


BIF, June 2019

Using genomics to improve meat quality in *Bos Indicus* influenced cattle



UF IFAS
UNIVERSITY of FLORIDA

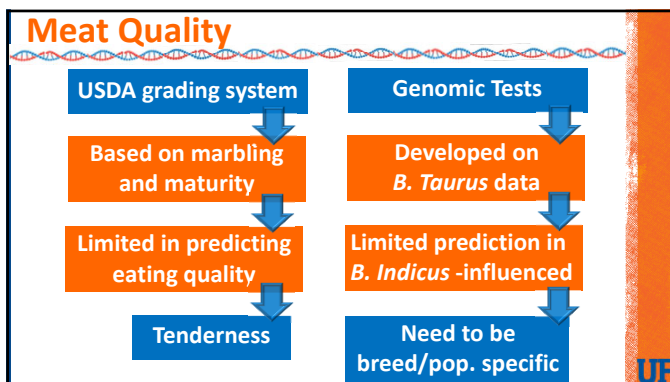
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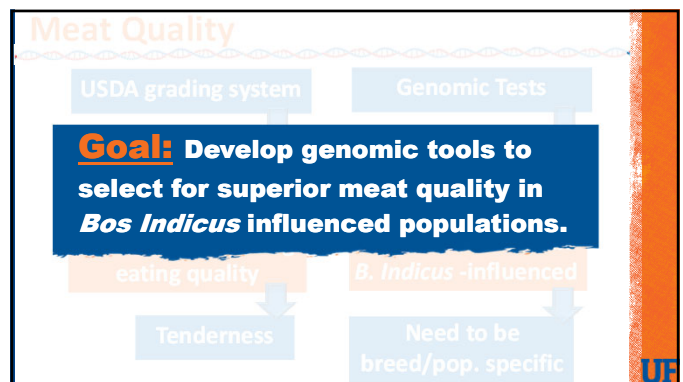
Meat Quality

- Top priority for beef industry
 - Great power to influence demand
 - Can be improved
- Very important for *B. indicus* crosses
 - Routinely penalized for relatively **low marbling** score.
 - Routinely penalized for **perceived** inadequate **tenderness**

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Phenotypic Level

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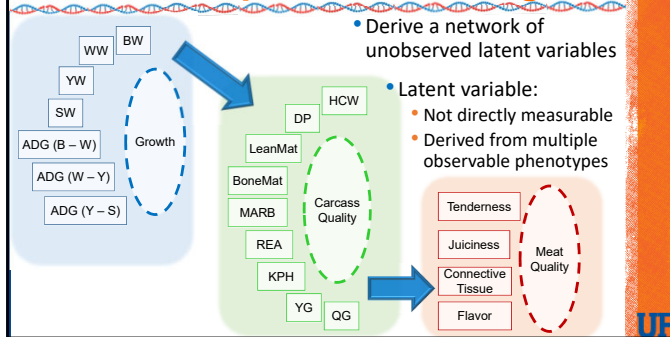
How do we define meat quality?



- Marbling
- Warner-Bratzler Shear Force
- Tenderness (sensory panel)
- Juiciness (sensory panel)
- Connective Tissue (sensory panel)
- Beef Flavor (sensory panel)
- Off-flavors (painty/fishy, livery/metallic)

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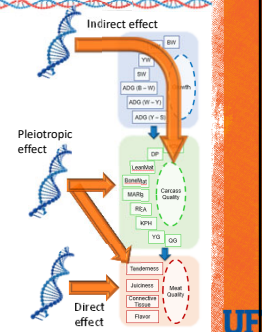
Structural equation modeling



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Structural Equation (SE) Modeling

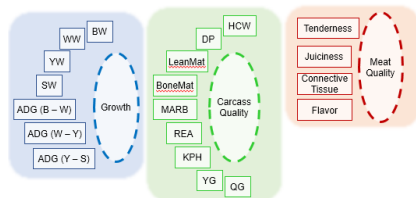
- The **SE** modeling analysis + **GWAS** = powerful approach to uncover:
 - genomic regions **directly** controlling variation in latent variables
 - genomic regions **indirectly** controlling variation in latent variables
 - genomic regions with **pleiotropic** effect responsible for the observed genetic correlations



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Population

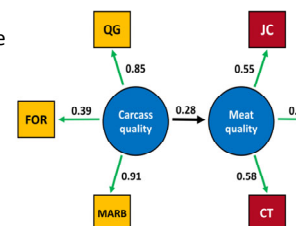
- B. Indicus* influenced: **UF** Angus x Brahman (Multibreed) Herd
 - Animals from 100%Angus to 100% Brahman (6 breed groups)
 - 726** steers (2007 – 2015) with **250K** genotypes
 - Used **22** observed phenotypes



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Final model for structural equation

