Gene Expression of Skeletal Muscle of Red Face Hereford Steers

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Introduction

Meat quality and tenderness are two of the most consumer valued characteristics of steak, with tenderness as one of the most important palatability attributes of meat. Agriculture is the largest industry in Montana, and an understanding of how selection pressures on economic important traits, such as meat tenderness and muscle growth, gives insight into the methods by which producers may practically select for tenderness in their own herds. The objective of this study was to evaluate the relationship between quality grade and genetic growth patterns on meat tenderness. The research aimed to evaluate the impacts of gene expression on quality grade. Muscle samples from 16 different Hereford cross steers were taken following harvest and RNA was extracted from these samples to evaluate which genes were being actively transcribed in the muscle at time of harvest. Gene set enrichment analysis, transcription factor analysis and network and pathway analysis was used to identify genes and gene networks that relate to growth rate and carcass quality.

Materials and Methods

- 16 red faced Hereford steers (Fort Keogh Agricultural Research Station)
- Harvested after all steers had been fed a minimum of 270 days in the feedlot
- Carcass data were collected (hot carcass weight, fat thickness, ribeye area, maturity, marbling)
- The striploin was removed 24 hr postmortem
  - One steak per steer was aged for 1, 3, 7, 14, and 21 days at 4ºC
- Shear force measurements were conducted following the methods of Boles et al. (2009).
- Loin muscle biopsy collected and snap frozen in liquid nitrogen
- RNA was extracted from the loin muscle and pooled based upon carcass quality grade
- Extracted RNA were sequenced on an Ion Torrent PGM (Colorado State University)
  - Aligned to bovine consensus sequence (BTAU 4.2) and gene expression determined using CLC Bio Genome Workbench software
  - Differentially expressed genes calculated using Strand NGS RNA seq. module
  - A functional analysis was run using DAVID bioinformatics software
- Carcass data and shear force was analyzed
  - Individual animal was the experimental unit
- Significance was determined *a priori* $P < 0.05$.

Results and Discussion

- Standard carcasses were significantly lighter, had less fat, and had a smaller loin muscle area than Select and Choice carcasses
- There was a significant increase in shear force between Choice and Select quality grades
  - No significant difference in shear force from Choice to Standard
- Shear force significantly decreased as length of postmortem aging increased
- Upon analysis of differentially expressed genes, a significant number of differences were observed between Choice and Standard carcass pools (1258 genes, $P < 0.01$).
- A functional analysis revealed differences in the underlying pathways regulating muscle cell growth and proliferation.

Table I: High Fold Change Differentially Expressed Genes

Gene ID	*Fold Change*	*Regulation*	*Function*
Q0VD21	13.56	Up	heparan sulfate (Glucosamine)
CATH	12.37	Up	cathepsin H
ITPRIPL2	11.13	Up	inositol 1,4,5-triphosphate receptor interacting protein
BACE2	9.28	Up	beta-site APP-cleaving enzyme
E2F3	-10.24	Down	E2F transcription factor 3
PI42C	-10.51	Down	phosphatidylinositol-5-phosphate 4-kinase
RFC2	-11.77	Down	replication factor C (activator)
A6QQD5	-12.53	Down	solute carrier (fatty acid transporter)

Table II: Gene Ontology Term Enrichment Analysis

Term	*Count*	*%*	*P-value*
Transcription	101	3.4	<0.00001
Regulation of protein kinase activity	25	0.8	<0.01
Lipid biosynthetic process	34	1.1	<0.01
Regulation of muscle adaption	4	0.1	<0.01
Growth	17	0.6	<0.05
Protein autoubiquitination	4	0.1	<0.05
Nitric oxide metabolic process	4	0.1	<0.05
Protein maturation	14	0.5	<0.05
Positive regulation of developmental process	23	0.8	<0.05
Regulation of cell proliferation	7	0.2	<0.05
Regulation of muscle hypertrophy	3	0.1	<0.05

Summary and Conclusions

Shear force measurements were impacted by quality grade, rib eye area, and fat thickness. As expected, we found Choice carcasses had a lower shear value then Select carcasses. However, Standard carcasses had a lower shear force value than Select. This is potentially due to the physiological age of the animals that were Standard. This is supported by the lighter carcass weights, lower marbling values, and less fat on the carcasses. A functional analysis of differentially expressed genes between Choice and Standard carcass pools revealed differences in the underlying pathways regulating muscle cell growth and proliferation. Biological processes such as growth, muscle hypertrophy, protein kinase activity, and lipid biosynthetic pathway were found to enriched in the differentially expressed gene set. Suggesting that the previously observed differences in the growth patterns between Choice and Standard cattle were due to identifiable differences in the regulation of cellular processes and growth. Meat quality and tenderness are two of the most important traits for beef production, and this research helps to shed light on the genetic and molecular basis of these traits, and how selection and growth may interact in these economically significant characteristics.

Table III. Carcass characteristics of Red Faced Hereford Steers, after 270 days on feed.

Class	*Shear Force(N)*	*HCW(Kg)*	*Fat(cm)*	*REA(cm^2)*	*KPH(%)*	*YG*
Standard	66.3^{b}	250.6^{b}	0.43^{b}	57.68^{c}	1.60^{c}	2.46^{ab}
Select	84.3^{a}	282.9^{a}	0.64^{a}	67.23^{b}	1.80^{b}	2.62^{a}
Choice	71.3^{b}	283.2^{a}	0.58^{a}	72.13^{a}	2.08^{a}	2.35^{b}
P value	< 0.0001	< 0.0001	0.0104	< 0.0001	< 0.0001	0.0077

[1] 200 = Traces, 300 = Slight, 400 = Small

[a, b, c] means within column with different superscripts are significantly different $P \leq 0.05$

References

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