

5th Euro-Global Summit and Expo on

Food & Beverages

June 16-18, 2015 Alicante, Spain



Genomics applied to beef quality traits

Luciana C. A. Regitano

Embrapa

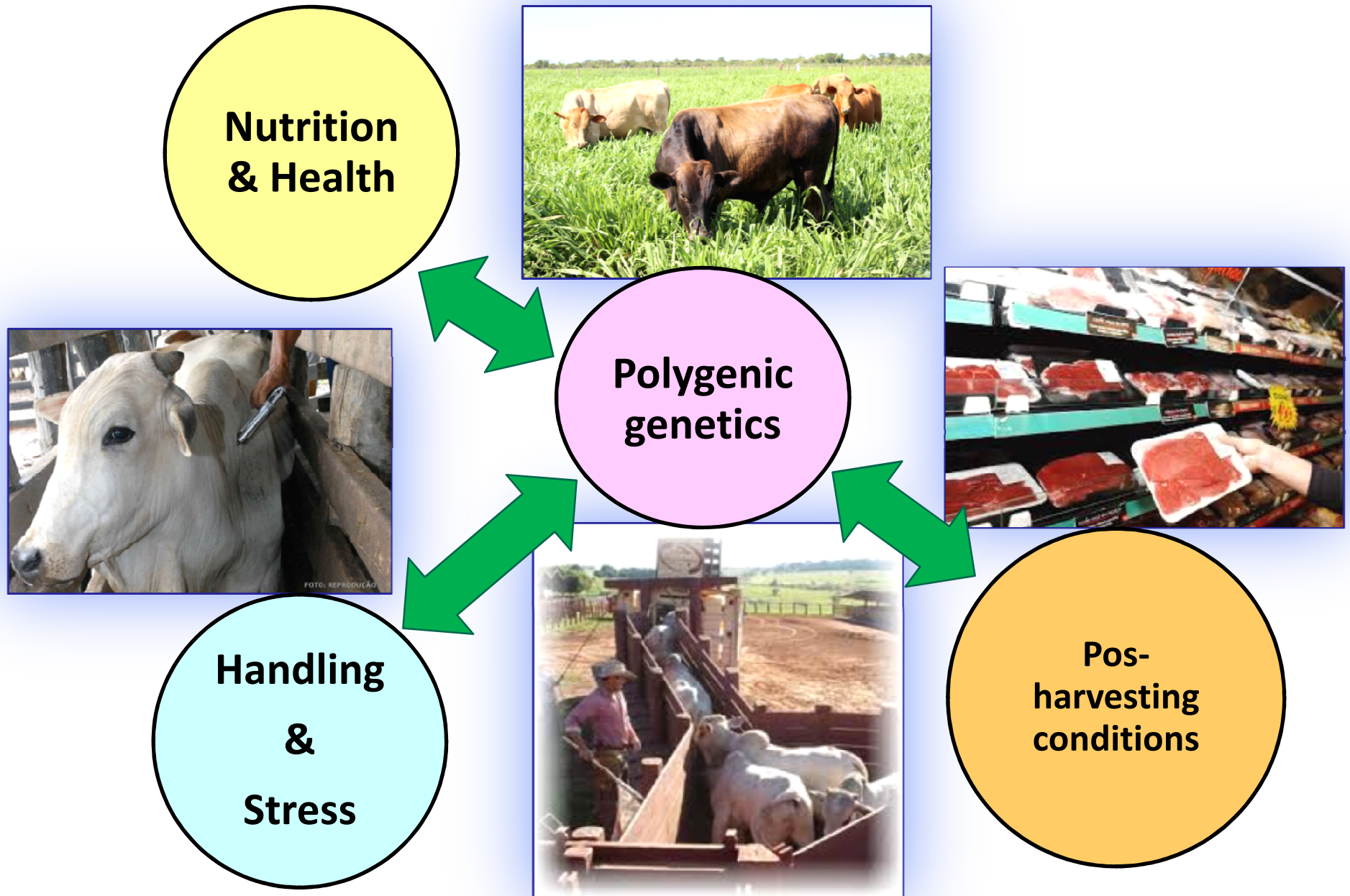
Southeast Livestock

“**Beef quality**” represents a variety of attributes

- ❖ Objective factors, as the **ratio fat/protein, fatty acids profile, mineral content...**
- ❖ Subjective factors, related to **palatability**