- The final structural model: **carcass** quality (**independent** latent variable) and **meat** quality (**dependent** latent variable)
- Carcass quality** was measured by FOR, marbling and QG
- Meat quality** was measured by connective tissue, juiciness and tenderness
- Growth** did not fit the model



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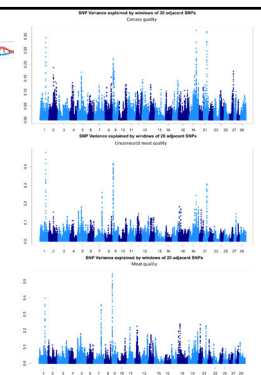
DNA Level

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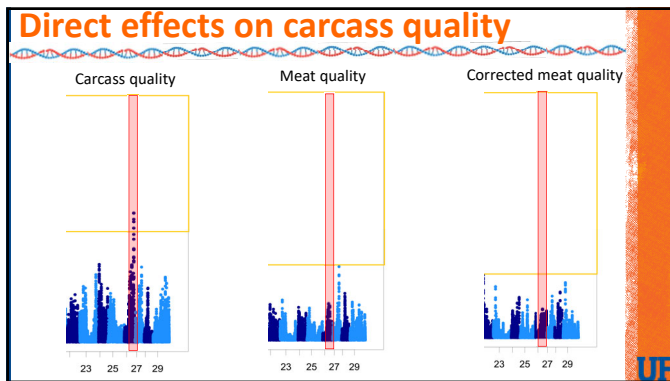
GWAS

- 571** associated genomic regions (643 genes)
 - Carcass quality**: 159 regions / 179 genes
 - Meat quality**: 242 regions / 266 genes
 - Carcass and meat quality**: 106 regions / 114 genes
 - Indirect effect on meat quality**: 64 regions / 84 genes

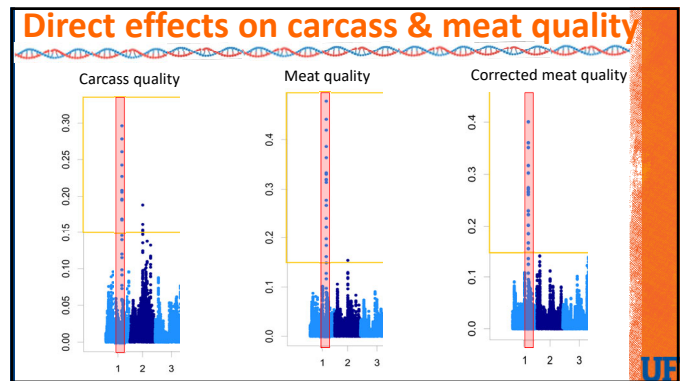
ssGBLUP (BLUP90), MAF>0.05, SNP calling rate > 0.9, 112,267 SNPs, window size = 20 SNPs



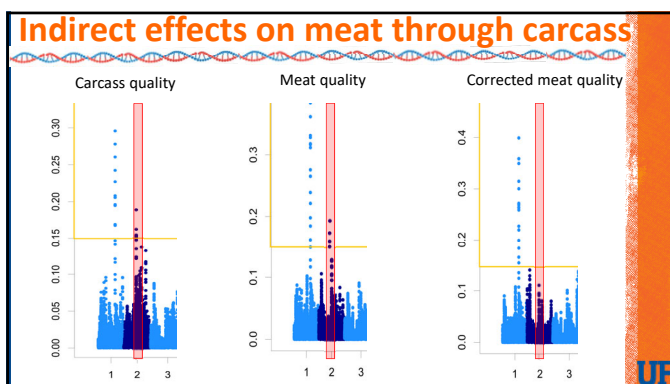
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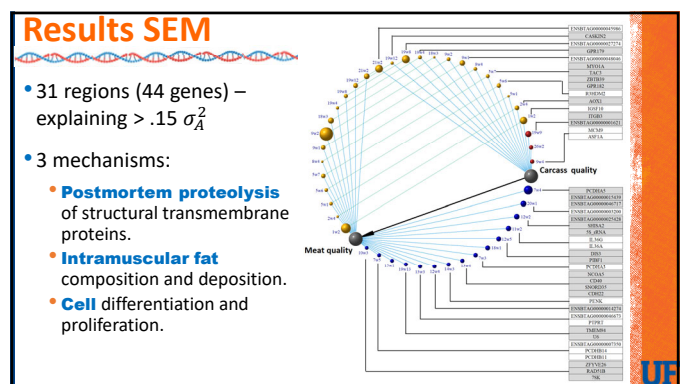
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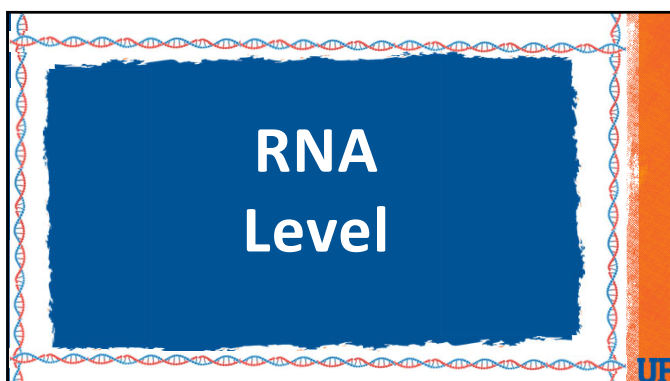
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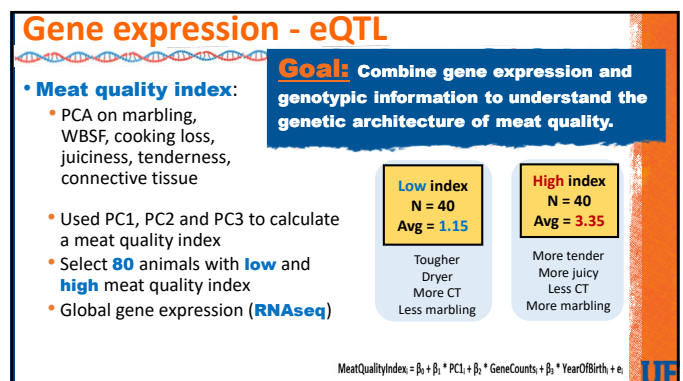
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Differentially expressed genes

