



Sequence-based GWAS on feed efficiency and carcass traits in French Charolais bulls



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Context of the study



■ Improvement of feed efficiency is of major interest for beef breeders

■ Productions

- Carcass weight increased by 56 kg in the last 20 years
- The price of carcass kilogram increased by 15%

■ Resources

- The consumption of forage increased by 10% to 20% and concentrate by 29%
- The feeding cost surged by 50%

 **Beef breeders are more and more concerned by feed efficiency**

■ Feed efficiency improvement is possible: heritability of residual feed intake (RFI) for French Charolais bulls is 0.26 (Taussat et al, 2019)



Context of the study



- Feed efficiency is related to carcass composition (Taussat et al, 2019):

Genetic correlations	Carcass yield	Muscle % in carcass	Fat % in carcass
RFI	-0.18	-0.47	0.48

- However, feed intake is difficult and expensive to measure on large scale
 - ➔ A way to improve feed efficiency is using the genomic evaluation:
 - Reference population composed of phenotyped and genotyped animals
 - Estimation of allele effects at each variant (SNP, causal mutations, ...)
 - Prediction of breeding values for the genotyped population
- ➔ **Goal of this study: find genes related to feed efficiency and carcass traits:**
 - To better understand the genetic determinism of these traits
 - To find candidate causal mutations for genomic evaluation

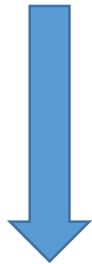


Materials and methods

■ Animal management:

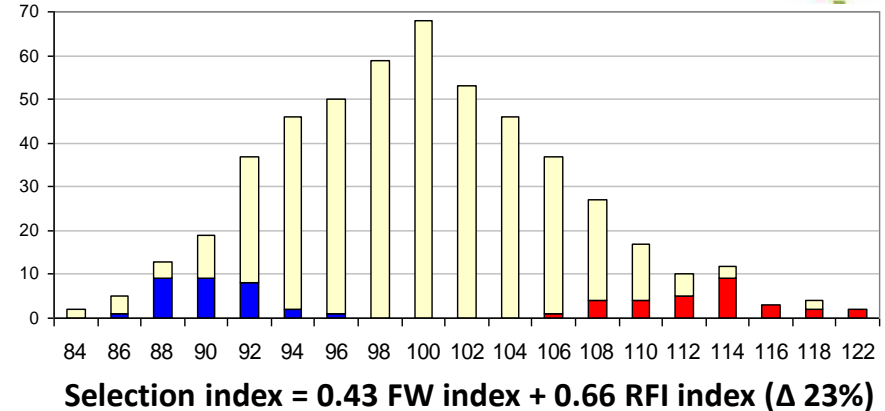
**60 Charolais sires selected divergently
for final weight and RFI**

Representative females
of French population



1,477 Charolais young bulls, born from 1988 to 2009:

- Fattened in the experimental station on INRA with pelleted diet ad libitum (composed of 29% dehydrated alfalfa hay, 29% dehydrated beet pulp, and 21% bran)
- Measure of daily feed intake (FI), final weight (FW) and average daily gain (ADG)
- Slaughtered at 17 mo of age on average, in the experimental slaughterhouse of INRA in Theix
 - Carcass weight
 - Dissection of 6th rib to estimate % of muscle and fat in carcass



Materials and methods



■ Phenotypes

■ Feed efficiency criteria:

- **FE**: feed efficiency ratio = ADG / FI (kg/kg)
- **RFI**: computed by a regression of FI on metabolic body weight and ADG (kg/d)

■ Slaughter traits:

- **CY**: carcass yield = hot carcass weight / empty body weight
- **MU**: carcass muscle percentage
- **FAT**: carcass fat percentage

