Genome-wide association and gene enrichment analyses of meat tenderness in an Angus-Brahman population



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Beef Industry Future Outlook

- Strong "high-quality" branded beef programs:
 - Consumers are willing to pay for assured quality.
- Important to maintain and increase current consumers brand loyalty (meeting and exceeding quality expectations).
- Important to expand consumer base.
- Improving quality critical for beef industry.
- Tenderness the most important sensory attribute.



Improving Beef Tenderness

• Beef tenderness:

- Measured by Warner-Bratzler shear force (kg).
- Trait measured after slaughter & expensive.
- 15 40% of the variation due to genetics.
- Sustainable strategy to deliver a consistently superior quality product:
 - Develop effective selection and management genomic tools.
 - Assist producers to produce cattle that fit customer expectations.

Population

- Bos Indicus influenced cattle: UF Angus x Brahman Herd
 - 6,870 animals: from 100%Angus to 100% Brahman
 - ~ 780 animals with 250K genotypes
 - **1,941** with carcass traits: **marbling score**, hot carcass weight, dressing %, ribeye area, back fat thickness, yield grade, quality grade, KPH.
 - 1,253 with meat quality phenotypes
 - Warner-Bratzler Shear Force (WBSF)
 - 640 with sensory panels (Tenderness, Juiciness, Connective tissue, Flavor: beef, painty/fishy, livery/metallic)

Objective

Identify **genomic regions** associated with meat **tenderness** related traits - using a **GWAS** approach followed by a **gene enrichment** analysis.













Genome-wide association

- Identify SNPs and chromosomal regions associated with meat tenderness related traits.
- Genotypes: **Bovine GGP F250** functional chip.
 - 221,077 SNPs => 115,287 SNPs

MAF > 0.05

Calling rate > 0.85

- Data processing and analysis Genetics Q-K analysis workflow of JMP-Genomics 6.0 software.
 - Mixed Model GWAS using a single locus (EMMAX)
 - Genomic relationship matrix
 - Fixed effect: year of birth

GWAS – SNP list for enrichment

- SNPs at < 0.05
 - 2,134 for WBSF
 - 2,191 for tenderness
 - 2,060 for connective tissue
- SNPs in genes ± 3kb





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Gene Enrichment

Gene list

- GO pathways DAVID
 - Cellular component
 - Molecular function
 - Biological process

10 3 11 8 12 9 5 6 13

16,384 genes with expression In skeletal muscle

Background list



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Hypergeometric Test

Benjamini-Hochberg p-value correction to each pathway





Gene Enrichment Results - 6 pathways

Trait	GO term	GO term name	p-value	Genes in gene list	Genes GO term
Tenderness	GO: 0005789	Endoplasmic reticulum membrane	0.0042	20	214
Connective Tiss.	GO: 0005789	Endoplasmic reticulum membrane	0.0103	23	214
WBSF	GO: 0005789	Endoplasmic reticulum membrane	0.0021	22	213
Connective Tiss.	GO: 0000122	Negative regulation of transcription from RNA polymerase II promoter	0.0004	19	225
Connective Tiss.	GO: 0005743	Mitochondrial inner membrane	0.0128	17	168
Connective Tiss.	GO: 0045944	Positive regulation of transcription from RNA polymerase II promoter	0.0195	40	319

Gene Enrichment across traits

• The "Endoplasmic reticulum membrane" pathway - enriched across traits





REEP1 - Receptor Accessory Protein 1 gene - In the gene enrichment

analysis for **Connective Tissue**, **Juiciness** and **Tenderness**.

REEP1 - required for endoplasmic reticulum (ER) network formation, shaping and remodeling.

- The protein links ER tubules to the cytoskeleton.

Conclusions

- Quality of beef important to drive demand.
- Selection and management genomic tools sustainable strategy.
- Enrichment of genes in six GO terms.
- Several genes involved in negative regulation of transcription and cell growth and proliferation.
- GWAS + gene enrichment analysis:
 - reveal the **genetic architecture** of complex traits.
 - novel information regarding biological mechanisms and genes that lead to complex phenotypes, like meat quality.



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Questions?

