., 2010; Allais et al., 2010) expecting a correlated response of adult cows when improving young bull beef traits. Measuring adult cows for genetic evaluation is obviously laborious. Genetic improvement of these traits may be obtained either as a correlated response to a selection of young bull traits or directly with a marker assisted selection. The objective of the present work is to study the genetic determinism (polygenic and QTL) of carcass and meat quality traits measured on adult beef cows in comparison with similar traits measured on young bulls.

### Materials and Methods

**Animals.** In the INRA experimental herd of Bourges, 1,386 purebred Charolais entire male calves were finished as young bulls in the last 22 years and slaughtered

either at 15 or 19 months of age. The purebred Charolais females of this herd were systematically culled at 7 years of age, unless the last reproduction failed, so they were culled at 6 years therefore. Among these culled cows, 546 were fattened during  $5.7 \pm 1.7$  weeks in the last 16 years. During all these years, the management and diets remained the same and the environment was controlled. Animals were weighed two consecutively days at the end of the finishing period and transported to a 200 km distant INRA experimental slaughterhouse. All these experimental animals were progeny of a sample of 72 Charolais sires.

**Data.** At slaughter the warm carcass was weighed and carcass yield (CY) calculated as the ratio to live weight at the end of fattening. The carcass muscularity (CM) was scored from 1 (poorly muscled) to 18 (extremely muscled). Warm removable fat from the carcass cavity (CIF) was weighed. At 24 hours post mortem the 6<sup>th</sup> rib was excised from the carcass and dissected into muscle, fat and bone. The carcass rib fat content (CRF) was calculated as the ratio of fat to the sum of muscle and fat. As Renand et al. (2001) showed that meat quality attributes of young bulls depended on the intramuscular lipid and total collagen contents, these two muscle characteristics were measured on part of the animals. The *Longissimus thoracis* muscle excised from the 6<sup>th</sup> rib was analyzed for intramuscular lipid content (ML) and muscle collagen content (MC) from the measurement of hydroxyproline content (collagen = 7.5 hydroxyproline). Blood sample was taken from 806 male calves and 468 adult females among the recorded animals and their sires. DNA was genotyped using the Illumina BovineSNP50® Beadchip.

**Statistical analyses.** The six adult female and the six young bull traits were analyzed jointly in a multivariate mixed model fitted with contemporary group fixed effects, regression on age at slaughter and 5,942 random animal effects including the 1,912 recorded animals and their ancestry up to the 4<sup>th</sup> generation. Variance components and genetic parameters were estimated by the Restricted Maximum Likelihood (REML) methodology using the VCE-6 software ([//ftp.tzv.fal.de/pub/vce6](http://ftp.tzv.fal.de/pub/vce6)) developed by Neumaier and Groeneveld, (1998).

The genotyping results of the BovineSNP50® Beadchip 54,609 SNP were edited for call rate ( $>0.98$ ), MAF ( $>0.02$ ) and Hardy-Weinberg disequilibrium ( $p$ -value  $<10^{-4}$ ). Eventually 45,160 SNP on the 29 autosomal chromosomes were kept for genome-wide association studies. Paternity of 51 animals was found incompatible and could be corrected with the compatible sire.

The SNP were mapped to the UMD 3.1 sequence assembly. QTL regions were detected using the GEMMA software that fits a univariate Bayesian sparse linear mixed model (BSLMM) using Markov Chain Monte Carlo in which SNP effects include two parts: the random small effects that all SNPs have and the additional fixed effects of some large effect SNPs (Zhou et al. (2012)). The dependent variable was the recorded traits adjusted for age and the contemporary group effects estimated in the previous REML analysis. For each trait analysis the average proportion ( $\pi$ ) of SNP retained as having an additional effect is computed and the probability ( $\gamma$ ) of each SNP to be a QTL. Eventually a Bayes Factor (BF) was computed for each SNP:

$$BF = 2 \ln \frac{\gamma/(1-\gamma)}{\pi/(1-\pi)}$$

SNP with  $BF > 6$  or  $BF > 10$  were considered as strongly or very strongly associated to a QTL.

### Results and Discussion

The main difference between adult cow and young bull carcasses is fatness. The 417 kg carcasses of adult cows have a slightly lower yield (-7%) and are slightly less muscled (-11%) as compared with the 404 kg young bull carcasses (table 1). Their carcasses contain markedly more fat: + 10 kg internal fat, + 5.5 % in the rib and more than twice lipid content in the LT muscle. No difference is observed in collagen content. In a sub-sample of 192 cows, the solubility of collagen is 12.3 % ( $\pm 3.8$ ) which is markedly lower than the 25.2 % ( $\pm 3.8$ ) measured on a 106 young bull sample (Renand et al., 2001). The difference in muscle lipid content and other muscle characteristics such as more intense red color, are actually the primary reasons for the preference of the French consumer for the adult cow meat.

