42nd Annual Senepol Cattle Breeders Convention
Huntsville, Alabama, Sept. 2019

Beef Cattle Improvement in the Genomics Era

UF IFAS UNIVERSITY of FLORIDA

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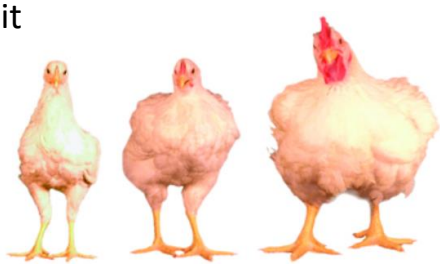
1

Traditional Animal Breeding

- **Selective breeding** for economically important traits
- Traditionally based on **phenotypic** recording
  - Estimation of breeding values from phenotypic records and pedigrees
  - Knowledge of heritability of each trait
- **Successful**
  - but **slow** process especially for certain traits

Time to market weight for meat chickens decreased from **16** to **5** weeks in **30** years



Fed identical diets, kept in similar conditions for 56 days.

Strains:	1957	1978	2005
56-d weight:	905g	1,808g	4,202g

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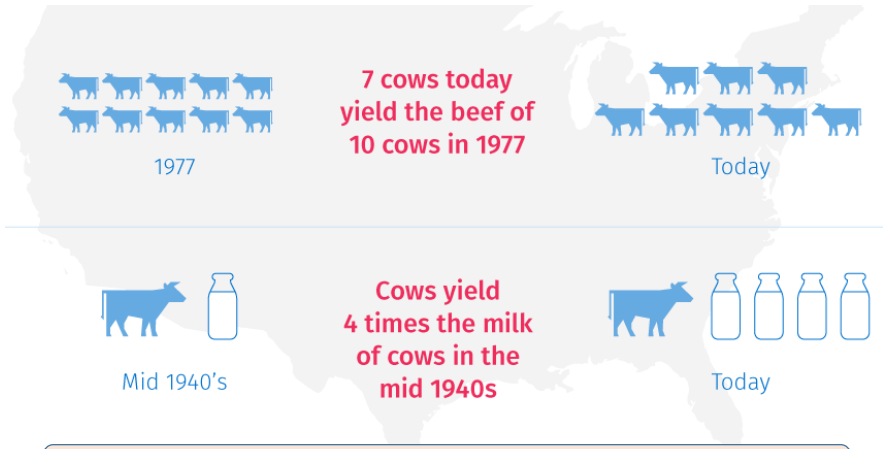
2

Impact of innovation in US



Need to go faster to feed 9.5 billion by 2050

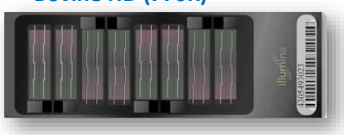
1. J.L. Capper. "The environmental impact of beef production in the United States: 1977 compared with 2007." Journal of Animal Science. 2011
2. J.L. Capper, R.A. Cady, and D.E. Bauman. "The environmental impact of dairy production: 1944 compared with 2007." Journal of Animal Science. 2009

3

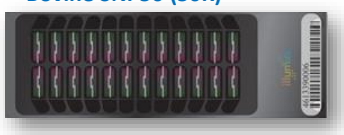
The opportunity

- New genomic technologies
  - Cost of DNA markers 1,000 times cheaper than 5 years ago
  - "SNP chips" -> 800,000 DNA markers at once
  - Whole genome sequencing cheaper and cheaper
- Can we use this technology to greatly increase genetic gain in animal breeding?

Bovine HD (770K)



Bovine SNP50 (50K)



4

Impact of genomics in beef cattle

- Most – if not all – economically important traits are complex (quantitative) traits

1. Controlled by **many genes**
   - Genomic tests - subset of these genes (and most times, not the genes themselves)
   - Accuracy associated with how much of the underlying genetics the test accounts for
2. Under **environmental** influence
   - Same genetics will perform differently in different environments
   - Accuracy associated with the environmental variation

5

Rate of genetic change

- Depends on 4 factors:
  - Selection **intensity**
    - How choosy we are in selecting individuals as parents
    - Can improve (increase) through management
  - **Accuracy** of genetic prediction
    - How close the EBV is to the true BV
    - Can improve (increase) through more/better records
  - **Generation interval**
    - Time between 2 generations
    - Can improve (decrease) through management or genomic selection
  - Amount of **genetic variation** in the trait
    - Genetic variation in a population (constant over short period of time)

