Regions of the Genome Associated with Mid-Lactation Feed Efficiency in Dairy Cattle

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Summary and Implications

Regions of the genome associated with variation in feed efficiency and dry matter intake were identified using data from 3306 Holstein cows from Europe and North America. For feed efficiency, regions that explained the most variation were located on chromosomes 18, 5, and 3. For dry matter intake, top regions were 26, 5, and 25. For both traits no one region explained more than 2.8 percent of the total genetic variation. From these results we conclude that feed efficiency and intake are genetically and biologically complex traits that are impacted by many factors and the exploitation of no one particular gene will generate large genetic gains in these traits.

Introduction

Increases in feed efficiency are continually sought in part because of their potential for economic and environmental improvements. While management and feeding practices have been employed to improve the feed efficiency of the dairy cow, genetic improvements have been minimal, largely due to the equipment and labor demands of recording feed intake on large numbers of individual cows, which is necessary to gain meaningful insights to quantitative traits. Consequently, collaboration between United States and European researchers was established in order to pool data for the exploration of the genetics of feed efficiency. The goal of this study was to identify regions of the genome associated with feed efficiency and dry matter intake (DMI).

Materials and Methods

Individual feed intake, milk production, milk composition, and body weight data were collected on 3306 cows from Canada, the Netherlands, Scotland, and the United States. Data outside 50 to 200 days in milk were removed and the remaining were corrected for location, experiment, diet, parity (first or second and later), and days in milk. Feed efficiency was calculated as residual feed intake (RFI), or the difference between actual DMI and that expected based on milk energy output, metabolic body weight, and change in body weight.

All cows were genotyped with 50k SNPs or had imputed genotypes of this size. Regions of the genome explaining genetic variation were determined using Bayesian methodology employed by the program GenSel. Genes located in or nearby the top 10 regions identified by GenSel were obtained using Ensembl and then clustered based on function using the bioinformatics resource, DAVID.

Results and Discussion

The top regions explaining genetic variation for feed efficiency together explained 4.22 percent of the total genetic variation in this trait (Table 1.) and were located, in order by most genetic variation explained, on chromosomes 18, 5, and 3. For DMI, locations explaining the most genetic variation were on chromosomes 26, 5, and 25. Together, these three regions explained 4.66 of the total genetic variance of DMI. For each trait, of the top ten regions explaining variation, three were in common between both traits.

853 genes were identified for feed efficiency and 942 for DMI. The top cluster for DMI showed enrichment for olfactory genes and the top cluster for feed efficiency showed enrichment for chemokine genes.

The absence of a region explaining a large proportion of the genetic variance for feed efficiency and DMI suggests that these traits are impacted by many genes each having a small effect. Perhaps this can be considered intuitive when one considers that DMI is impacted by milk production, body size, and body tissue reserves. However, based on the calculation of RFI, variation in these traits would not have an impact on feed efficiency. Nonetheless, there are many metabolic processes that occur after consuming a meal that could influence feed efficiency. Genetic variation in efficiency of digesting carbohydrates and proteins or in cellular metabolic processes all could contribute to the genetic variation of feed efficiency.

