Differences In QTL Regions Affecting Residual Feed Intake In Steers Fed Grower And Finisher Diets

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Introduction

Feed efficiency (FE) is an important aspect of beef cattle production. Although different FE measures exist, residual feed intake (RFI) is becoming more popular because it is independent of growth and production. At various stages of growth, different feed formulations are fed to young, growing cattle. Selecting cattle that are feed efficient across diets will increase profitability of the industry.

Some studies have reported quantitative trait loci (QTL) affecting FE measured on steers fed the finisher diet (Sherman et al., 2009; Nkrumah et al., 2007). It is important to know whether the same QTL affect FE when animals are fed other types of feed. Hence, we set out to investigate if similar QTL affect RFI when growing steers are fed grower and finisher diets.

Material and methods

Animals and management. All animals were located at the University of Alberta ranch at Kinsella, Alberta and were cared for according to the Canadian Council on Animal Care (CCAC, 1993) guidelines. A total of 490 steers were used in the three-year trial (2006-2009). These steers were born in the spring of each year from multiple hybrid sires mated to hybrid dams on pasture. All steers had been vaccinated for IBR, PI3, BVD, BRSV, *haemophilus somnus*, *pasteurella multocida* and clostridial diseases four weeks before arriving at the feeding facility. Upon arrival, each steer was treated with a pour-on parasiticide that controls warble larvae, mites, lice and horn fly. Each steer was also identified with a radio frequency (RF) transponder button (half duplex RFID, Alflex USA, Inc., Dallas/Ft. Worth Airport, TX 75261-2266) in its right, or left ear. The transponder button was located five to six cm from the base of the ear, in the middle, with the transponder button on the inside part of the ear.

There were two successive feeding periods in each of the three years. The first feeding period (P1) ran from November to January while the second feeding period (P2) ran from February to May. A 14-day transition period was allowed between P1 and P2. The animals were offered one of two types of feed (grower and finisher diet) in any feeding period. The composition of the grower diet on an as-fed basis was 74% oats, 20% hay and 6% feedlot supplement while the finisher diet contained 10% alfalfa pellets, 28.3% oats, 56.7% barley and 5% feedlot-32 supplement. Feed and clean drinking water were offered *ad libitum* throughout the test periods.

Each year (except the first year), the animals were divided into two groups. In the first year, all steers (n=175) were fed a grower diet in P1 followed by the finisher diet in P2. In the second year 84 steers were fed the grower diet in P1 and the finisher diet in P2, while 88 were fed the finisher diet in P1 and P2. In the third year, 72 steers were fed a grower diet in

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P1, then the finisher diet in P2, while 71 were fed the grower diet in P1 and P2. In total 402 steers were evaluated on the grower diet while 419 were evaluated on the finisher diet.

Data collection and trait derivation. A minimum of 63 days (Wang et al., 2006) of reliable data is required for the calculation of RFI. The data required include intake measurement, body weight measurements and ultrasound back-fat (UBF) thickness. Feed intake was measured daily on each steer using the GrowSafe feeding system (GrowSafe Systems Ltd., Airdrie, Alberta, Canada). The weights of all steers were measured once every 2 weeks throughout the test periods while UBF was measured at the beginning and at the end of the feeding period with an Aloka 500V real-time ultrasound with a 17.5 cm, 3.5MHz probe (Overseas Monitor Corporation Ltd., Richmond, British Columbia, Canada).
For data integrity and quality control purposes, the GrowSafe system has an internal audit system that calculates the daily assigned feed disappearance (AFD) for each feeding node. The AFD should be sufficiently high (>95%) for each day's data to be included for data analysis. Data collected on the days that had low AFD were excluded from all analyses. Other data integrity (not shown) include the dry matter intake (DMI) correlations with mid-metabolic weight (MWT), average daily gain (ADG), UBF and expected DMI (e-DMI). RFI is the difference between the actual feed intake and the e-DMI. The e-DMI was obtained as a regression of ADG, MWT and UBF on standardized DMI using PROC GLM of SAS Version 9.2 (SAS Inst., Inc., Cary, NC).