6

Potential Benefits of Genomics

- Benefits are greatest for economically important traits that:
  - Are difficult or expensive to measure
  - Measured late in life or after death
  - Not currently selected for because are not routinely measured
  - Have lower heritability
- Benefits:
  - Determine the value of animal at birth
  - Increase accuracy of selection
  - Reduce generation interval
  - Increase selection intensity
  - Increase rate of genetic gain

7

Genomic Selection

- Key to genetic change: **selection**
- **Genetic change** - use animals better than the average, as parents of the next generation
- Incorporation of DNA information into genetic evaluations – stepwise evolution since 2000.
- Goal: **increase the accuracy** of predicting genetic merit (EPD)

For breeders to make the **best use of genomic** data, it needs to be **combined** with traditional sources of information (i.e. phenotypes and pedigrees) into traditional genetic evaluations.

8

Incorporation of genomic information

Which traits?

- Traits **with** routine genetic evaluations obtained from phenotypic and pedigree information.
  - Enhanced **accuracy** of genetic evaluations
- Traits **without** routine evaluations.
  - Will allow selection for **novel** but economically important traits

9

Traits with current genetic evaluation

- Traits **with** routine genetic evaluations obtained from phenotypic and pedigree information.
  - Enhanced **accuracy** of genetic evaluations

Pedigree estimated EPDs, no ultrasound scan data

OLD	CWT	MARB	RE	FAT
EPD	I +15	I +.79	I +.41	I -.001
Acc	.05	.05	.05	.05

Genomics added

NEW	CWT	MARB	RE	FAT
EPD	+ 18	+ .71	+ .50	+.004
Acc	.30	.38	.35	.28

10

Traits with current genetic evaluation

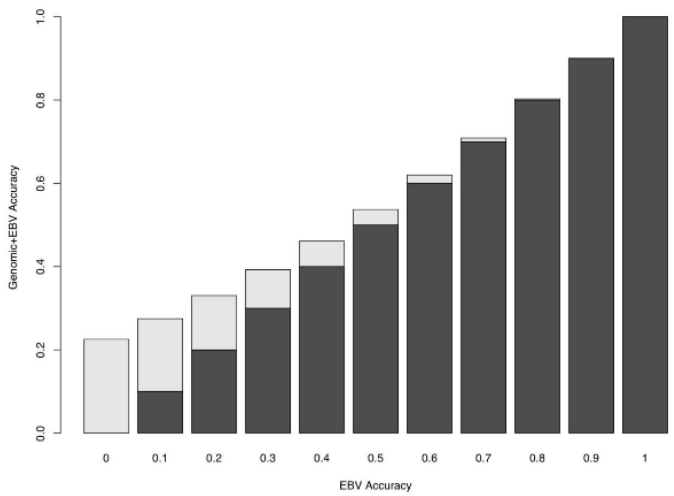
Enhanced accuracy of genetic evaluations

- More pronounced in **young** animals with no recorded progeny – high value for selection of replacement animals.
- The increase in **accuracy** will depend on:
  - Available records on relatives
  - Heritability of the trait
  - Proportion of variation accounted for by the test

11

Adding Genomic Information

- Increase in accuracy from integrating genomic information that explains 40% of the genetic variation into EBV



M. Spangler, *Integrating molecular data into NCE: expectations, benefits, and needs*

12

Population specific tests

- Current marker panels (genetic tests) are likely to work best in the populations where discovery occurred
- Predictive power decreases as the target population becomes more genetically distant

Discovery	Target	
Angus	Angus	Closest relationship
Angus	Charolais	⬇
Angus	*Bos Indicus*	Most distant relationship

- Same erosion will occur over time (over generations if panels are not retrained).

13

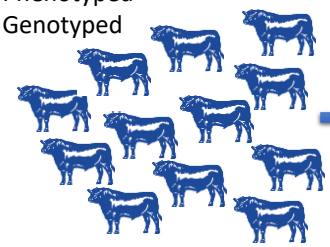
Novel traits

- Genomic information (SNPs)
  - Increase the accuracy of EPDs
  - Add "novel" traits to our suite of available EPD (cattle health – BRD, feed efficiency, healthfulness, nutritional value, disease resistance, thermotolerance, reproductive traits)
- Large resource populations with phenotypes are required for discovery and validation.
- Need breed specific prediction equations.

14

Principles of Genomic Selection

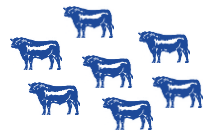
Large Training Population
- Phenotyped
- Genotyped



Prediction equation

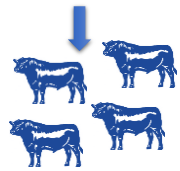
Genomic breeding value = $w_1x_1 + w_2x_2 + w_3x_3$.....