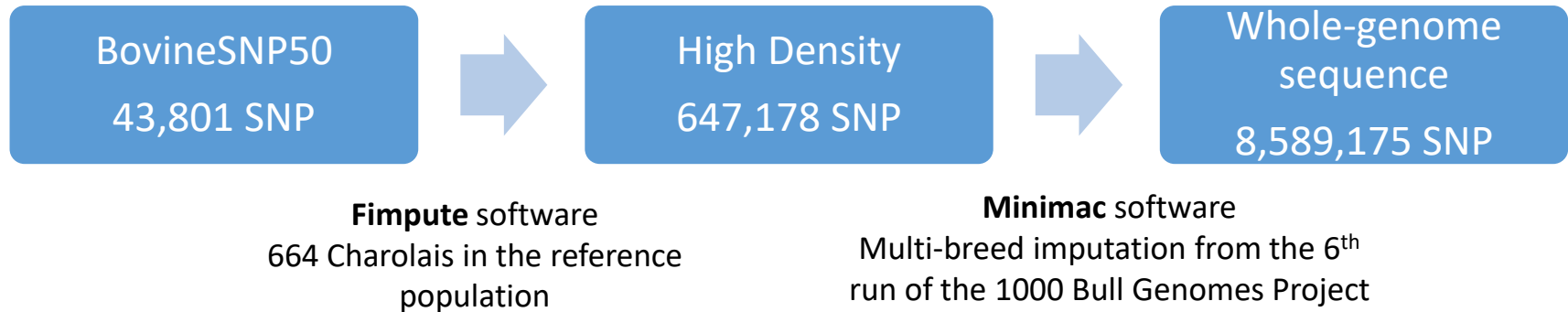
■ All phenotypes were adjusted for fixed effects of **years** (22 yr), **age of the dam** (3,4,5,6 yr and over) and **twinning** (single or twin) and **slaughter age** as covariate



Materials and methods

■ Genotypes

- A subset of **789 Charolais young bulls** were genotyped with the **BOVINESNP50** and imputed to the whole-genome sequence:



■ Genome-Wide Association Studies (GWAS)

- We used **GCTA** software
- $y = a + b x + g + e$ with: - **y** the adjusted phenotype, - **a** the general mean,
- **b** the fixed effect of the SNP, - **x** the SNP genotype,
- **g** the polygenic effect - **e** the residual effect.
- A corrected Bonferroni threshold of 5.5 was used (p-value < 3,10e⁻⁶)



