QTL FOR FEED INTAKE AND ASSOCIATED TRAITS

W.S. Pitchford, M.L. Fenton, A.J. Kister and C.D.K. Bottema

Livestock Systems Alliance, Adelaide University, Roseworthy SA 5371, Australia

INTRODUCTION

In typical beef cattle production systems, the breeding herd accounts for 65-85% of the total feed requirements (Ferrell and Jenkins, 1984 ; Montaldo-Bermudez *et al*., 1990) and 65-75% of this is used for maintenance. Primarily, the very large maintenance requirement is because cattle are a large, slowly maturing species with a low annual reproductive rate. Furthermore, only a single product is harvested (meat). Any improvement in the efficiency with which breeding cows maintain body weight, will result in an increase in total meat production for a given amount of feed.

The key to selection for increased efficiency is to be able to accurately measure feed intake, a trait that is both difficult and expensive to measure. A less expensive alternative would be to use a DNA test for markers of genes affecting intake. This approach has the potential to significantly reduce the generation interval. The aim of this project is to locate regions (quantitative trait loci, QTL) in the cattle genome that contain genes affecting intake.

METHODS

Cattle herd design and feed intake measurement. The Adelaide-AgResearch Cattle Gene Mapping Project comprised a cross between two diverse *Bos taurus* breeds (Jersey and Limousin) where F_1 bulls were crossed back to both parent breeds. There were three bulls used in Australia and three in New Zealand (half brothers of Australian bulls) with 120-140 progeny per F_1 sire. Feed intake measurements were conducted on the Adelaide progeny only. The Adelaide mapping progeny included 366 backcross calves : 77 born April 1996, 153 born April 1997, and 136 born April 1998. Heifers and steers were measured separately each year so there were six cohorts (1996-heifers, …, 1998-steers). In all cohorts, as expected, just over 10% of animals were shy feeders and were removed from the intake testing pens and fed separately. Thus, there was feed intake data available for 323 animals (Table 1). Additional data on number of feeding sessions and total time in feeders was also obtained. The 1996 and 1997 drops were tested at similar weights but 1998 drop had lighter heifers and heavier steers. The 1998-drop steers had very low gains (average 0.03kg/d) because they entered the intake test after spending significant time on high energy feed.

Feed intake measurements were conducted using an automated system with up to eight animals per feeder. Each time cattle enter the feeder, their ID is recorded with their weight, the amount of time feeding and the amount of feed eaten.

Gene mapping. Microsatellite markers (3-9 per chromosome) were genotyped for all 29 autosomes. In the half-sib design utilised, sires were all classified as having the genotype "AB". Thus, progeny would either inherit an "A" or "B" from the sire and another allele ("A",

"B", or "C") from the dam. Genotyped probabilities were calculated using "QTL Express" (Seaton *et al.* 2001) every centi-Morgan on all autosomes.

Statistical analysis. Feed intake data was processed by calculating least-squares means for each animal over the test period. Day was included in the model to allow for weather, personnel, time of feeding, and any other factor that would affect the intake of all cattle. Intake and growth traits were normally distributed, but the number of eating sessions and time spent eating were skewed and were subsequently transformed by taking the natural logarithm (Table 1).

Before proceeding with mapping, the data were investigated by fitting a model containing fixed effects of cohort (1996 heifers, …, 1998 steers), breed of dam (Jersey or Limousin) and sire (361, 368 or 398). Significance was defined as $P<0.05$ for the analysis of fixed effects as well as QTL mapping. Permutation tests (Seaton et al. 2001) showed that the chromosome-wide significance level was F-value of 4.4 ($P<0.05$) or 5.8 ($P<0.01$).

Table 1. Summary of data collected

Trait	Abrev.	No.	Mean	CV (%)	Min.	Max.
Daily feed intake (kg/day)	Intake	323	12.94	17	6.37	18.95
No. meals ($\log_n$(No./day))	LnMeals	314	1.96	30	0.65	3.48
Time eating ($\log_n$(min/day))	LnTime	314	4.56	7	3.83	5.37
Eating rate (g/sec)	Rate	314	2.44	30	1.05	4.71

RESULTS AND DISCUSSION

Data collected. When back transformed, the mean, minimum and maximum values for number of meals (sessions) per day were 7, 2, and 32 and for time eating (minutes) per day were 96, 46, and 215 respectively. The maximum value for feeding sessions (32) was probably high because some animals had the tendency to come in and out of the feeders frequently while eating. Feed intake was more variable (CV=17%, Table 1) than time spent eating, but less variable than the number of meals. Intake was moderately correlated (0.34) with eating time, but not with the number of meals (-0.09). Eating rate was more highly correlated with eating time (-0.78) than with intake (0.29).

Fixed effects. Cohort differences were highly significant for every trait (Table 2). The 1996-drop was the only group where steers and heifers were fed at the same time. From the 1996-drop results, it can be concluded that compared to heifers, steers were 8% heavier, gained weight 17% faster, ate 4% more (Table 2), ate 13% less meals, spent 4% less time eating and ate 2% faster.