Selection Candidates
- Genotypes used to predict genetic merit



- Training Pop: many animals with phenotypes and genotypes
- Estimate effect of each marker, generate a prediction equation
- Apply the prediction equation to a group of animals with genotypes

Not predictive in other breeds/lines



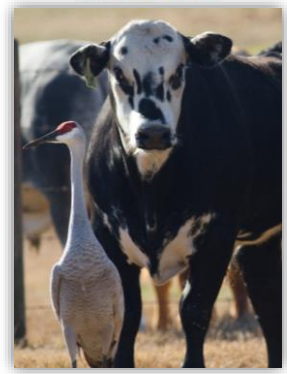
Selected breeders
- Based on genomic breeding values

Adapted from Hayes and Goddard. 2009. Nature Reviews Genetics 10, 381-391

15

Challenges for the Beef Cattle Industry

- Little use of AI
- Relatively few high accuracy sires for training
- Multiple competing selection goals – cow/calf, feedlot, processor – little data/value sharing between sectors
- Few/no records on many economically-relevant traits
- Many breeds, some small with limited resources
- Crossbreeding is important
- No one wants to pay, as value is not recovered by breeder



16

Available Genomic Tests

17

Genomic testing

- Available through breed associations, partnered with companies providing genotyping services (Zoetis, Neogen/GeneSeek)
  - Several types of tests main difference is the number of genetic markers included

50K = 50,000 SNP

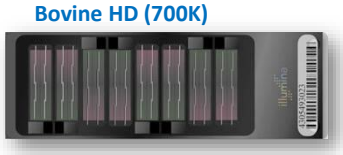
$75-90 for the high-density chips

$45-55 for the low-density imputation chips

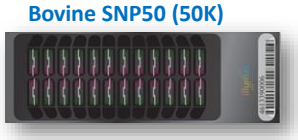
  - Breed assoc. include genomic info into genetic evaluations

genomic-enhanced EPD

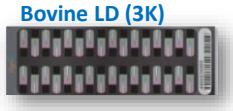
Bovine HD (700K)



Bovine SNP50 (50K)



Bovine LD (3K)



18

Other tests

- Simple genetic conditions
  - Horned/polled
  - Coat color
  - Genetic abnormalities
- Costs vary, large number of labs providing the tests, price range **$22 - 45**
- Stand alone test for parentage: **$18 - 30**
- Many of these simple genetic tests can be purchased less expensively as an **add-on** to the higher density genotyping tests.

19

Commercial cattle testing

- Several tests marketed for use on commercial cattle
- Not directly part of a breed association genetic evaluation program
- No independent, peer-reviewed papers in the scientific literature documenting the field performance.

20

Training population - impact

- The **accuracy drops** when utilized in a **crossbred** commercial cattle population
- Correlation between test and true BV **~ 0.3** when estimating the genetic merit of commercial crossbred animals.
- Correlation likely to be **even lower** in animals comprised of breeds **not in the original training** set.

The lower the correlation, the more possible inaccuracy there is in the ranking based upon that test.

21

Carcass merit/meat quality in *Bos Indicus* influenced cattle

Genomics of thermotolerance

UF-ANS Beef Cattle Research

22

Two areas of interest

Meat Quality

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

Thermotolerance

- Climatic stress - major limiting factor of production efficiency
- Genomic tools can help select
  - Animals with superior ability for both **thermal adaptation** and **food production**
  - Energy-efficient, **sustainable** approach to meet the challenge of global climate change.

