


Healthfulness of beef: A genome wide association study using crossbred cattle.

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Introduction

- Increase in health conscious consumers.
- Modifications in animal diets can alter the nutrient profile of beef.
- Identification of genetic variants would allow producers to select for more desirable nutrient profiles of beef.
- Novel traits – niche market opportunities
- Ultimately increase value and consumer satisfaction of beef.
- Selection aided by genomic predictors may serve as an applicable tool improve nutrient profiles
 - Phenotypic data can be expensive and difficult to collect




Objectives

- Determine the proportion of phenotypic variation explained by the Illumina BovineSNP50KBead-Chip for cholesterol (CH), polyunsaturated fatty acids (PUFA), monounsaturated fatty acids (MUFA), protein, potassium, iron and sodium.
- Identify chromosomal regions that harbor major genetic variants underlying the variation of these traits.




Materials and Methods

- 239 Crossbred steers and heifers (Angus, Simmental and Piedmontese)
 - Genotyped for 0, 1, or 2 copies of Myostatin mutation (C313Y)
- Split into 4 groups and fed over a two year period (2010 to 2012)
 - 2 groups each year, heifers and steer groups each year
- Ad libitum access to water and were fed a diet that met or exceeded NRC requirements
- ½ inch steaks cut from eye of round (ST) and longissimus dorsi (LTL)
- Steaks trimmed to 1/8th inch of subcutaneous fat
- Midwest Laboratories, Inc. performed lipid and mineral analysis




Materials and Methods

- Fatty acids and cholesterol were analyzed as a % of total fat and mg/100g of wet tissue
- Potassium, iron and sodium were analyzed as ppm of whole tissue
- Interpretation of the two scales is dramatically different
 - Low PUFA in mg/100g of whole tissue would have low total lipid and would have a relatively high PUFA as a % of total fat.




PUFA	MUFA
C18:2 trans	C14:1 trans
C18:2	C14:1
C18:3 gamma	C16:1 trans
C18:3 alpha	C16:1 alpha
C20:2	C17:1
C20:3	C18:1 trans
C20:4	C20:1
C20:5	C22:1
C22:2	C24:1
C22:5	
C22:6	



Statistical Analysis

- Outliers were removed for the data >3 S.D.
- GenSel software was used to fit a BayesC algorithm with group (year and sex) fitted as fixed
 - π 0.95
 - 150,000 iterations, first 50,000 discarded
- BayesC – Bayesian mixture model is fitted with a set prior number of SNP having an effect each iteration and the other SNP having a null effect at that iteration.
- a priori heritability estimate used
- GEBV - summing posterior mean marker effects by marker genotype across all SNP
- SNP were blocked into 1 Megabase (Mb) windows
 - Top 0.5% (n=13) compared across cuts
 - Candidate gene approach conducted




Summary of lipid traits

Trait	n	Mean	± S.D.
ST Cholesterol (mg/100g)	225	46.26	4.73
ST Cholesterol (% of fat)	223	1.94	2.48
LTL Cholesterol (mg/100g)	225	45.76	4.48
LTL Cholesterol (% of fat)	222	0.50	0.45
ST PUFA (mg/100g)	227	378.87	132.31
ST PUFA (% of fat)	222	8.50	5.20
LTL PUFA (mg/100g)	224	572.60	180.07
LTL PUFA (% of fat)	223	5.27	2.21
ST MUFA (mg/100g)	227	2461.14	1977.84
ST MUFA (% of fat)	223	45.11	5.50
LTL MUFA (mg/100g)	227	6087.70	3233.42
LTL MUFA (% of fat)	224	46.25	4.31

Summary of mineral and protein traits

Trait	n	Mean	± S.D.
ST Protein %	227	22.91	1.33
LTL Protein %	225	21.69	1.86
ST Iron ppm	226	13.92	2.62
LTL Iron ppm	224	13.65	2.06
ST Sodium ppm	226	3484.30	227.99
LTL Sodium ppm	227	3015.18	268.71
LTL Potassium ppm	227	393.92	29.02
ST Potassium ppm	226	418.69	32.14




