

# Genomic insights for feeding behavior traits in beef cattle

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# Introduction

Animal behavior studies have been viewed as an attempt to look at the entire production system, assessing individual activities regarding the social and physical environment that animals are exposed to.

## Feeding behavior related traits:

- Respiratory diseases (Quimby et al., 2001; González et al., 2008)
- Metritis (Weary et al., 2009)
- Evaluation of acidosis (Schwartzkopf-Genswein et al., 2003; Robles et al., 2007)
- Strategies for bunk management (Schwartzkopf-Genswein et al., 2002; 2004)

# Introduction

*Important aspects of feeding behavior:*

- Individual variability in feed efficiency and performance traits;
- Individual capacity of adaptability to the environment provided by man;
- Animal health status and welfare

**All these aspects are of considerable importance for the development of sustainable breeding programs**

# Introduction

There is a need to understand the genetic and biological mechanisms underlying feeding behavior traits and their association with feed efficiency and performance traits

Identify genomic regions and candidate genes associated with feeding behavior traits including feeding event frequency and daily feeding duration in crossbred beef cattle

# Material and methods

Automated GrowSafe feeding system (GrowSafe Systems Ltd., Airdrie, Alberta, Canada)

Performance tests carried out between 2003 and 2013

- Average test duration was  $80 \pm 6$  days

Crossbred beef cattle

- Angus, Charolais, Hereford, BeefBooster, and Kinsella Composite

Illumina BovineSNP50 BeadChip array

- located on sex chromosomes
- monomorphic and markers with  $MAF < 0.01$
- HWE ( $p\text{-value} < 1^{-6}$ )
- SNPs and Individuals with call rate  $< 0.90$



# Material and methods

## Feeding Event Frequency

$\sum$  feed events/performance duration (d)

*event* = bunk visit with feed consume > 0Kg and intervals between the last 2 readings of the same transponder > 300s.

## Daily Feeding Duration

$\sum$  feed duration time/performance duration (d)

*duration time* (min) = difference between the feeding event end and start times.

Basarab *et al.* (2003)

# Material and methods

Weighted single-step GBLUP (WssGBLUP) methodology using BLUPF90 programs (Wang et al., 2012; Misztal et al., 2016)

Single-trait animal model

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{e}$$

- direct additive genetic effects =  $\mathbf{a} \sim N(0, \mathbf{H}\sigma_a^2)$
- residual effect =  $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$

Fixed effect - Contemporary groups (animal sex, herd of origin, year of birth, and management group)

Covariates - Animal weight at the beginning of the test

Breed composition (ADMIXTURE software, Alexander et al. 2009)

# Material and methods

*Summary of data set structure and descriptive statistics*

	FREQ (events/d)	DUR (min/d)
No. animals	3,509	3,511
Mean $\pm$ SD	55.94 $\pm$ 29.92	100.89 $\pm$
Live weight (kg)	373 $\pm$ 74	37.53
No. genotypes (after QC)	3,529	
No. SNPs (after QC)	37,298	

## Post GWAS analysis

biomaRt  Bioconductor  
DATA SOURCE SOFTWARE FOR BIOINFORMATICS



**CattleQTLdb**

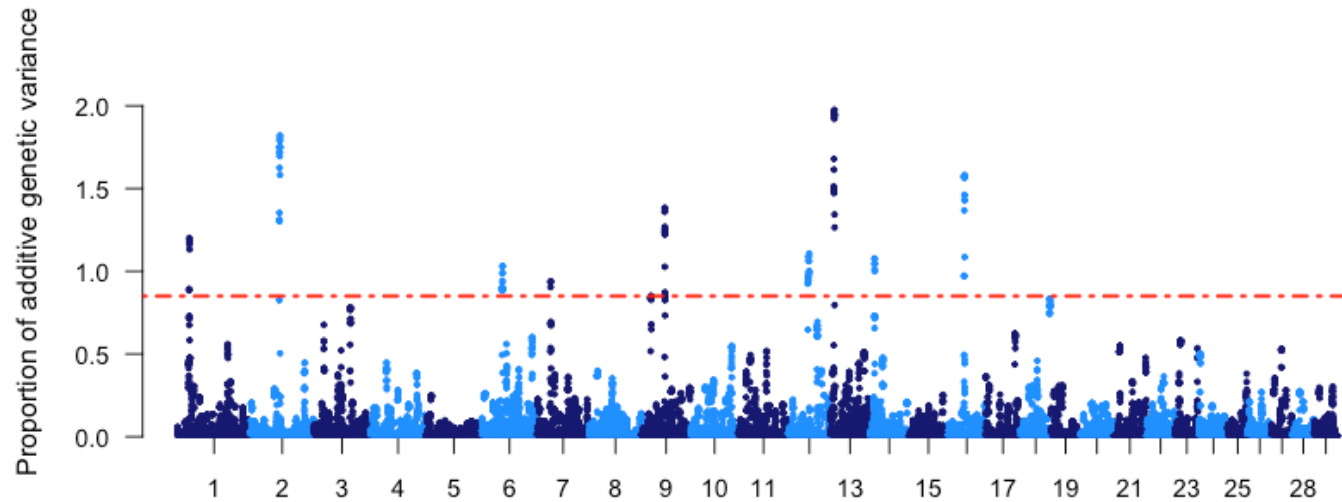
(Durinck *et al.*, 2009; Huang *et al.*, 2009; Hu *et al.*, 2013)