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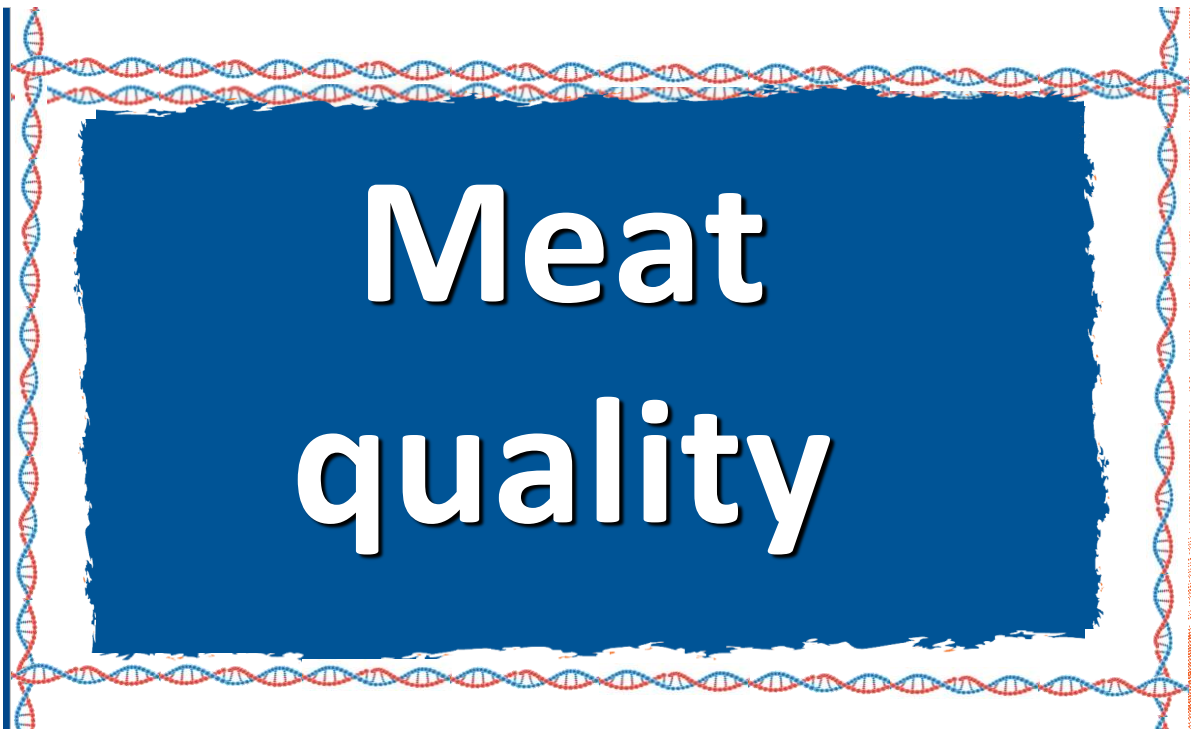
23