Results – Number of SNP



■ 3,167 SNP are highly associated with traits

	RFI	FE	CY	MU	FAT
RFI	51	7	0	0	0
FE		109	0	0	0
CY			2,269	869	893
MU				1,394	1,073
FAT					1,243

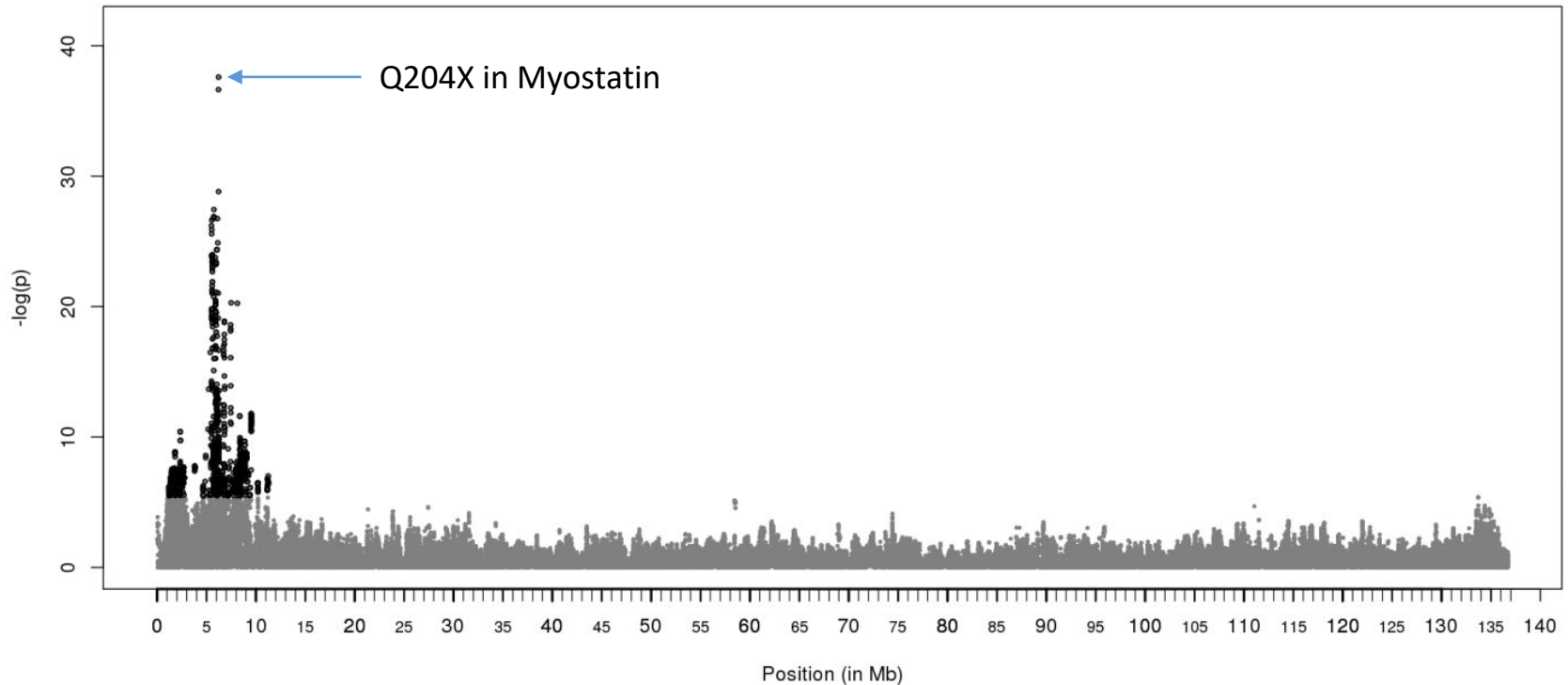


Results – Number of SNP



■ 3,167 SNP are highly associated with traits

Manhattan plot for CY in BTA2



Results – Number of SNP



■ 3,167 SNP are highly associated with traits

	RFI	FE	CY	MU	FAT
RFI	51	7	0	0	0
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Diagram illustrating the breakdown of highly associated SNPs (3,167 total) into Intragenic SNPs:

- 51 SNPs from RFI
- 109 SNPs from FE
- 10 SNPs from RFI are Intragenic
- 59 SNPs from FE are Intragenic

No high significant SNP in common between feed efficiency and carcass traits



Results – Genes associated with feed efficiency



■ 1 gene only associated with RFI:

- **MMP13** (matrix metalloproteinase 13) on **BTA15**
 - Peptidase activity
 - Calcium ion binding
 - Collagen binding
- In QTL of FCR (Sherman et al., 2009)

■ 2 genes associated with RFI and FE:

- **CAPN7** (calpain 7) on **BTA1**: calpain family is known to be related to meat quality
 - Protein binding
 - Peptidase activity
- **CACNA1E** (calcium voltage-gated channel subunit alpha1 E) on **BTA16**
 - Voltage-gated calcium channel activity
 - Calcium ion binding
- In QTL of rib eye area (Hay et al., 2018)



Results – Genes associated with feed efficiency



■ 4 genes only associated with FE:

- **SLC35F4** (solute carrier family 35 member F4) on **BTA10**. Transmembrane transporter activity
- **SULT2A1** (bile salt sulfotransferase) on **BTA18**. Catalyzes the sulfonation of steroids and bile acids in the liver and adrenal glands
 - Protein binding
 - Transferase activity
- **GADL1** (glutamate decarboxylase like 1) on **BTA22**
 - Catalytic activity
 - Carboxy-lyase activity
 - In QTL of marbling score (McClure et al., 2010) and backfat thickness (Li et al., 2017)
- **ZNF407** (zinc finger protein 407) on **BTA24**. May be involved in transcriptional regulation
 - In QTL of marbling score and longissimus muscle area (McClure et al., 2010)