**Table 1. Adult cow and young bull performances\***

Trait		Adult cows	Young bulls
Slaughter age	months	16.8 $\pm$ 2.0	80.8 $\pm$ 5.4
Carcass		(n = 546)	(n = 1,386)
Yield	CY %	54.5 $\pm$ 1.8	58.8 $\pm$ 2.0
Muscularity	CM /18	9.1 $\pm$ 1.1	10.3 $\pm$ 1.3
Intern. Fat	CIF kg	26.2 $\pm$ 6.6	16.3 $\pm$ 6.0
Rib Fat	CRF %	21.9 $\pm$ 4.8	16.1 $\pm$ 4.2
LT Muscle		(n = 468)	(n = 806)
Lipids	ML mg/g	40.0 $\pm$ 15.6	18.1 $\pm$ 8.5
Collagen	MC mg/g	4.4 $\pm$ 0.5	4.4 $\pm$ 1.0

\*mean  $\pm$  s.d.

The coefficients of variation are roughly similar for adult cow and young bull performances. The estimates of heritability coefficients are reported in table 2. Most traits are moderately heritable with heritability coefficients between 0.20 and 0.36 in accordance with average values found in the literature (Burrow et al., 2001). Young bull muscularity score and intramuscular lipid content are slightly less heritable, around 0.15. To the contrary, collagen content of adult cows shows a very high heritability (0.70). All traits, except internal fat, are

genetically and positively correlated across gender: carcass yield and muscularity are moderately correlated (+0.4 to +0.6) while rib fat, intramuscular lipid and collagen contents are highly correlated (+0.7 to 0.9). Internal fat weight of cows appears independent of the same trait of young bulls. Moreover (results not in tables), while in young bulls CIF is closely correlated to CRF and ML (+0.6 to 0.8), these correlations are much lower in adult cows (+0.1 to +0.3). These results point out that the biology of fat storage in carcass cavity by adult cows is largely different from storage in other fat deposits and from the fattening process of finishing animals.

**Table 2. Estimates of heritability and genetic correlation coefficients among and between adult cow and young bull performances**

	Adult cow		Young bull		Genetic correlation*	
	h <sup>2</sup> *		h <sup>2</sup> *			
CY	0.34	0.07	0.37	0.03	+ 0.59	0.06
CM	0.30	0.07	0.14	0.03	+ 0.38	0.10
CIF	0.28	0.06	0.20	0.03	0.00	0.09
CRF	0.28	0.04	0.35	0.03	+ 0.89	0.04
ML	0.36	0.08	0.15	0.03	+ 0.68	0.09
MC	0.70	0.10	0.26	0.04	+ 0.69	0.07

\*  $\pm$  s.e.

The numbers of SNP significantly associated with traits vary greatly among traits and gender. There were between 100 and 120 significant SNP for CY and CRF in both genders but none for CIF. Most of the highly significant SNP are in QTL regions for CY and CRF (Table 3). Due to the limited number of data available, very few QTL regions could be found for other muscle characteristics.

**Table 3. Number of very strong SNP and QTL\* for adult cow and young bull performances**

	Adult cow		Young bull	
	SNP	QTL	SNP	QTL
CY	11	8	10	8
CM	4	3	2	1
CIF	0	0	0	0
CRF	12	8	15	12
ML	1	1	0	0
MC	1	1	0	0

\*region < 3Mb containing at least one very strong SNP (BF>10)

A number of strong SNP are located in the same 14 QTL regions associated with CRF of both adult cows and young bulls (table 4). These common QTL certainly contribute to the very high genetic correlation between both traits. Similarly, 12 common QTL regions are related to CY of both genders. Interestingly there are three QTL regions related to CY and CRF of both cows and young bulls. The extremely strong QTL region on chromosome 2: 5.54-6.61, contains the *myostatin* gene which is known to have mutations with significant effect on carcass yield and fatness (Allais et al., 2010). The sires were genotyped for the Q204X mutation in the *myostatin* gene (Dunner et al.,

2003) and 27 actually carried a mutated allele. The effect and the high frequency of the mutated allele in that experimental population explain the very high BF (Fig. 1).