Meat quality



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24

Meat Quality

USDA grading system

Based on marbling and maturity

Limited in predicting eating quality

Tenderness

Genomic Tests

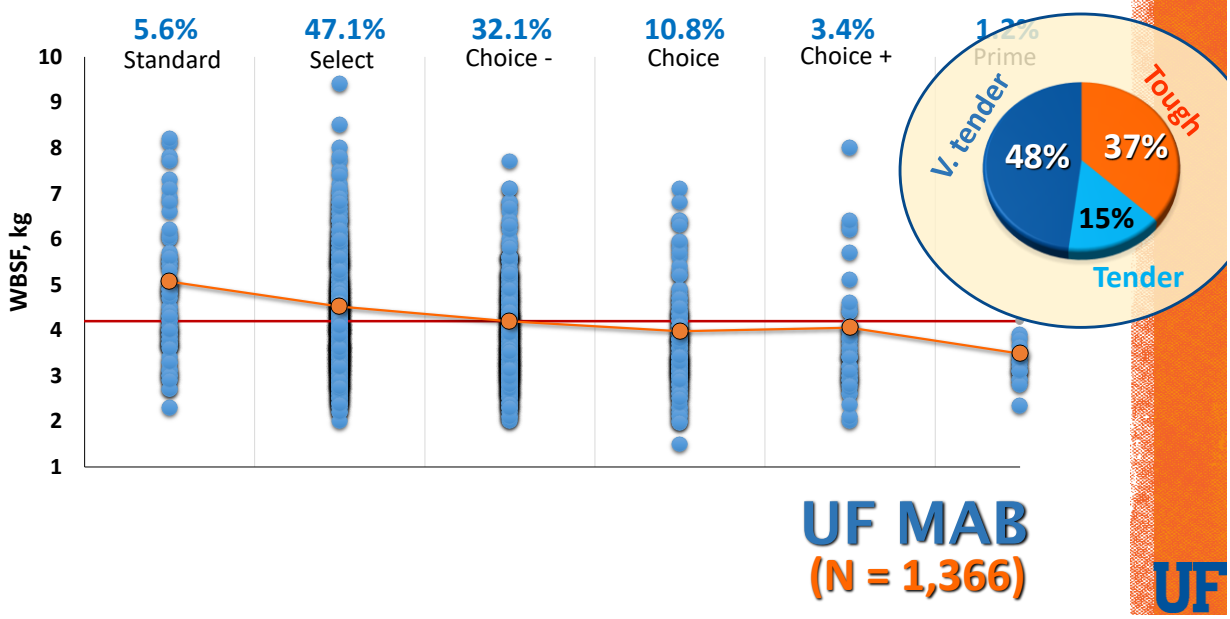
Developed on *B. Taurus* data

Limited prediction in *B. Indicus* -influenced

Need to be breed specific

25

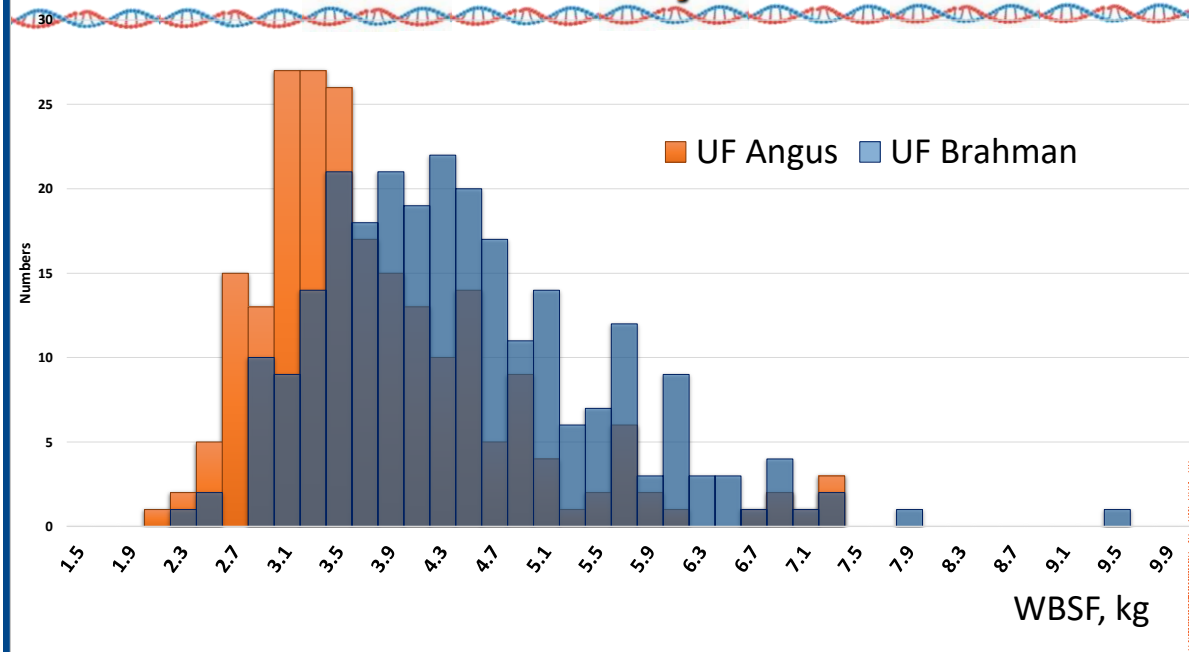
Tenderness by USDA Quality Grade



UF MAB
(N = 1,366)

26

Variation in WBSF – by breed



27

Genetic tests Tenderness

28

Genomics Tests

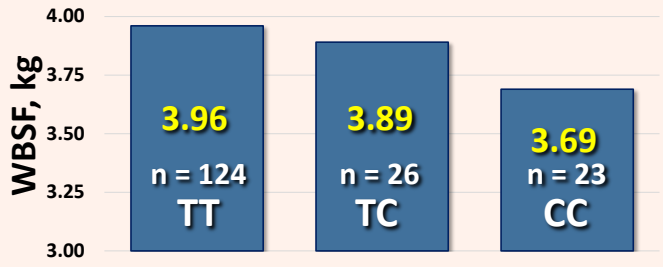
SNP – genetic marker

..GACG**C**CGTGG..
..GACG**T**CGTGG..