Results – Genes associated with carcass traits

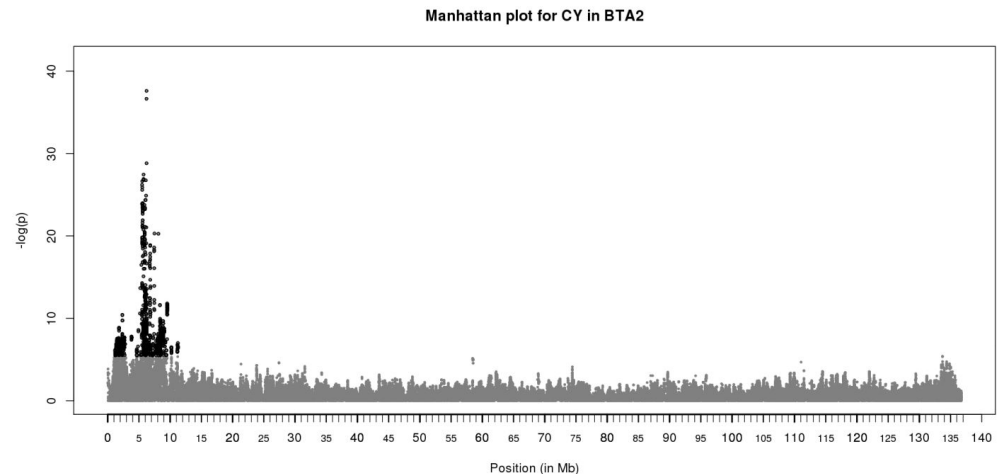


■ We found the causal mutation of myostatin (MSTN) in BTA2 for:

- CY: **+1.7%** with a p-value = **$2.6e^{-38}$**
- MU: **+2%** with a p-value = **$2.3e^{-26}$**
- FAT: **-2%** with a p-value = **$3.7e^{-26}$**

■ But also for:

- RFI: **-0.24 kg/d** with a p-value = **$3.5e^{-4}$**
- FE: **+0.003 kg/kg** with a p-value = **$3.7e^{-3}$**
- FI: **-0.36 kg/d** with a p-value = **$4.9e^{-5}$**



Results – Genes associated with carcass traits



■ Some genes associated with carcass traits:

- **BTA11** for FAT: **CCDC85A** (coiled-coil domain containing 85A)
 - Found for kidney, pelvic and heart fat percentage (Imumorin et al., 2011) and FA-C18:0 in longissimus dorsi (Cesar et al., 2014)

- **BTA15** for CY: **GALNT18** (polypeptide N-acetylgalactosaminyltransferase 18)
 - Transferase activity
 - Carbohydrate binding
 - In QTL of shear force (McClure et al., 2012) and FA-C13:0 of longissimus muscle (Saatchi et al., 2013)



Take home messages



- **The highest significant SNP for feed efficiency are not the same for carcass traits**
- **But, with the exemple of MSTN, genes co-associated between feed efficiency and body composition can be found**
- **Several candidate genes were identified, with protein and energetic activities for RFI and FE**
 - **Peptidase activity (MMP13, CAPN7)**
 - **Protein binding (CAPN7, SULT2A1)**
 - **Collagen binding (MMP13)**
 - **Calcium ion binding (MMP13, CACNA1E)**
 - **Transferase activity (GALNT18, SULT2A1)**
 - **Carbohydrate binding (GALNT18)**
 - **Voltage-gated calcium channel activity (CACNA1E)**



Conclusion

- This study showed the complex genetic determinism of feed efficiency, with several metabolic processes highlighted
- Using the whole-genome sequence allows to find highly significant variants in several genes
- This analysis need a large number of animals
- Next step: identify network of genes co-associated between feed efficiency and body composition
- Future analysis: test genomic evaluation including highly significant variants



THANK YOU FOR YOUR ATTENTION!



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Results – Number of SNP

- 3,167 SNP are highly associated with traits

	RFI	FCE	FI	ADG	FW	CY	MU	FAT
RFI	51	7	3	0	0	0	0	0
FCE		109	0	0	0	0	0	0
FI			17	0	0	0	0	0
ADG				3	0	0	0	0
FW					122	0	0	0
CY						2,269	869	893
MU							1,394	1,073
FAT								1,243

No high significant SNP in common between feed efficiency and carcass traits



Results – Genes associated with FCE, FI and FW



■ 1 gene associated with RFI and FI

- **SULT6B1** (sulfotransferase family 6B member 1) on **BTA11**. Implies in 3'-phosphoadenosine 5'-phosphosulfate metabolic process.
 - Transferase activity
 - Found for RFI by Sherman et al. (2009), marbling score, longissimus muscle area and carcass weight by McClure et al. (2010) and FA-C16:1 in subcutaneous fat over longissimus dorsi by Morris et al. (2010).

■ FI

- **PARD3** (par-3 family cell polarity regulator): adapter protein involved in asymmetrical cell division and cell polarization processes
 - Protein binding
 - Lipid binding

■ FW

- **STMN2** (stathmin 2): regulator of microtubule stability
 - Protein binding
 - Tubulin binding
 - Calcium-dependent protein binding
- **ZFHX4** (zinc finger homeobox 4): may play a role in neural and muscle differentiation