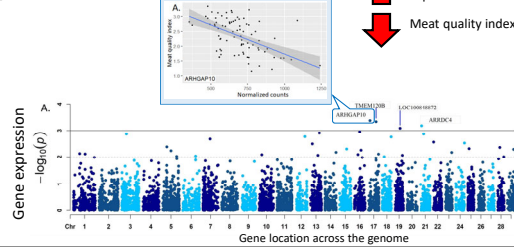
Associated genes = 208

P-value ≤ 0.05

Tested genes = 8,799

ARHGAP10 - regulates actin cytoskeleton remodeling.
↑ expression, more stable actin cytoskeleton structure.

↑ Expression
↓ Meat quality index

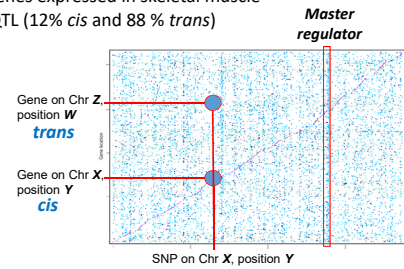


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Map genomic regions for gene expression

- Use gene expression as a trait, for each gene run a GWAS (250K)
 - 8,588 autosomal genes expressed in skeletal muscle
 - 8,377 identified eQTL (12% *cis* and 88 % *trans*)

Hot spot: A SNP with at least 20 *trans* associations
Harboring gene or the adjacent gene => **Master regulator**

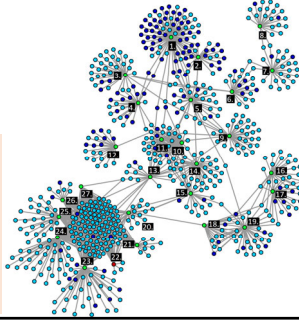


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Network of expression master regulators

- Master regulator
- Diff master regulator
- Regulated gene
- Diff regulated gene

- 27 expression master regulators
- Associated with 674 regulated genes
- Classified as membrane associated or cytoskeletal proteins, transcription factors and DNA methylases.



| | |
|----|---------------------|
| 1 | NTF3 |
| 2 | PDE8B |
| 3 | GAD1 |
| 4 | ZNF445 |
| 5 | FAT4 |
| 6 | PCGF5 |
| 7 | ALAD |
| 8 | ZNF804A |
| 9 | ENSRIBAG00000035487 |
| 10 | PAWR |
| 11 | PSD4 |
| 12 | OR451 |
| 13 | RUNX1T1 |
| 14 | TTC25 |
| 15 | ENSRIBAG00000011638 |
| 16 | CSAD |
| 17 | KIT7 |
| 18 | MYH14 |
| 19 | KLK4 |
| 20 | KCNJ1 |
| 21 | TOR1AIP1 |
| 22 | KOMMA |
| 23 | OR3P1 |
| 24 | ENSRIBAG00000000336 |
| 25 | TMA5F1 |
| 26 | SIPAL12 |
| 27 | GPR88 |

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Conclusions

- Different types of analyses combined with multiple layers of omics information:
 - At the **phenotypic** level – structural equation modeling
 - At the **DNA** level – GWAS on individual traits and latent variables
 - At the **RNA** level – global gene expression in samples with extreme meat quality
- Provides new insight in the regulatory **network architecture** in LD muscle
- Positional identification of gene expression **master regulators**

Goal: Develop genomic tools to select for superior meat quality in *Bos Indicus* influenced populations.

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