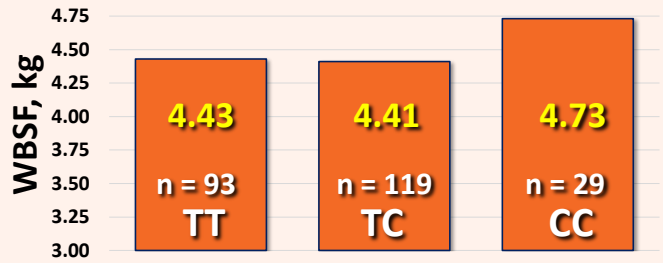
C C **C T** **T T**

3 possible genotypes

UF Angus, n = 153

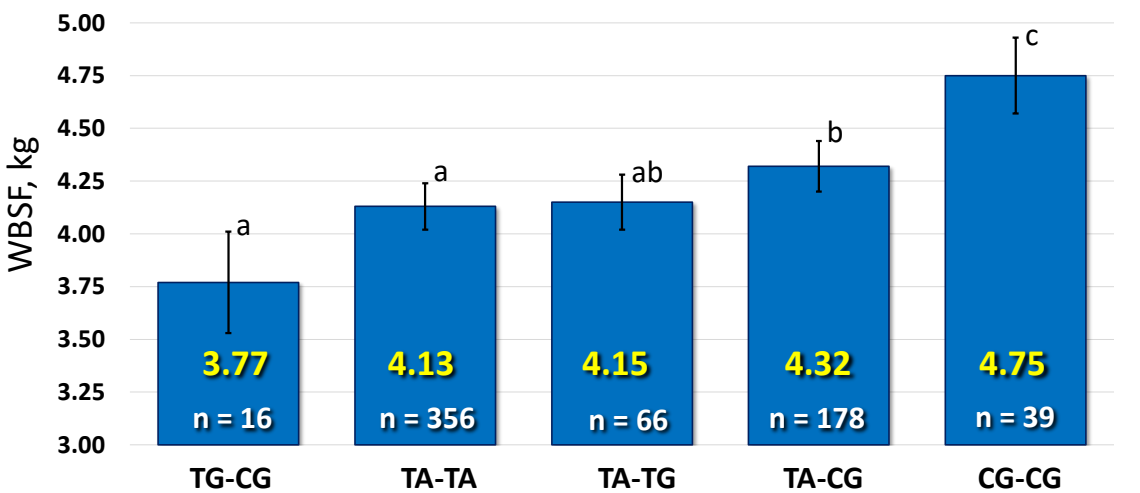


UF Brahman, n = 241



29

Combination of markers in calpastatin



30

Breed-specific genomic tools

- To meet consumer expectation, the average **tenderness** needs to be **improved** and the **variation** in meat tenderness must be **controlled/managed**
- To be effective - genomic tools need to be developed in the **target** populations

Large resource populations with phenotypes are required for discovery and estimation.

31

Thermo-tolerance

32

In response to heat stress, cattle will regulate:

Heat Production

- Modulating basal metabolic rate
- Changing: feed intake, growth, lactation, activity

Heat Exchange

- Blood flow to the skin
- Evaporative heat loss through sweating & panting

Goal: Develop genomic tools to select for superior ability for both thermal adaptation and food production.

33

Research Populations – pilot data

- UF Multibreed Angus x Brahman Herd
  - Summer 2017, 2018
  - **335 cows**: from 100% Brahman to 100% Angus

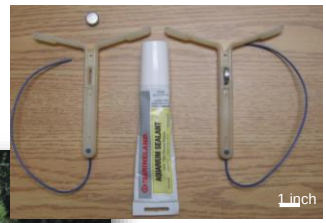
Breed Group		Angus %	Brahman %
1	Angus	100	0
2	75%A	75	25
3	Brangus	62.5	37.5
4	50%A	50	50
5	25%A	25	75
6	Brahman	0	100

34

Internal Body Temperature

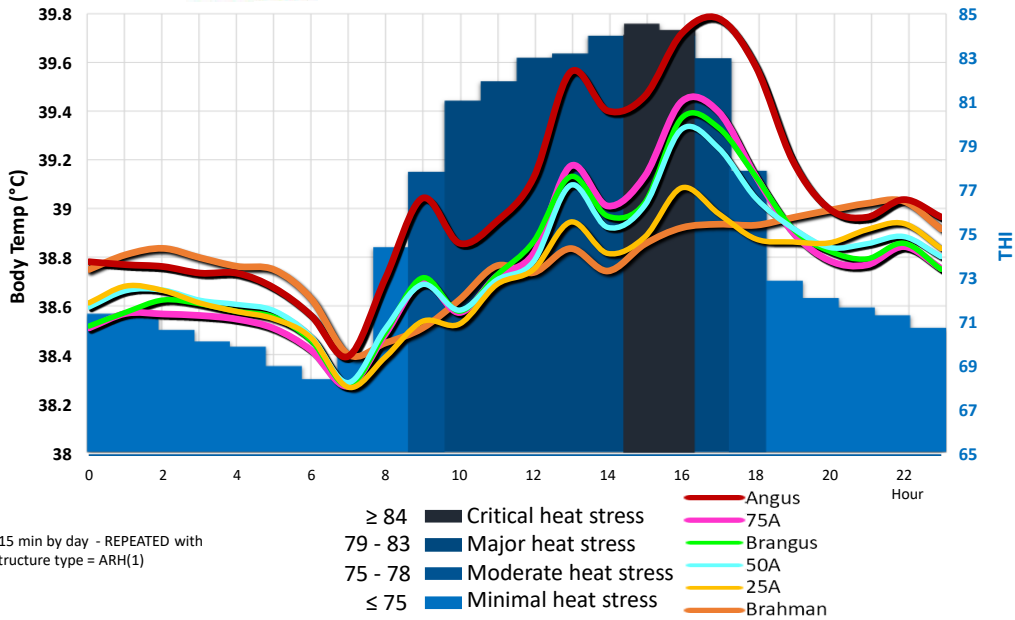
- Vaginal **temperature** at 5-min intervals for 5 days
- Air temperature and relative humidity - recorded continuously in the pastures