Acknowledgements

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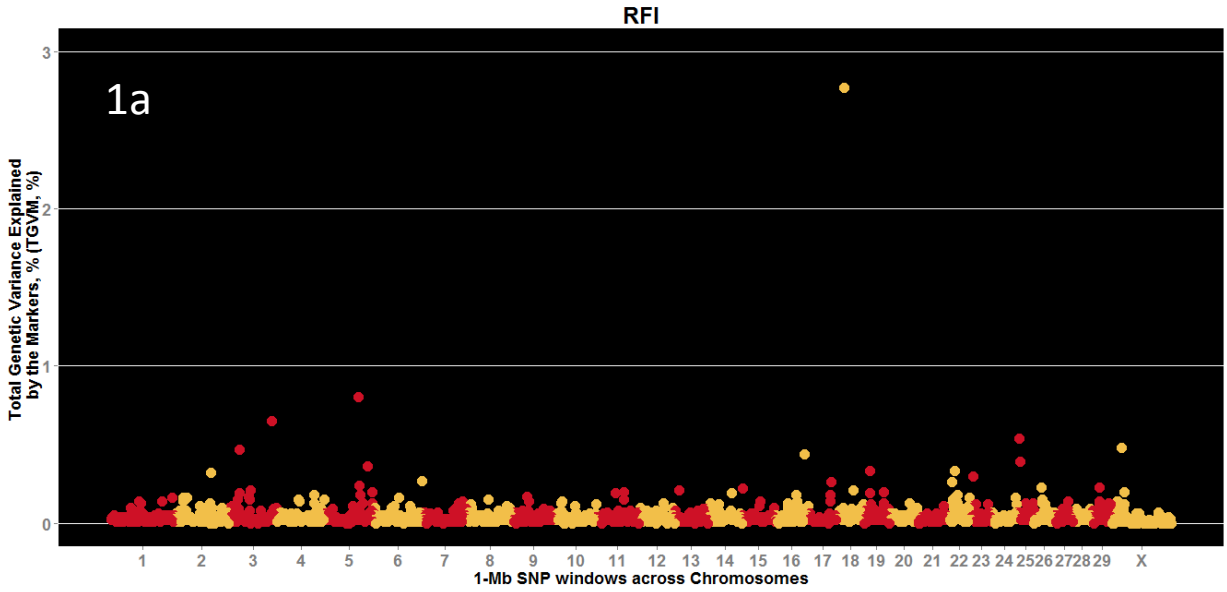
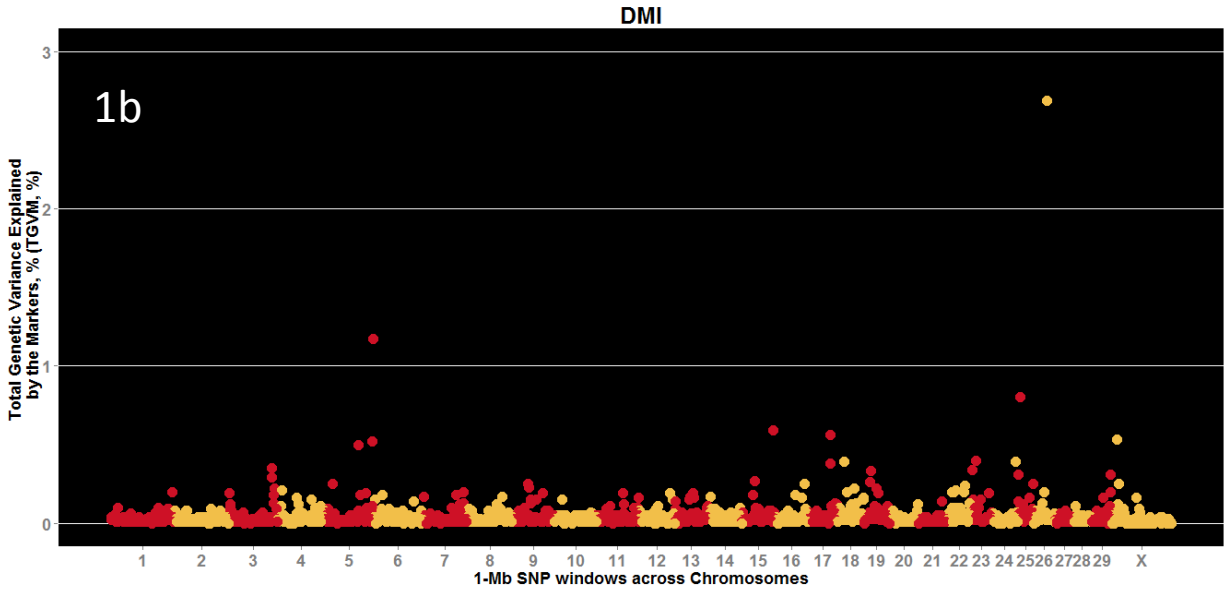
Table 1. Top ten chromosome (Chr.) regions (Megabases, Mb) explaining genetic variation (%Gen. Var.) in feed efficiency (RFI) and dry matter intake (DMI).

	RFI			DMI		
Rank	Chr.	Mb	%Gen. Var.	Chr.	Mb	%Gen. Var.
1	18	15	2.77	26	32	2.69
2	5	83	0.50	5	121	1.17
3	3	108	0.65	25	8	0.80
4	25	4	0.54	15	79	0.59
5	X	13	0.48	17	56	0.56
6	3	27	0.47	X	1	0.53
7	16	73	0.44	5	117	0.52
8	25	8	0.39	5	83	0.50
9	5	106	0.36	23	3	0.40
10	19	16	0.33	18	15	0.39

Figure 1: Manhattan plot showing the percent of genetic variance explained by windows of SNPs on each of the chromosomes (labeled on the x-axis) for feed efficiency (RFI, 1a) and dry matter intake (DMI, 1b).




DMI
1b
Total Genetic Variance Explained by the Markers, % (TGVM, %)
0
1
2
3
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 X
1-Mb SNP windows across Chromosomes