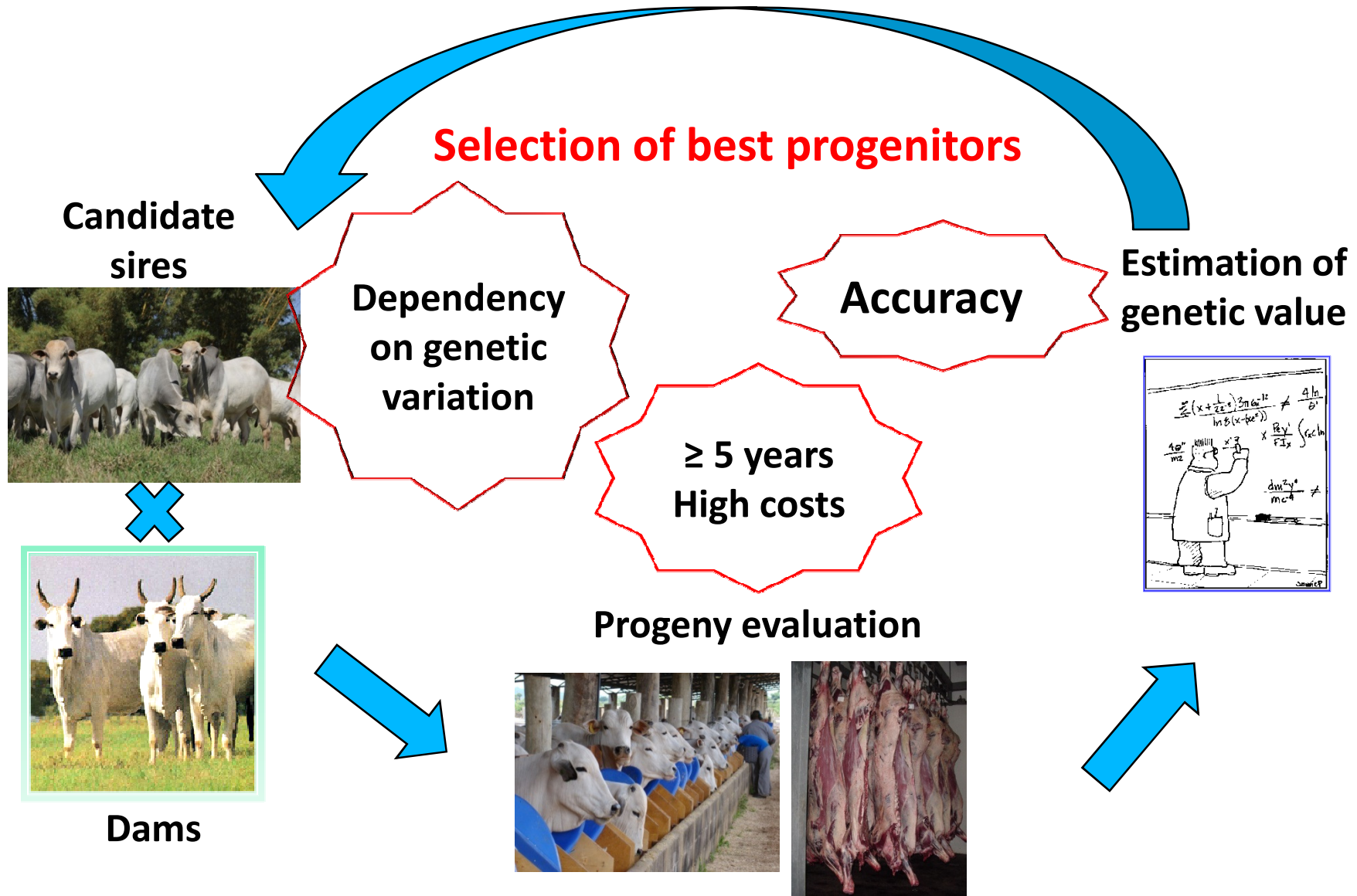
Beef quality traits are multifactorial



***Is it possible to explore genetic
variation to produce a better
beef?***



Genetic selection for beef quality



How could genomics help?

