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, performance and carcass 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 ± 6 days

Crossbred beef cattle

- Angus, Hereford, BeefBooster, Kinsella Composite and Charolais

Illumina BovineSNP50 BeadChip array

- SNP markers with unknown genomic position
- located on sex chromosomes
- monomorphic and markers with MAF < 0.01
- HWE (p-value < 1^{-6})
- SNPs and Individuals with call rate < 0.90

(www.beefcentral.com/genetics/genetics-new-net-feed-intake-testing-station-open-for-business/)

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.

Feeding Event Frequency

$\sum$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

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

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

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 ± SD	55.94 ± 29.92	100.89 ± 37.53
Live weight (kg)	373 ± 74	
No. genotypes (after QC)	3,529	
No. SNPs (after QC)	37,298	

Post GWAS analysis

biomaRt

Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

DAVID BIOINFORMATICS DATABASE

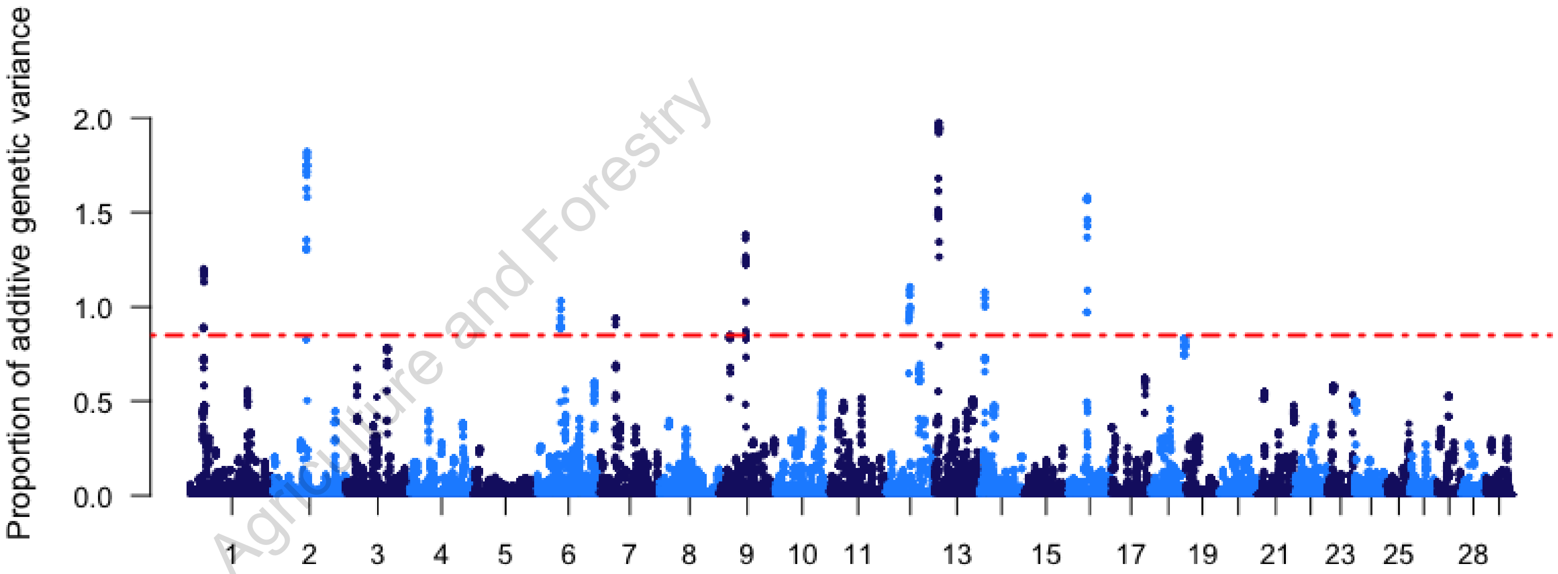
CattleQTLdb

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

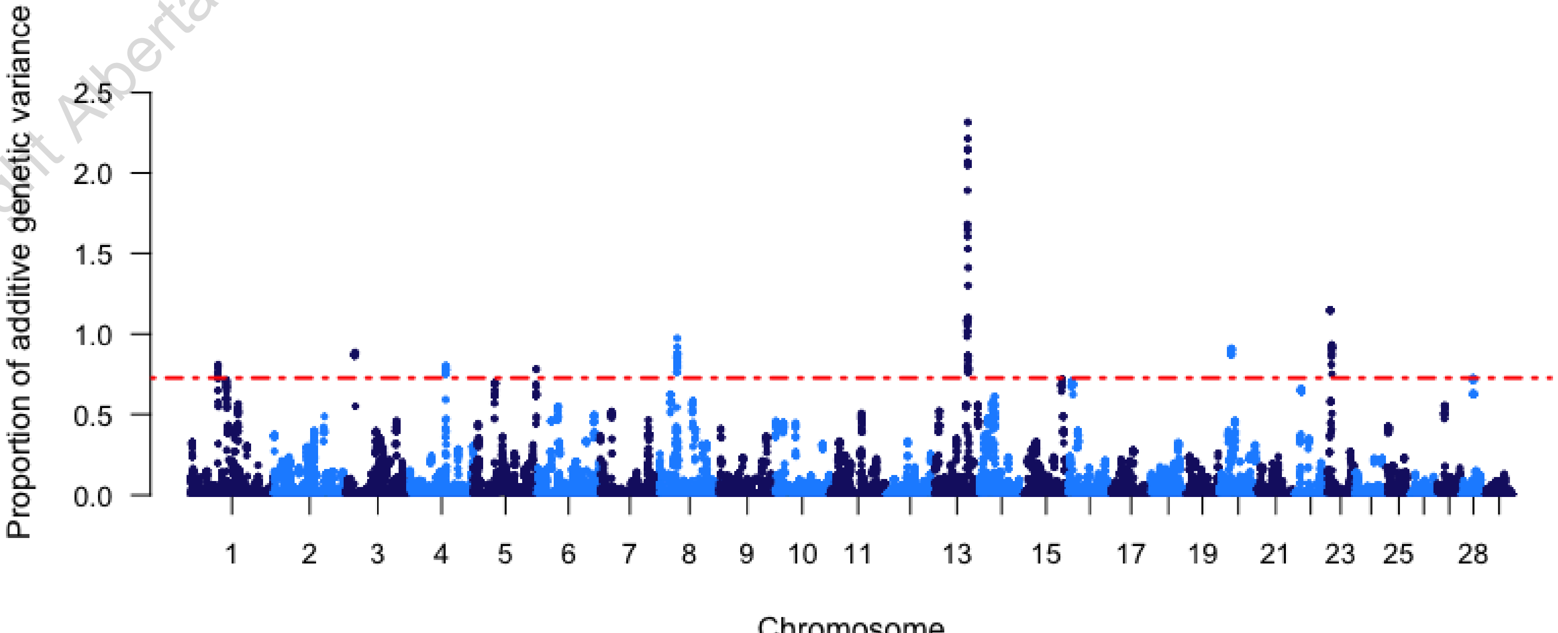
Results

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

Feeding Event Frequency



Daily Feeding Duration



Results

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

Feeding event frequency

BTA[1]	Location (bp)	Var (%)[2]
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
	17 genes	12.96%

Daily feeding duration

BTA[1]	Location (bp)	Var (%)[2]
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
	163 genes	10.27%

[1]BTA = *Bos taurus* chromosomes; [2]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)

Feeding Event Frequency

- *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.

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