THI = temperature-humidity index



35

Breed effect on body temperature



vagtmp every 15 min by day - REPEATED with cov structure type = ARH(1)

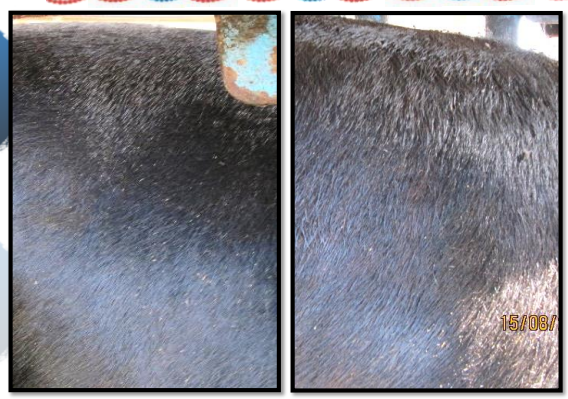
36

Factors important in thermotolerance

Coat Hair

Sweat Glands

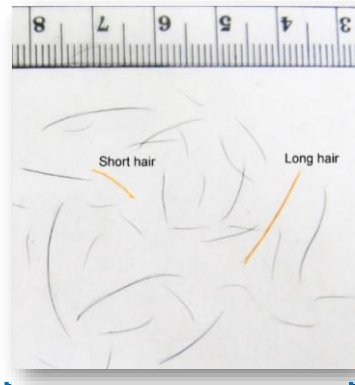
Other Skin Prop.



Score 1
Excessively Smooth

Score 2
Fairly Smooth

Coat score
1. excessively smooth
2. fairly smooth
3. long coat
4. woolly
5. excessively woolly coat



Long Hair Length
Long Hair Diameter
Short Hair Length
Short Hair Diameter

37

Factors important in thermotolerance

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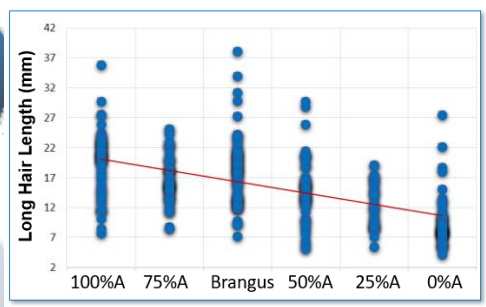
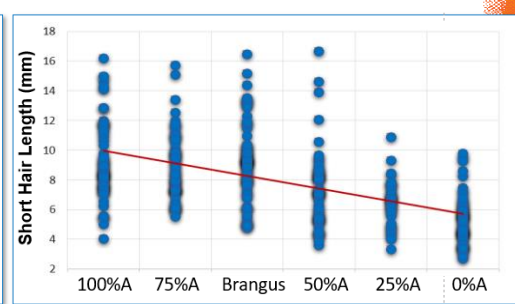
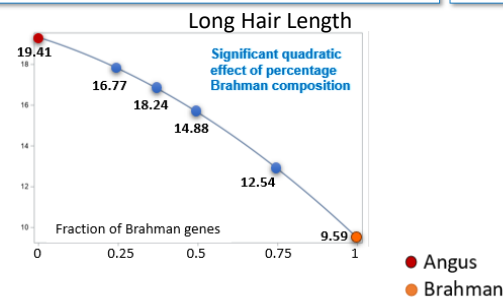
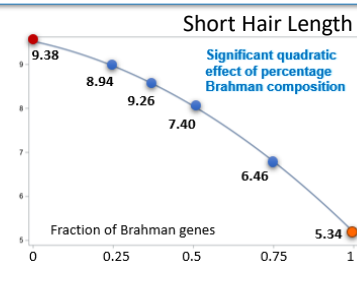
Other Skin Prop.