Genotyping, parentage determination and QTL mapping. Blood samples or ear tissues were collected from each animal for DNA extraction. Genotyping was done using the Illumina BovineSNP50 Beadchip. The sire of each steer was determined using a subset of the SNP output which met a specific criteria (100% snp frequency, 95% animal call rate and 0.1 minor allele frequency). Approximately 29000 SNP were then used to determine the sires executed in a program developed in the Livestock Genomics group, University of Alberta.

The SNP for QTL mapping (approx. 41,000) were filtered from the genotyping output with 0.05 minor allele frequency and 95% animal call rate. Sire heterozygosity was calculated using Haploview (Barrett et al., 2005). The SNP with low sire heterozygosity (<0.30) were considered less informative and were excluded from the filtered set. The total available SNP for QTL mapping was 28222 at approximately 0.1 cM spacing. In order to increase power of QTL detection, an F2 design was implemented in R/QTL (Broman et al., 2003) using a single QTL model. The procedure uses an interval mapping approach (Lander and Bostein, 1989) with the EM algorithm for the genome scan. Mapping was carried out within each diet-fed group while a LOD threshold of 3 was considered significant for the QTL.

Results and discussion.

The beef sector (especially in North America) is regarded as segmented which may lead to divergent breeding goals. Identifying QTL that are specific to either diet or common to both of them will be helpful for the genetic progress of feed efficiency in the industry. Few studies have investigated RFI-QTL in beef cattle (Moore et al., 2006; Nkrumah et al., 2007; Barendse et al., 2007; Sherman et al., 2009). Most of these studies used a half sib design for the analysis. The appropriateness of the F2 design (used in this study) for the analysis of half-sib groups may cause some bias. However, it was implemented in order to increase the

number of steers to be used for the analysis, thereby increasing power of the analysis. Some sires' genotypes were unavailable which would exclude such families from a half-sib analysis. The F2 also maintains the use of the three genotypes (2 homozygotes and a heterozygote genotypes). The underlying assumption is that the genotype frequencies would approximate those found in the F2 design. Implementing this design in R/QTL enabled us to incorporate a high density of markers which may not be feasible in programs for half-sib analysis.

Significant QTL represented by SNP were observed in most chromosomes. Given that an interval for RFI QTL can span from 5 to 49 cM in some studies (Sherman et al., 2009), we considered that SNP located within an interval of 20 cM within a chromosome may represent the same QTL. There were more significant QTL in the finisher fed group than in the grower fed group. The finisher group had more SNP per chromosome. Considering the distance between markers, most of the markers were not independent. The reason for the higher number of significant SNP is unclear but may be related to the effect of high energy on the genes affecting RFI. The heritability estimated in the finisher diet was higher than the grower diet (Durunna et al., unpublished).

Figures 1 and 2 show the QTL plot for all chromosomes for the grower fed and finisher fed groups, respectively. Significant QTL that were common to both feeding environments were observed in chromosomes 1, 2, 4, 10, 11, 16, 17, 19 and 20. These QTL would be more important for selection purposes since they may have similar effects on RFI across different diets. The animals that are selected based on these regions would be generalists and would be expected to perform more uniformly across diets. On the other hand, some QTL were observed in either the grower fed or the finisher fed group. Significant QTL specific to the grower fed group were located in different regions from 6 chromosomes (13, 14, 15, 24, 28 and 29). The finisher-diet specific regions were found in chromosomes 5, 8, 12, 18, and 21.

Environmental interactions arise when certain QTL, previously detected in one environment, fail to show up in another environment. Such differential expressions, due to differences in scale or rank (James, 2009) in different environments may be an indication of QTL-by-environment interaction. Steers with such genes may be efficient on the grower diet but inefficient on the finisher diet or vice versa. Animals selected for these QTL may be regarded as specialists because their performance will depend on the diet they were fed.