**Table 4. Common QTL\* across adult cow and young bull performances**

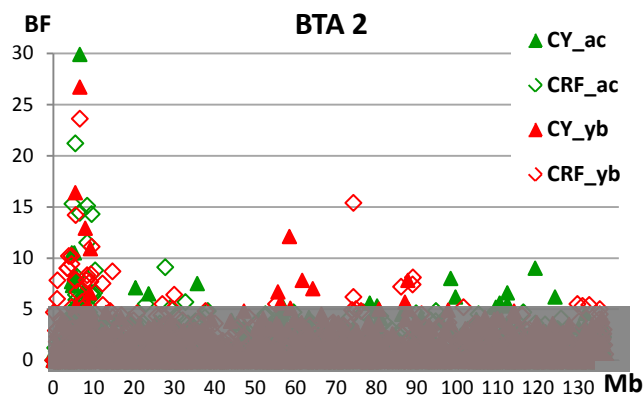
BTA	SNP position (Mb)		Traits in common
	first	last	
2	5.54	6.61	CY CRF
2	27.76	29.95	CRF
3	53.38	55.54	CY
3	102.16	105.02	CRF
4	33.53	34.50	CY
7	17.69	20.28	CRF
7	22.94	25.23	CY CRF
7	48.85	49.51	CY
8	72.78	75.39	CRF
9	50.54	51.40	CRF
10	26.77	28.29	CRF ML
11	1.92	4.10	CRF
11	80.11	80.92	CRF
12	51.34	52.49	CY
12	66.62	68.85	CY
16	48.23	50.80	CY
20	53.33	54.51	CRF
21	59.37	62.00	CRF
22	16.99	18.66	CRF
26	34.07	34.07	CY
27	30.09	31.70	CY
29	36.24	37.86	CY
29	46.65	49.08	CY CRF

\* region < 3Mb containing at least one strong SNP ( $BF > 6$ ) for the same trait measured on both genders

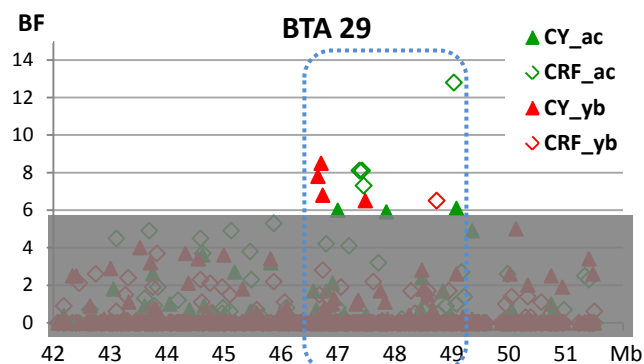
Two other QTL regions are related to the same 4 traits (CY and CRF of cows and young bulls) on chromosomes 7:22.94-25.23 and 29:46.65-49.08 (Fig 2).

### Conclusion

The genetic determinism of carcass yield and rib fat contents of adult cows is largely related to the genetic determinism of the same traits measured in finishing young bulls. The high genetic correlations observed between both types of animals partly result from common QTL regions. Selection on young bull traits based either on polygenes or markers will give a correlated response for similar traits of adult cows. That conclusion is not valid however for muscle characteristics such as lipid or collagen contents since no associated marker could be detected due to a limited experimental population. It should be noticed that the ability of cows to store fat in the carcass cavity is independent of the other carcass quality traits and should be considered as a specific trait of cows related to their energy metabolism for production functions.



**Figure 1. BF factors of SNP detected on chromosome 2 for adult cow (\_ac) and young bull (\_yb) traits**



**Figure 2. BF factors of SNP detected on chromosome 29 for adult cow (\_ac) and young bull (\_yb) traits**

### Acknowledgments

This research was supported by ANR (project Mugène) and Région Centre (project DéfiViande).

### Literature Cited

- Allais, A., Levéziel, H., Payet-Duprat, N., et al. (2010). *J. Anim. Sci.*, 88, 446-454.
- Bouquet, A., Fouilloux, M.N., Renand, G., et al. (2010). *Livest. Sci.*, 129, 38-48.
- Burrow, H.M., Moore, S.S., Johnston, D.J., et al (2001). *Aust. J. Exp. Agric.*, 41, 893-919.
- Dunner S., Miranda, E., Amigues, Y., et al. (2003). *Genet. Sel. Evol.*, 35, 103-118.
- Institut de l'Élevage (2013). *Chiffres clés 2013:Productions bovines*. 12 pp.
- Neumaier, A., and Groeneveld, E. (1998). *Genet. Sel. Evol.*, 30, 3-26.
- Renand, G., Picard, B., Touraille, C. et al. (2001). *Meat Sci.*, 59, 49-60.
- Zhou, X., Carbonetto, P., and Stephens, M. (2012). *PLoS Genetics*, 9, e1003264.