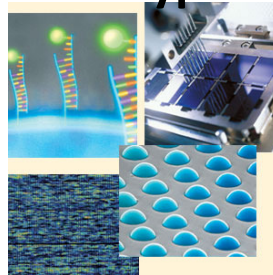
Training population

Breeding population

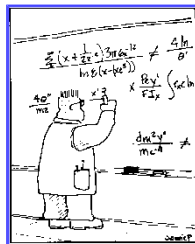
Phenotypes



Genotypes



Estimation of marker effects on phenotypes



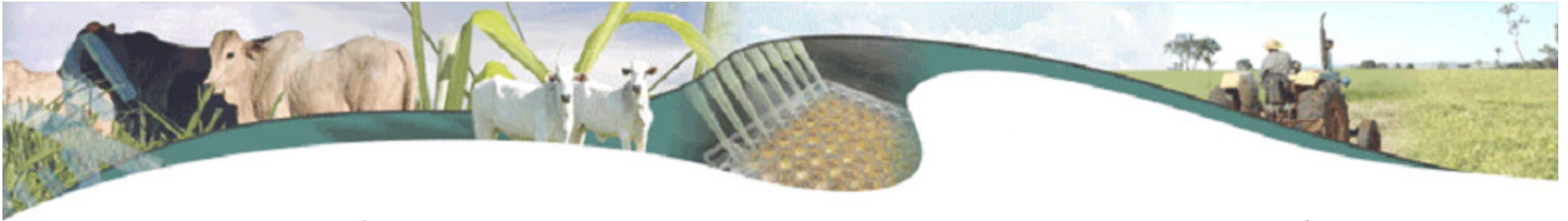
↓ Time



“Genomic value”
based on DNA data

↑ Accuracy

Predictive equation



Embrapa's experience



34 Sires



Commercial Dams



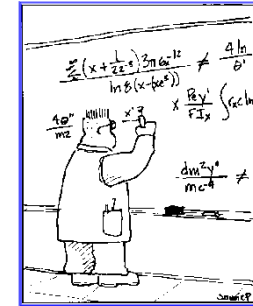
X

~800 steers / 3 years / 5 farms



- Feed efficiency
- Carcass traits
- Meat quality
- Temper

Quantitative analysis



Illumina HD
SNP genotyping



Gene expression
(RNAseq/qPCR)

Proteomics

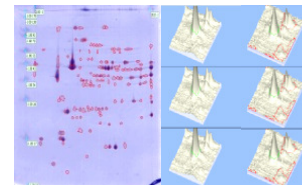
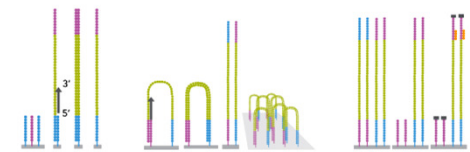
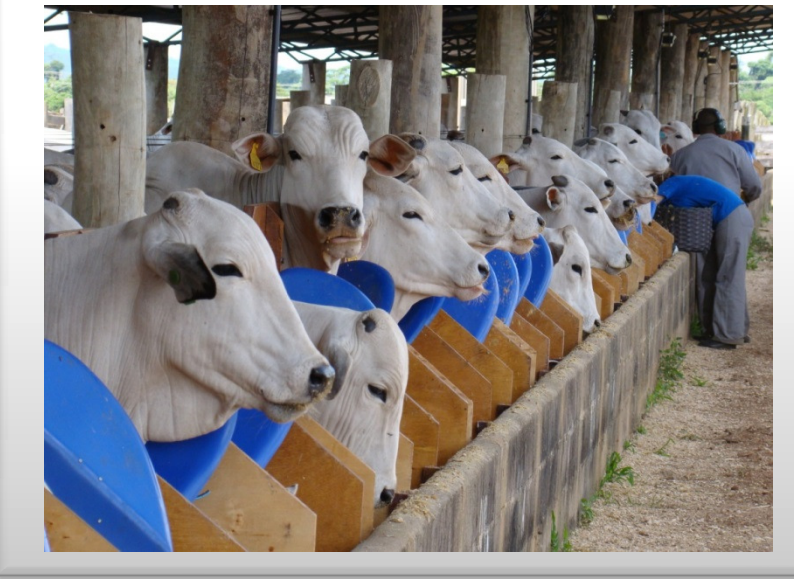


FIGURE 3. CLUSTER GENERATION BY ISOTHERMAL BRIDGE AMPLIFICATION



Cluster generation from single-molecule DNA templates occurs within the sealed Illumina flow cell on the cBot instrument, and involves immobilization and 3' extension, bridge amplification, linearization, and hybridization.



Beef quality traits



Rib Eye Area

Marbling

pH

Fat Thickness

Minerals and fatty acids profiles

Shear Force

Water retention

Color (fat and meat)