We detected more QTL for the finisher diet than that reported by Sherman et al. (2009). They used 400 steers in a half sib analysis and found significant QTL for RFI on chromosomes 1, 3, 4, 6, 7, 9, 11, 12, 13, 14, 17, 18, 19, 21, 22, 23, 24, 25, 26, 28. They pooled half sibs across families which could reduce the ability of QTL detection. We did not observe any QTL on chromosomes 22, 25, and 26. This is in contrast with the study of Sherman et al. (2009) who observed significant QTL in these regions while Nkrumah et al. (2007) detected QTL on chromosome 26 but not on 22 and 25. A later study by Sherman et al. (2010) found SNP that were associated with RFI in chromosomes 1, 2, 4, 6, 8, 10, 11, 12, 15, 18, 19, 23, 24, 25, 26, 28 and 29.

There is need for further using research using other QTL mapping tools to study the differential expression of RFI QTL when beef steers are fed different feed formulations. This will help advance our knowledge about genes controlling feed efficiency for applications in marker assisted selection or genomic selection.

Conclusion

Our study investigated whether similar QTL affect RFI performance in steers fed a grower or a finisher diet. We used RFI performances obtained from steers fed grower and finisher diets in feeding trials. The results indicated that some SNP/ QTL were specific to either the grower fed group or the finisher fed group. These differences may indicate that a QTL-by-environment interaction exists for RFI.

Figure 1: QTL plot for all chromosomes in the grower fed group

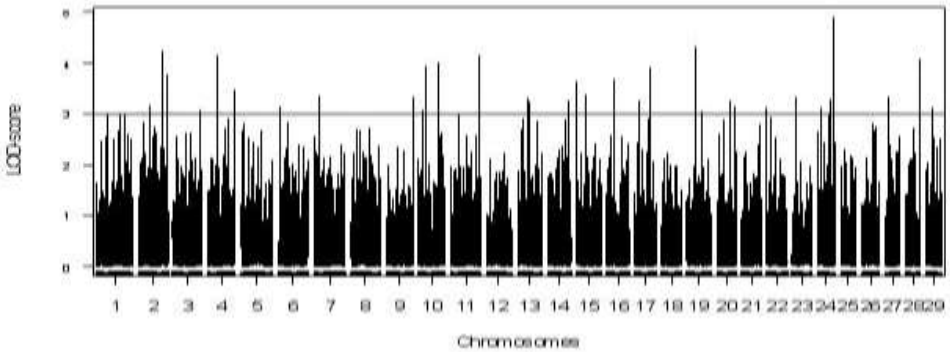
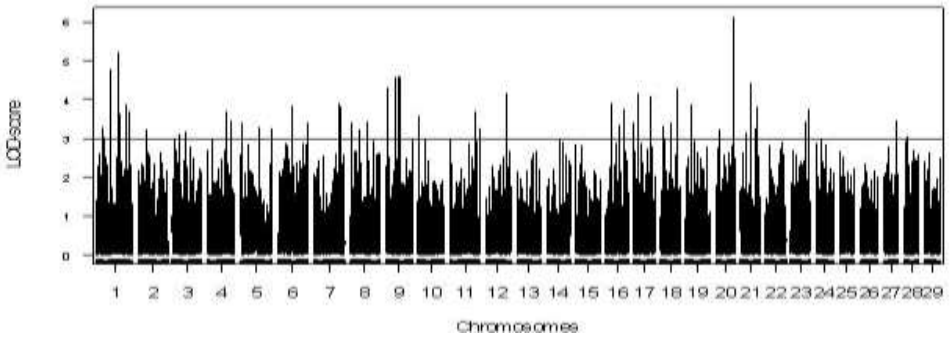


Figure 2: QTL plot for all chromosomes in the finisher fed group



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