

# Genome-Wide Association Study of Feed Efficiency in Beef Cattle

## A.S. Leaflet R2855

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### Summary and Implications

Feed costs comprise the majority of beef production costs and feed intake has long been recognized as an economically relevant trait for beef cattle. Residual feed intake (RFI) is a function of feed intake and performance and reflects whether animals eat more or less than expected for a given level of production. The objectives of this study were to map quantitative trait loci (QTL) associated with feedlot RFI in 4 different beef cattle populations. A total of 13 significant QTL over 10 different chromosomes were detected. The identified QTL had no overlap across 4 beef cattle populations reflecting different genetic makeup of RFI across different beef populations. Further genotyping and statistical analyses are needed to find the casual mutations. Once found, knowledge of such mutations would create new opportunities for the selection of more efficient animals.

### Introduction

Feed costs comprise the majority of beef production costs and improving feed efficiency has long been recognized as a desirable change for beef cattle (Koch et al., 1963). Improvements in the efficiency of feed utilization could lead to increased economic returns in the entire beef cattle production system (Archer et al., 1999).

Feed efficiency is also important for social reasons because of environmental concerns about methane emissions of cattle and competition from alternative uses of traditional livestock feedstuffs, particularly corn- and soybean-based biofuels.

The objectives of this study were to map QTL associated with feedlot RFI in 4 different beef cattle populations.

### Materials and Methods

Feedlot average daily gain, daily dry matter intake and metabolic body weight were measured in 4 different beef cattle populations consisted of 1,160 Cycle VII steers (derived from Cycle VII of the USMARC Germplasm Evaluation Project), 1,658 Angus steers, 870 Hereford animals and 1,445 Simmental sired (Simmental×Angus) steers genotyped either by BovineSNP50 or BovineHD assays.

A Bayes-B model implemented in GenSel software was used to simultaneously analyze all of the markers and QTL were identified by characterizing the proportion of additive genetic variation explained by non-overlapping 1-Mb regions of the genome.

### Results and Discussions

A total of 13 significant 1-Mb genome windows distributed over 10 different chromosomes were detected as QTL associated with RFI (Table 1). The identified QTL had no overlap across 4 beef cattle populations reflecting different genetic makeup of RFI across different beef populations.

Some of the identified QTL regions harbor good candidate genes. For example, the QTL on BTA14 at 25Mb carry a well-known gene, PLAG1 that has major effect on body size and body weights in cattle. The QTL on BTA20 at 4Mb has been identified as a major pleiotropic QTL associated with body weights in several beef cattle breeds (unpublished data).

Further genotyping and statistical analyses are needed to find the casual mutations. Once found, knowledge of such mutations would create new opportunities for the selection of more efficient animals.

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**Table 1. The significant 1-Mb genome windows associated with residual feed intake in 4 different beef populations.**

BTA_Mb <sup>1</sup>	Population	Start SNP	End SNP	Number of SNPs	Genetic variance (%)	PPI <sup>2</sup>
5_113	Cycle VII	<i>rs110075037</i>	<i>rs110611098</i>	23	1.19	0.74
6_50	Angus	<i>rs133728493</i>	<i>rs136948693</i>	304	2.21	0.63
8_9	Cycle VII	<i>rs29020666</i>	<i>rs29020862</i>	24	0.88	0.57
10_85	Simmental	<i>rs110164488</i>	<i>rs43652141</i>	230	1.58	0.61
14_25	Cycle VII	<i>rs41627954</i>	<i>rs42298470</i>	20	0.80	0.56
14_41	Simmental	<i>rs42509065</i>	<i>rs133984439</i>	201	1.75	0.52
14_43	Cycle VII	<i>rs109845775</i>	<i>rs110706635</i>	12	1.95	0.75
15_82	Simmental	<i>rs110524424</i>	<i>rs42781637</i>	380	2.40	0.73
18_37	Simmental	<i>rs110857287</i>	<i>rs43211307</i>	241	1.35	0.59
19_37	Cycle VII	<i>rs109433582</i>	<i>rs110497942</i>	22	0.73	0.55
19_54	Hereford	<i>rs134654442</i>	<i>rs110630064</i>	353	1.45	0.54
20_4	Hereford	<i>rs134565601</i>	<i>rs43094976</i>	299	1.57	0.64
25_7	Simmental	<i>rs110477162</i>	<i>rs110037478</i>	289	1.45	0.51

<sup>1</sup>Bovine chromosome and n<sup>th</sup> 1-Mb window of the same chromosome started from zero. <sup>2</sup>PPI: posterior probability of inclusion.