Trait	Heritability
ST Cholesterol (mg/100g)	0.45 (0.11)
ST Cholesterol (% of fat)	0.45 (0.10)
LTL Cholesterol (mg/100g)	0.50 (0.06)
LTL Cholesterol (% of fat)	0.50 (0.09)
ST Poly Unsaturated Fatty Acids (mg/100g)	0.45 (0.04)
ST Poly Unsaturated Fatty Acids (% of fat)	0.65 (0.06)
LTL Poly Unsaturated Fatty Acids (mg/100g)	0.70 (0.08)
LTL Poly Unsaturated Fatty Acids (% of fat)	0.70 (0.08)
ST Mono Unsaturated Fatty Acids (mg/100g)	0.60 (0.10)
ST Mono Unsaturated Fatty Acids (% of fat)	0.60 (0.08)
LTL Mono Unsaturated Fatty Acids (mg/100g)	0.85 (0.04)
LTL Mono Unsaturated Fatty Acids (% of fat)	0.40 (0.10)

Trait	Heritability
ST Protein %	0.75 (0.06)
LTL Protein %	0.70 (0.08)
ST Iron ppm	0.35 (0.09)
LTL Iron ppm	0.35 (0.13)
ST Sodium ppm	0.05 (0.05)
LTL Sodium ppm	0.15 (0.08)
ST Potassium ppm	0.65 (0.09)
LTL Potassium ppm	0.75 (0.08)

GEBV Correlations

- Follow the phenotypic correlations
- Low to moderate and varied in direction
 - Among protein and minerals
 - Iron and protein -0.32
 - Sodium and protein -0.09 (ST)
 - Sodium and protein 0.15 (ST and LTL)
 - Sodium and protein 0.25 (LTL)
 - Lipids with protein and minerals
 - PUFA and protein 0.59 (ST)
 - MUFA and protein -0.53 (ST)
 - CH and protein 0.35 (ST)



GEBV Correlations

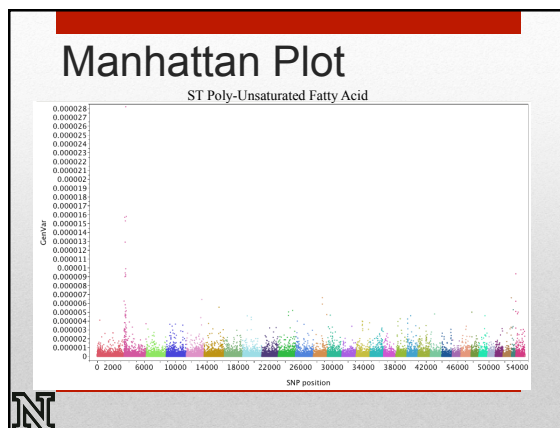
- Moderate to strong
 - Among lipid traits
 - % - MUFA negative with PUFA and CH
 - mg/100g - MUFA and PUFA were positively correlated
 - CH negatively correlated with MUFA and PUFA

GEBV Correlations

- Interpretation is conditional upon the measurement scale
- Example: When the gravimetric amount of PUFA is low the amount of PUFA relative to total fatty acids can be high due to the amount of total fatty acids being low.

GEBV Correlations

- The expectation that the increase in adipose tissue that CH increases, PUFA decreases and MUFA increases on a percent fat basis is challenged in the case of the double muscling genotype.
- Raes et al. (2001) found the Belgian Blue breeds has low proportions of MUFA and high PUFA in muscle lipid compared with normal genotype animals.
- Due to low concentrations of total lipid and high ratio of phospholipid (high in PUFA) and total lipid.



Candidate gene annotation

- GULP1 common gene found among lipid traits.
 - *Engulfment adaptor PTB domain containing 1*
 - Adaptor protein that binds and directs the trafficking of LPR1 which is involved in lipid homeostasis (He and Lin, 2010).
- ITGAV
 - Associated with metabolic processes and negative regulation of lipid transport and storage (Kim et al., 2013).

Other work

- Matescu et al. (2013) reported similar heritability estimates for iron and sodium.
- There are few reported estimates of heritability for fatty acids and cholesterol
 - Cesar et al. (2014) reported low to moderate heritability
 - Pitchford et al. (2002) reported low to moderate heritability
 - Cameron et al. (1990) reported moderate to high heritability

Conclusions

- These are novel traits that seem to be under genetic control and have genetic relationships among each other.
- Gravimetric scale seems to be the most straightforward measurement as proportions can be deceiving based on total fat content.
- Animals are re-ranked based on measurement scale.
- Further analysis of these novel traits will allow for better understanding of the genetic control



Acknowledgements

Co-authors

- Jeremy T. Howard, former graduate student
- Dr. Chris Calkins, UNL
- Dr. Matt Spangler, UNL

Data Collection

- Michelle Semler
- Michael Chao
- Justine Hosch
- Lasika Senaratne-Lenagala
- Kim Varnold
- Katherine Domenech-Perez

Project Funding

- University of Nebraska-Lincoln Layman Award



Questions?