Tenderness



The major attribute for consumer's choice

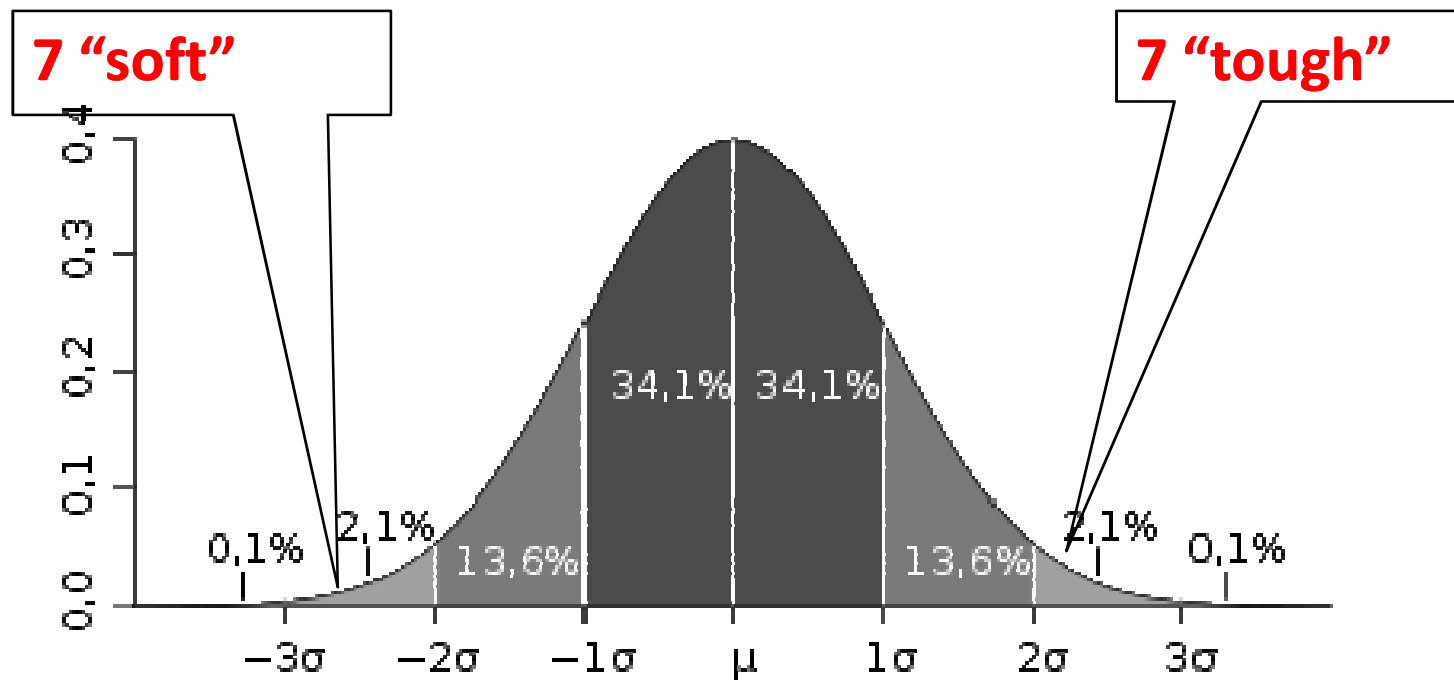
***KCNJ11 - Potassium inwardly rectifying channel,
subfamily J, member 11***

Rat model gene for diabetes

- Rat knockouts¹
 - **Reduced glycogen and body fat deposits**
 - **Lower muscle strenght**
- In bovine: **Maps to a tenderness QTL**

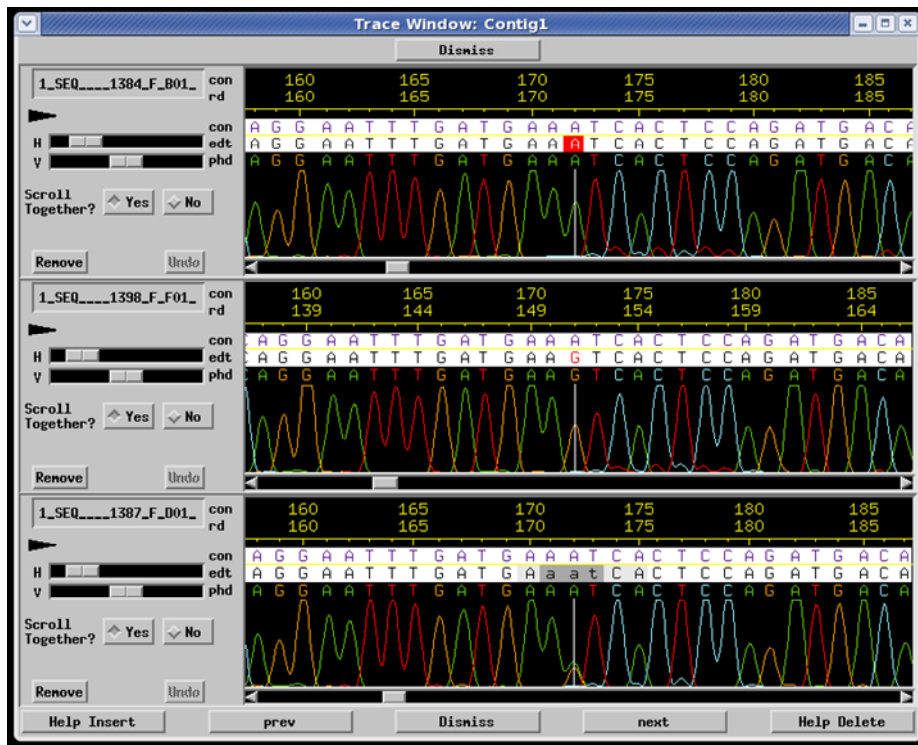
¹Alekseev et al. Cell Metabolism, 11: 58-69, 2010

Searching for variation in Nelore's *KCNJ11* gene



Extreme phenotype sampling

Sanger sequencing



22 SNPs



Frequency comparison
between groups



Full population genotyping

Identification of *KCNJ11* as a functional candidate gene for bovine meat tenderness