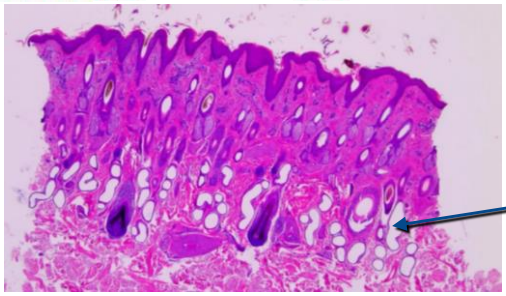
38

Factors important in thermotolerance

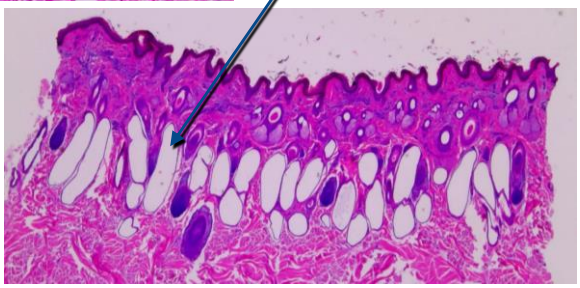
Coat Score

Sweat Glands

Other Skin Prop.



Angus



Brahman

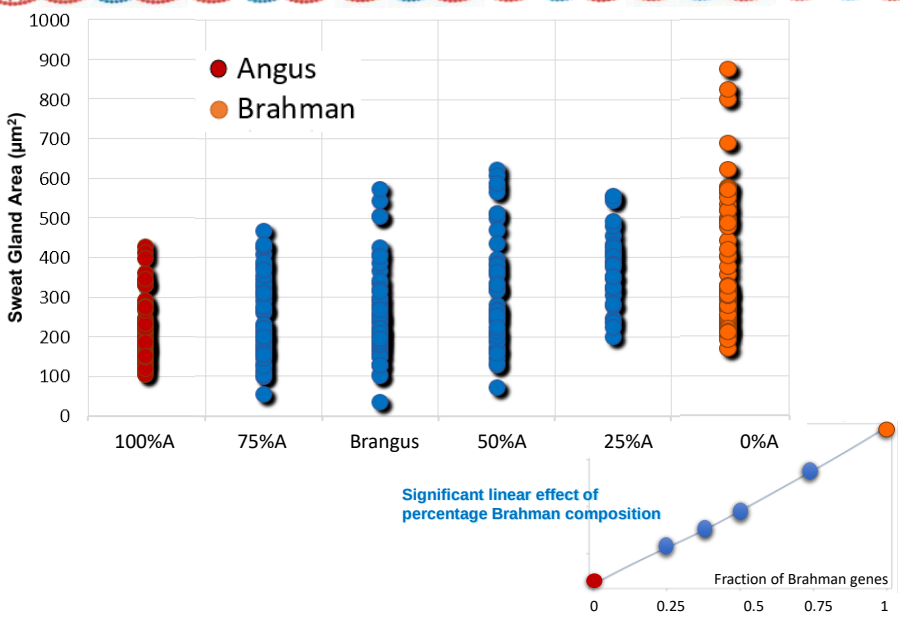
39

Factors important in thermotolerance

Coat Score

Sweat Glands

Other Skin Prop.



40

Future outlook / Summary Points

- Genomic information
  - Increase the **accuracy** of EPDs
  - Shorten the **generation interval**
  - Add "**novel**" traits to our suite of available EPD (feed efficiency, healthfulness, nutritional value, disease resistance, thermotolerance)
- **Large resource** populations with phenotypes are required for discovery and validation.
- Need **breed specific** prediction equations.

Genomics - technology to accelerate genetic progress.

41

Acknowledgments

University of Florida

- Dr. Pete Hansen
- Dr. Mauricio Elzo
- Dr. Dwain Johnson
- Dr. Tracy Scheffler
- Dr. Jason Schaffler
- Dr. Serdal Dikmen
- Danny Driver
- Michelle Driver
- Joel Leal, Heather Hamblen, Sarah Flowers, Kaitlyn Sarlo, Mesfin Gobena, Eduardo Rodriquez, Zaira Estrada
- Adriana Zolini, William Ortiz, Samantha Eifert, Lauren Peacock, Alexa Chiroussot

Seminole Tribe of Florida

- Alex Johns
- Phillip Clark
- Sheri Holmes
- Bobby Yates
- Mike Ciorocco
- Dayne Johns, etc.

Financial Support

- USDA-NIFA Grant 2017-67007-26143
- UF Agricultural Experim. Station
- UF ANS Hatch Project
- Seminole Tribe of Florida
- Brangus Breeders Association
- Florida Beef Council
- Florida Cattlemen's Association

42