Breed of dam differences were significant for weight (not presented) and feed intake (Table 2). Limousin cross (¾L¼J) cattle were 16% heavier, gained 11% more weight, ate 12% more and 17% faster than the Jersey cross (¼L¾J). While the differences appear large, there was no significant difference in most measures of efficiency, number of meals or time spent eating (Table 2).

Table 2. Least squares means and tests of significance for main effects

Trait	Intake	LnMeals	LnTime	Rate
Cohort	***	***	***	***
'96 Heifers	11.4±0.3	2.76±0.05	4.36±0.03	2.78±0.08
'96 Steers	11.9±0.3	2.62±0.06	4.32±0.03	2.84±0.10
'97 Heifers	12.3±0.2	1.98±0.04	4.66±0.02	2.06±0.07
'97 Steers	13.7±0.2	2.15±0.04	4.51±0.02	2.73±0.06
'98 Heifers	14.1±0.2	1.65±0.04	5.01±0.02	1.61±0.07
'98 Steers	13.4±0.2	1.26±0.04	4.31±0.02	3.17±0.07
Breed	***			***
Jersey	12.1±0.1	2.08±0.03	4.54±0.01	2.33±0.04
Limousin	13.5±0.2	2.06±0.03	4.53±0.01	2.73±0.04
Difference	12%	-2%	-1%	17%
Sire	***	**	***	
361	13.3±0.2	2.00±0.03	4.55±0.02	2.61±0.05
368	12.9±0.2	2.07±0.03	4.58±0.02	2.46±0.05
398	12.2±0.2	2.14±0.03	4.47±0.02	2.52±0.05
Difference[A]	-7%	11%	-9%	-1%
QTL **1**	***			*
Effect	-1.76±0.39			-0.25±0.11
Difference	-14%			-10%

*P<0.05, **P<0.01, ***P<0.001.
[A]Difference between 398 and average of other two sires calculated from back-transformed means.

As with breed effects, sire differences were significant for weight (not presented) and feed intake (Table 2). In contrast with breed effects, sire differences were also significant for efficiency, number of meals and time spent eating. Generally, sire 398 was different from the other two sires. Progeny of sire 398 progeny ate 7% less, had 11% more meals but spent 9% less total time eating than the average of the other two sires' progeny. Since Sire 398's progeny ate less and spent less time eating, there was no difference in eating rate (Table 2).

QTL mapping. The study identified five potential QTL with effects on feed intake. Most QTL were segregating in one family only indicating that the QTL or genes identified were not fixed in the parent "purebred" populations. One of the five QTL for feed intake was identified with an F-value of 7.5 (P<0.01, Table 2) and a corresponding calculated LOD score of 4.5 (Seaton *et al.* 2001). In the progeny of sire 398 (Table 2), the QTL resulted in animals that ate 14% less, spent 4% less time eating, and had a 10% lower eating rate (i.e. little effect on time spent eating, simply ate less). The effect on intake (14%) exactly accounted for the difference between 398 and the other sires (7%, Table 2) implying sire 398 was heterozygous for the QTL. However, the QTL effect on number of meals and time spent eating was smaller and did not account for the difference between sires in those traits (Table 2). Lastly, the QTL effect on

eating rate was larger (10%) than the difference between the sires (only 1%). There was no effect on the number of meals (LnMeals) at, or near, the largest QTL for feed intake. Indeed, LnMeals mapped to an entirely different chromosome. The amount of time feeding (LnTime), however, mapped near (20cM) the feed intake QTL.

Mouse studies were conducted in a parallel project to the cattle studies. Mouse lines were selected for high or low net feed intake based on a post-weaning test (Hughes *et al.* 1997). After seven generations of selection, the lines were approximately 30% different in feed intake with little difference in growth and body composition. These lines were crossed to produce F_1 sires and dams that were *inter se* mated to produce F_2 progeny. Mapping was conducted in two sire families.

Mice are not necessarily a good model for cattle because of gross differences in digestive systems. Comparative mapping between mice and cattle is further complicated by the fact that mapping traits in mice results in different sets of QTL depending upon the type of cross and strains used. Nevertheless, some of the feed intake QTL identified in our mouse mapping experiment were homologous to some of those identified in cattle.

ACKNOWLEDGEMENTS

The J.S. Davies Bequest to the University of Adelaide and Meat and Livestock Australia funded the project. Genotyping was conducted by AgResearch, Dunedin NZ. Contract feeding was conducted by the Cattle and Beef Quality Cooperative Research Centre at Tullimba Feedlot, Armidale NSW 2351 (1996-drop) and the South Australian Research and Development Institute at Struan Agricultural Centre, Naracoorte SA 5271 (1997 and 1998-drop). The input of farm and technical staff and students was invaluable.

REFERENCES

Ferrell, C.L. and Jenkins, T.G. (1984) *J. Anim. Sci.* **58** : 234-243.

Hughes, T.E., Archer, J.A. and Pitchford, W.S. (1997) *Proc. Ass. Adv. Anim. Breed. Genet.* **12** : 230-233.

Montaldo-Bermudez, M., Nielsen, M.K. and Deutscher, G.H. (1990) *J. Anim. Sci.* **68** : 2279-2288.

Seaton, G., Haley, C., Knott, S., Kearsey, M., and Visscher, P. (2001) QTL Express, http://qtl.cap.ed.ac.uk (December 5th 2001 version).