Polyana C. Tizioto,¹ Gustavo Gasparin,² Marcela M. Souza,¹ Mauricio A. Mudadu,³ Luiz L. Coutinho,² Gerson B. Mourão,² Patricia Tholon,³ Sarah L. C. Meirelles,⁴ Rymer R. Tullio,³ Antônio N. Rosa,⁵ Maurício M. Alencar,³ Sérgio R. Medeiros,⁵ Fabiane Siqueira,⁵ Gelson L. D. Feijó,⁵ Renata T. Nassu,³ and Luciana C. A. Regitano³

Table 6. Summary of the results of the mixed-model analysis of association among WBSF measures in Nelore and two polymorphisms in *KCNJ11* gene

WBSF	n	SNP1526 C>T				SNP2342T>C			
		Gen.	LS Means ±SE, kg/f	Add.	Dom.	Gen.	LS Means ± SE, kg/f	Add.	Dom.
0	461			ns	ns			0.3885	ns
		CC	8.86 ± 0.15			CC	9.14 ± 0.14		
		CT	8.72 ± 0.14			CT	8.70 ± 0.14		
7	423	TT	9.40 ± 0.51			TT	8.75 ± 0.16		
				ns	ns			0.3778	ns
		CC	5.38 ± 0.13			CC	5.50 ± 0.13		
14	434	CT	5.46 ± 0.13			CT	5.51 ± 0.13		
		TT	5.69 ± 0.50			TT	5.12 ± 0.15		
				ns	ns			ns	ns
		CC	4.33 ± 0.11			CC	4.35 ± 0.11		
		CT	4.49 ± 0.11			CT	4.54 ± 0.11		
		TT	4.57 ± 0.43			TT	4.26 ± 0.13		

WBSF measured at 24 h after slaughter = 0; measured at 7 days of aging = 7; measured at 14 days of aging = 14) n, Number of observations; Gen., genotype; LS Means ± SE, least square means adjusted by the model ± SE; Add., additive effect (kg/f); Dom., dominance deviation effect; ns, not significant ($P \leq 0.05$).

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Table 7. *Effect of the muscular expression level (Ct) of KCNJ11 gene on the WBSF measures in 137 Nelore steers*

WBSF	Estimated Effect, kg \pm SE	<i>P</i> Value
0	-0.07868 ± 0.066	0.2403
7	-0.1627 ± 0.068	0.0187*
14	-0.03891 ± 0.056	0.4877

* $P \leq 0.05$.

As from the mouse model → **Lower** gene expression = “**softer**” meat

Genome wide association

Physiol Genomics 45: 1012–1020, 2013.
First published September 10, 2013; doi:10.1152/physiolgenomics.00066.2013.

CALL FOR PAPERS | *Updates on Mapping Quantitative Trait Loci*

Genome scan for meat quality traits in Nelore beef cattle

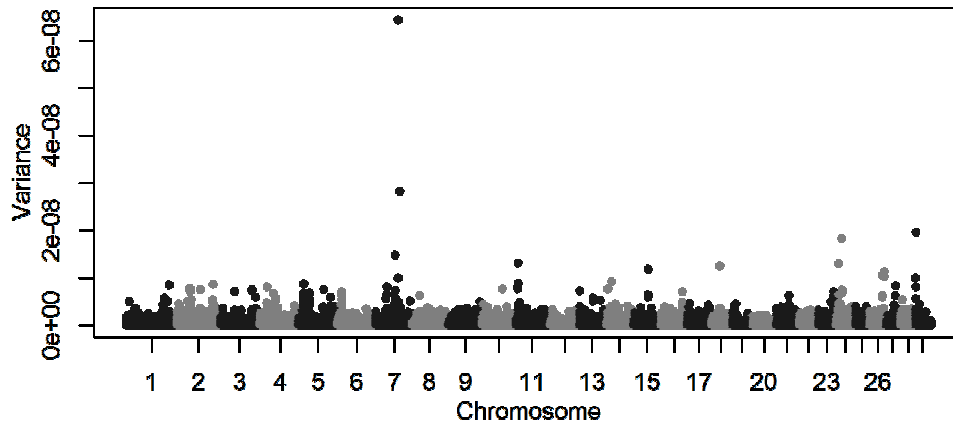
P. C. Tizloto,^{1,2} J. E. Decker,² J. F. Taylor,² R. D. Schnabel,² M. A. Mudadu,³ F. L. Silva,⁴ G. B. Mourão,⁴ L. L. Coutinho,⁴ P. Tholon,³ T. S. Sonstegard,⁵ A. N. Rosa,⁶ M. M. Alencar,³ R. R. Tullio,³ S. R. Medeiros,⁶ R. T. Nassu,³ G. L. D. Feijó,⁶ L. O. C. Silva,⁶ R. A. Torres,⁶ F. Siqueira,⁶ R. H. Hlga,⁷ and L. C. A. Regitano³

