Fatty Acid SNP Interaction Analysis in Angus Sired Beef Cattle

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Summary and Implications

The triacylglyceride (TAG) fatty acid content in meat from Angus-sired cattle was analyzed for non-additive genetic effects. A total of 11,482 significant DNA marker interactions (false discovery rate [FDR] < 0.05) were detected across thirty-seven different TAG fatty acids. Interactions were not evenly distributed amongst all fatty acids analyzed, and types of interactions (additive-by-additive, additive-by-dominance, and dominance-by-dominance) varied within each individual fatty acid. These results indicate that it may be possible to account for additional genetic variance amongst TAG fatty acids over and above individual markers.

Introduction

Increasing awareness of what people are eating has brought about a nutritionally minded group of consumers. Fatty acid consumption has been associated with some negative health traits such as cardiovascular disease, and as such has become an important point of contention amongst consumers. As such, additional research into how much genetic variance can be accounted for within the various fatty acids is an important undertaking in order to better understand how the traits are controlled and inherited. By better understanding the genetic variance that controls TAG fatty acids, we will be better equipped to select for animals with altered fatty acid composition as desired by the consumer market.

Materials and Methods

A subset, 1721 head of cattle, was utilized from the beef healthfulness study previously completed. TAG fatty acid fractions of the longissimus dorsi were collected after freeze grinding steaks into a powder. Total lipid fraction was extracted from this powder via a chloroform and methanol mixture, and then the TAG fraction was separated from the phospholipid fatty acid fraction via thin-layer chromatography and then quantitated by gas chromatography. These values were collected on forty-four different TAG fatty acids. All calves were genotype with the Illumina 54k SNP chip.

Statistical analyses were performed to identify interactions between SNPs that exhibited an additive-by-additive, additive-by-dominance or dominance-by-dominance interactions (Table 1). False discovery rate was estimated for SNP interactions to account for multiple testing. Genotype frequency filters were applied to the interactions remaining after FDR analysis, at 5, 10, 20, 50, and 100 animals per genotype combination. Interactions were then plotted for each individual fatty acid in order to visualize which chromosomes and which regions are responsible for the interactions discovered (Figure 1).

Results and Discussions

A total of 11,482 significant interactions (FDR < 0.05) were detected through our SNP interaction analysis (Table 1). A decreasing number of significantly detected interactions were seen as the filters became more stringent. Of particular note are TAG fatty acid traits 14:0, 18:1t10pt11, and the AI (atherogenic index). These three fatty acids had over 500 significant interactions despite requiring at minimum 100 animals of each genotype. Traits were also examined as a broader category such as Saturated Fatty Acids (SFA), Monounsaturated Fatty Acids (MUFA), Polyunsaturated Fatty Acids (PUFA), and Ratio/Calculation. The PUFA category of TAG fatty acids contained the smallest proportion of significant interactions from this study (0.077) while nearly half the total interactions discovered (0.483) were associated with MUFA.

Results for the TAG fatty acids indicate the potential to account for additional genetic variation amongst these traits in Angus-sired beef cattle. Combined with previous work that characterized individual SNP effects, this SNP interaction study contributed to the total variation that has been accounted for and will help with selection on various traits as the market demands.

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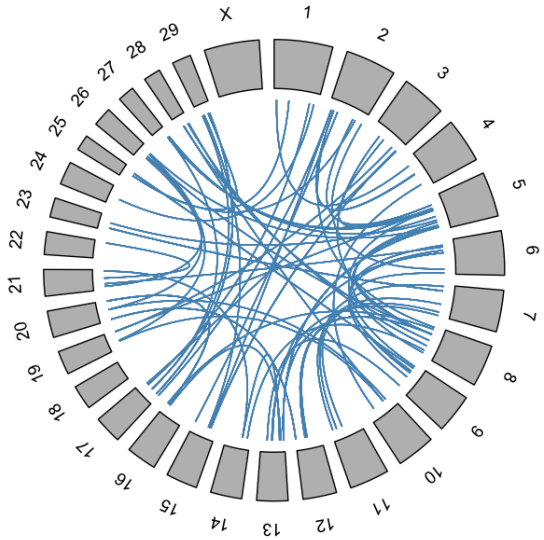
Table 1. Interaction type breakdown by individual TAG fatty acid at FDR significance and 5-animal filter

Trait	AA	AD	DD	Total Interactions
Saturated Fatty Acids				
SFA	242	141	14	397
12:0	11	197	22	230
14:0	953	46	10	1009
16:0	0	0	0	0
17:0	159	5	0	164
18:0	267	83	3	353
22:0	6	103	9	118
23:0	0	1	1	2
24:0	0	0	1	1
Monounsaturated Fatty Acids				
MUFA	1	0	0	1
14:1	3	0	0	3
16:1	269	146	17	432
17:1	263	2	0	265
18:1c9	0	1	0	1
18:1c11	877	30	9	916
18:1c12	0	1	0	1
18:1c13	10	316	126	452
18:1t6pt9	8	516	13	537
18:1t10pt11	2731	122	27	2880
18:1t12	0	0	0	0
18:1t15	51	2	1	54
Polyunsaturated Fatty Acids				
PUFA	2	98	0	100
18:2	0	1	0	1
18:3n3	0	0	0	0
20:2	2	13	0	15
20:4	1	15	23	39
20:5	3	57	10	70
22:6	0	8	15	23
CLAc9t11	0	21	2	23
CLAt10c12	18	4	2	24
n3	0	83	0	83
n6	139	349	20	508
Ratio/Calculation				
n3n6	6	124	1	131
PUFASFA	2	92	0	94
MCFA	397	92	3	492
LCFA	405	90	3	498
AI	1017	431	117	1565
Total	7843	3190	449	11482

Figure 1: SNP by SNP interactions for TAG fatty acid 18:0



Blue lines are significant SNP interactions, Grey blocks are chromosomes labeled 1 to X. 353 total significant interactions visualized at FDR < 0.05 and 5 animal filter