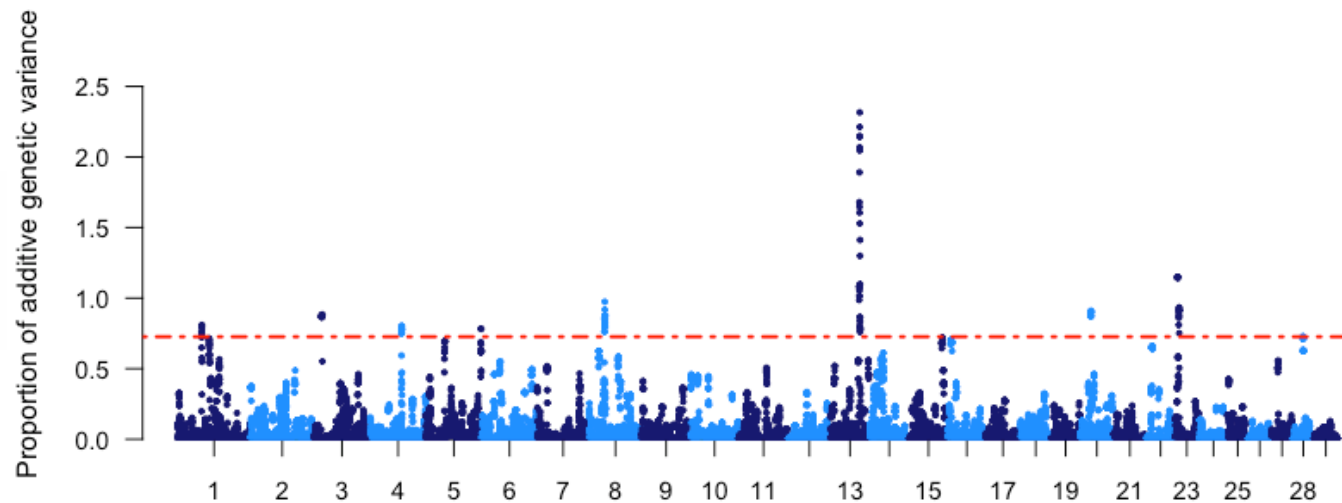
# Results

*Manhattan plot of additive genetic variance explained by windows of 20 adjacent SNPs for:*

Feeding Event Frequency



Daily Feeding Duration



Chromosome

# Results

*Summary of top 10 SNP-windows with major effects on feeding behavior traits.*

Feeding event frequency		
BTA <sup>1</sup>	Location (bp)	Var (%) <sup>2</sup>
1	25,685,179 - 27,465,349	1.20
2	63,516,470 - 65,069,037	1.82
6	44,622,597 - 45,412,181	1.03
7	29,579,813 - 31,136,178	0.94
9	20,247,290 - 21,490,009	0.85
9	49,865,815 - 50,804,011	1.38
12	45,002,070 - 45,952,853	1.11
13	8,347,568 - 9,556,357	1.97
14	11,154,590 - 11,983,913	1.08
16	35,723,500 - 36,565,106	1.58
<b>17 genes</b>		12.96%

Daily feeding duration		
BTA <sup>1</sup>	Location (bp)	Var (%) <sup>2</sup>
1	52,748,123 - 53,656,600	0.80
3	18,520,392 - 19,860,064	0.88
4	68,528,799 - 69,831,612	0.80
5	119,261,609 - 120,378,417	0.78
8	33,747,904 - 34,714,805	0.97
13	63,257,337 - 65,006,713	2.32
20	22,823,334 - 24,228,836	0.91
23	5,896,623 - 7,276,902	1.15
23	9,453,816 - 10,688,252	0.93
28	22,760,601 - 23,742,925	0.73
<b>163 genes</b>		10.27%

<sup>1</sup>BTA = *Bos taurus* chromosomes; <sup>2</sup>Var = Proportion of additive genetic variance

# Results

SNP windows overlapped with previously reported QTLs for feed efficiency (QTLdb database)

•DMI; ADG; RFI; FCR; YG

## Feeding Event Frequency

- *PPARGC1A* gene on BTA6 (44Mb)  
(peroxysome proliferator-activated receptor-gamma coactivator-1alpha)

Modulate feed intake (GO: 0002021)

Associated with intramuscular fat deposition, productive and reproductive traits in beef cattle  
(Ramayo-Caldas et al., 2014)

## Daily Feeding Duration

- *RORC*, *TNFAIP8L2* on BTA3
- *BPIFB1* on BTA 13
- *DBS*, *PSMB8*, *PSMB9*, *BOLA-DMA*, *BOLA-DMB*, *BOLA-DOA*, *BOLA-DOB*, *BOLA-DYB* on BTA23

Inflammatory bowel disease (KEGG\_PATHWAY)

Associated with intramuscular fat, marbling and carcass weight in different cattle breeds (Barendse et al., 2010)

# Conclusion

Identified major SNP windows and potential candidate genes, providing new insights for the biological understanding of feeding behavior in beef cattle.

Corroborate the possibility to use animal behavior as tool for early detection of health status and performance.

Further functional genomic studies are important to better understand the relevant pleiotropic pathways underlying feeding behavior and feed efficiency traits.

# ACKNOWLEDGEMENTS



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