¹Departamento de Genética e Evolução, Universidade Federal de São Carlos, São Carlos, São Paulo, Brazil; ²Division of Animal Sciences, University of Missouri, Columbia, Missouri; ³Brazilian Agricultural Research Corporation (Embrapa) Pecuária Sudeste, São Carlos, São Paulo, Brazil; ⁴Departamento de Zootecnia, Universidade de São Paulo/Escola Superior de Agricultura Luiz de Queiroz, Piracicaba, São Paulo, Brazil; ⁵Agricultural Research Service, United States Department of Agriculture (USDA), Beltsville, Maryland; ⁶Embrapa Gado de Corte, Campo Grande, Mato Grosso do Sul, Brazil; and ⁷Embrapa Informática Agropecuária, Campinas, São Paulo, Brazil

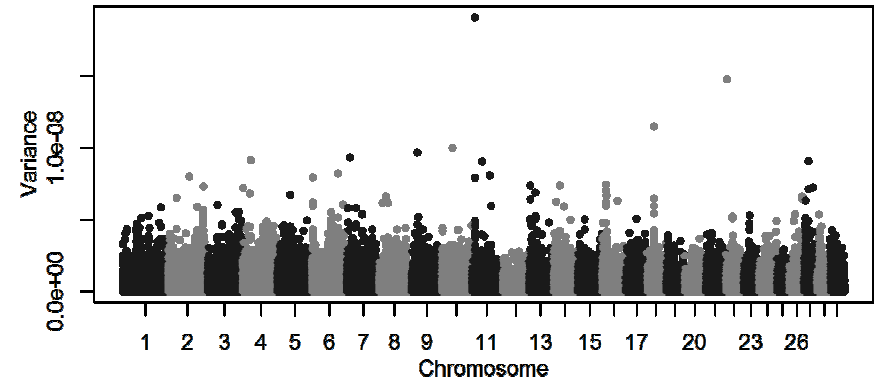
Submitted 1 May 2013; accepted in final form 3 September 2013

Shear force at different aging times

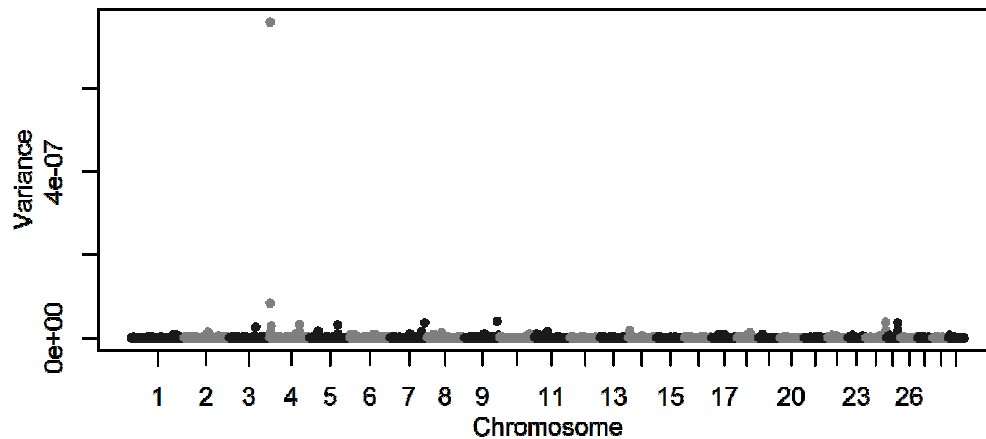
Shear Force at 24 hs



Shear Force at 7 days



Shear Force at 14 days



***What about
Fat and Fatty acids
profiles?***



GWAS – Fat

Cesar *et al.* *BMC Genetics* 2014, **15**:39
<http://www.biomedcentral.com/1471-2156/15/39>



RESEARCH ARTICLE

Open Access

Genome-wide association study for intramuscular fat deposition and composition in Nelore cattle

Aline SM Cesar¹, Luciana CA Regitano², Gerson B Mourão¹, Rymer R Tullio², Dante PD Lanna¹, Renata T Nassu², Maurício A Mudado², Priscila SN Oliveira³, Michele L do Nascimento¹, Amália S Chaves¹, Maurício M Alencar², Tad S Sonstegard⁴, Dorian J Garrick⁵, James M Reecy⁵ and Luiz L Coutinho^{1*}

Table 1 Descriptive statistics, variance components and heritability by GBLUP for IMF deposition and composition in Nellore

Trait	Terminology ¹	N	Mean ± SE ²	Genetic variance	Residual variance	Total variance	h ² ± SE
IMF (%)	Intramuscular fat	382	2.77 ± 0.05	0.196	0.490	0.686	0.29 ± 0.16

Lean beef every day is effective in lowering total and LDL “bad” cholesterol (DASH, Dietary Approaches to Stop Hypertension).

C18:0	Stearic acid	378	14.98 ± 0.14	1.3380	5.348	6.686	0.20 ± 0.12
C18:1 cis-9	Oleic acid	378	37.46 ± 0.22	2.0720	10.826	12.898	0.16 ± 0.11

C18:0 (stearic acid)=== > humans convert to oleic acid, the main monounsaturated fatty acid in olive oil, associated with several health benefits

¹IUPAC Compendium of Chemical Terminology.

²SE Standard error.

³MUFA, PUFA and SFA were the total of all monounsaturated, polyunsaturated and saturated fatty acids, respectively.

⁴n-3 and n-6 were total of omega 3 and 6 fatty acids.

⁵Atherogenic index = [12:0 + 4(14:0) + 16:0]/(SFA + PUFA).

RESEARCH ARTICLE

Putative Regulatory Factors Associated with Intramuscular Fat Content

Aline S. M. Cesar¹, Luciana C. A. Regitano², James E. Koltes³, Eric R. Fritz-Waters³, Dante P. D. Lanna¹, Gustavo Gasparin¹, Gerson B. Mourão¹, Priscila S. N. Oliveira⁴, James M. Reecy³, Luiz L. Coutinho^{1*}

RNA-Sequencing: High vs Low IMF

77 Differentially Expressed Genes (FDR 10%)

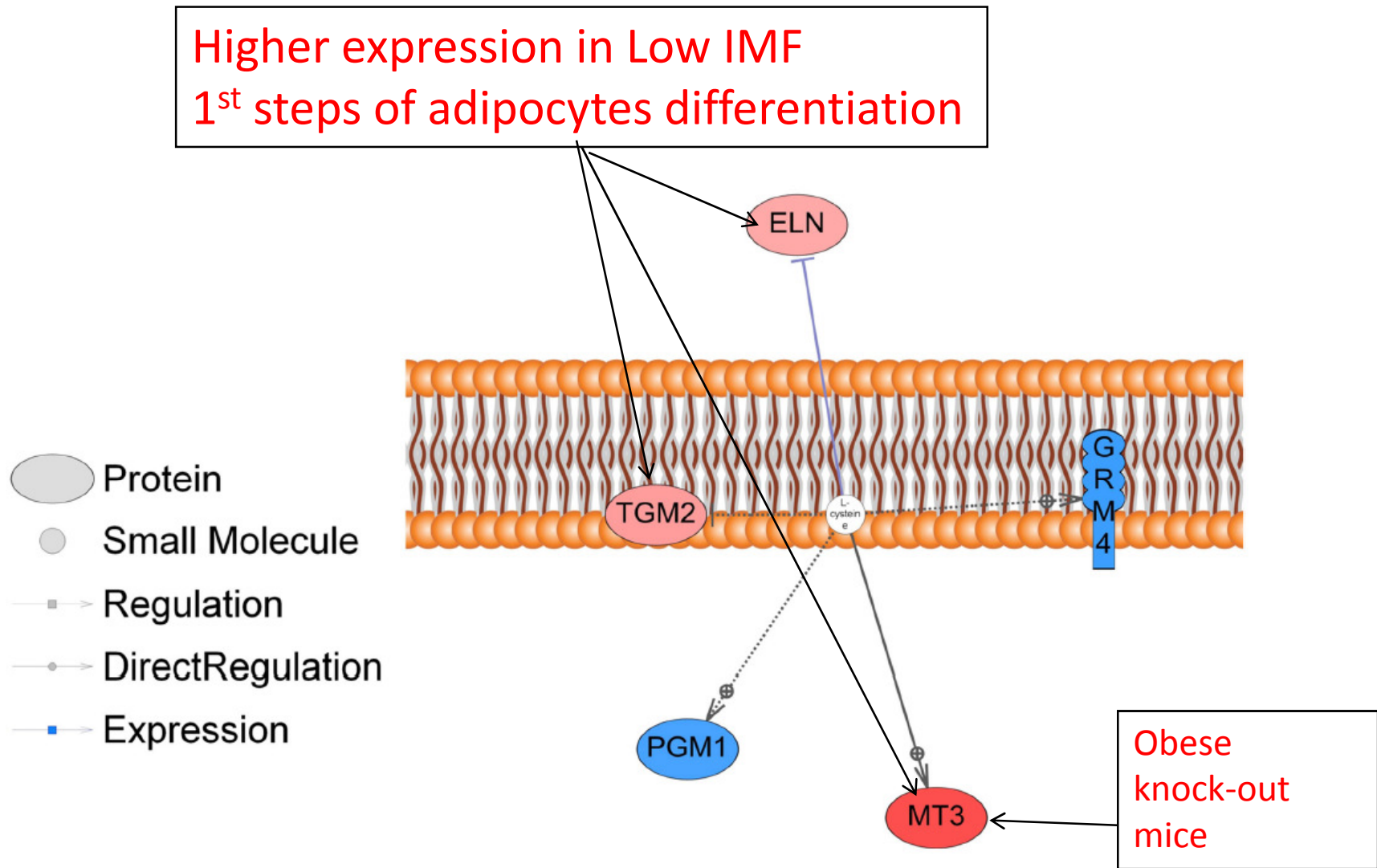


Fig. 1- L-cysteine pathway genes identified as differentially expressed between High and Low IMF

Minerals

They are **fundamental** in metabolism regulation, including muscle function and energy utilization.

Would genetic variation be expected in normal animals?



Genetic parameters for concentrations of minerals in longissimus muscle and their associations with palatability traits in Angus cattle¹

R. G. Mateescu,^{*2} A. J. Garmyn,^{*} R. G. Tait Jr.,[†] Q. Duan,[†] Q. Liu,[‡] M. S. Mayes,[†] D. J. Garrick,[†]
A. L. Van Eenennaam,[§] D. L. VanOverbeke,^{*} G. G. Hilton,^{*} D. C. Beitz,^{†‡} and J. M. Reecy[†]

^{*}Department of Animal Science, Oklahoma State University, Ames 50011; [†]Department of Biochemistry, Iowa State University, Ames 50011; and [§]Department of Animal Science, Iowa State University, Ames 50011.

Iron-deficiency anemia is still the main public health problem and reaches 30% of world population
(World Health Organization, 2015)

Table 5. Genetic (σ^2_a) and residual (σ^2_e) variance components for calcium, copper, iron, magnesium, manganese, and potassium concentrations ($\mu\text{g/g}$ muscle) in LM from Angus cattle obtained by single trait REML analysis.

Trait ¹	σ^2_a	σ^2_e	$h^2 \pm SE$
Calcium	0.00003	277.74	0.000 \pm 0.03
Copper	0.00025	0.49	0.000 \pm 0.04
Iron	3.69	3.09	0.544 \pm 0.09
Magnesium	36.78	530.83	0.065 \pm 0.04
Manganese	0.00006	0.007	0.009 \pm 0.03
Phosphorus	1,105.10	29,630.5	0.036 \pm 0.03
Potassium	3,989.63	104,989.0	0.037 \pm 0.03
Sodium	591.32	2574.71	0.187 \pm 0.06
Zinc	4.73	47.10	0.091 \pm 0.04

N= 2.825 Angus

Genome-wide association study of concentrations of iron and other minerals in longissimus muscle of Angus cattle¹

R. G. Mateescu,^{*2} D. J. Garrick,[†] R. G. Tait Jr.,[†] A. J. Garmyn,^{*} Q. Duan,[‡] Q. Liu,[§] M. S. Mayes,[†] A. L. Van Eenennaam,[#] D. L. VanOverbeke,^{*} G. G. Hilton,^{*} D. C. Beitz,^{†§} and J. M. Reecy[†]

^{*}Department of Animal Science, Oklahoma State University, Stillwater 74078; [†]Department of Animal Science, Iowa State University, Ames 50011; [‡]Department of Genetics, University of North Carolina, Chapel Hill 27599; [§]Department of Biochemistry, Biophysics and Molecular Biology, Iowa State University, Ames 50011; and [#]Department of Animal Science, University of California, Davis 95616

Iron

✓ Seven regions in six chromosomes (1, 2, 7, 10, 15 e 28)

✓ Explained phenotypic variance = 0.37, $h^2 = 0.48$

✓ BTA 1 (9 Mb) - *TFR1* (*Transferrin receptor 1 gene*)

✓ BTA2

SLC11A1 (*Solute Carrier Family 11*)

ABCB6 (*ATP-Binding Cassette, Sub-Family B (MDR/TAP), Member 6*)

RESEARCH

Open Access

Detection of quantitative trait loci for mineral content of Nelore *longissimus dorsi* muscle

Polyana C Tizioto^{1,2}, Jeremy F Taylor², Jared E Decker², Caio F Gromboni³, Mauricio A Mudadu⁴, Robert D Schnabel², Luiz L Coutinho⁵, Gerson B Mourão⁵, Priscila SN Oliveira¹, Marcela M Souza¹, James M Reecy⁷, Renata T Nassu⁴, Flavia A Bressani⁴, Patricia Tholon⁴, Tad S Sonstegard⁶, Mauricio M Alencar⁴, Rymer R Tullio⁴, Ana RA Nogueira⁴ and Luciana CA Regitano^{4*}

- ✓ Mineral contents are **moderately inherited** ($h^2 = 0.29$ to 0.36)
- ✓ **Several small effect QTLs**
- ✓ Large effect region for iron in BTA 12 (72 Mb):
 - 6.5% of additive genetic variation of [Fe]
 - ATP-binding cassette genes**

Final considerations

Genomic analysis is able to depict genetic variation for beef quality traits, and can be a good alternative to improve beef quality.

Final considerations

Will industry pay for quality?

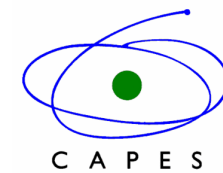




UNIVERSITY OF WISCONSIN-MADISON



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Thank you!

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Embrapa Southeast Cattle