

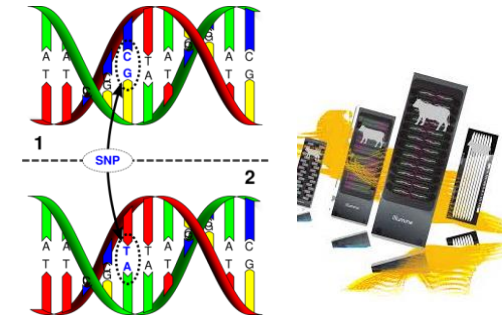
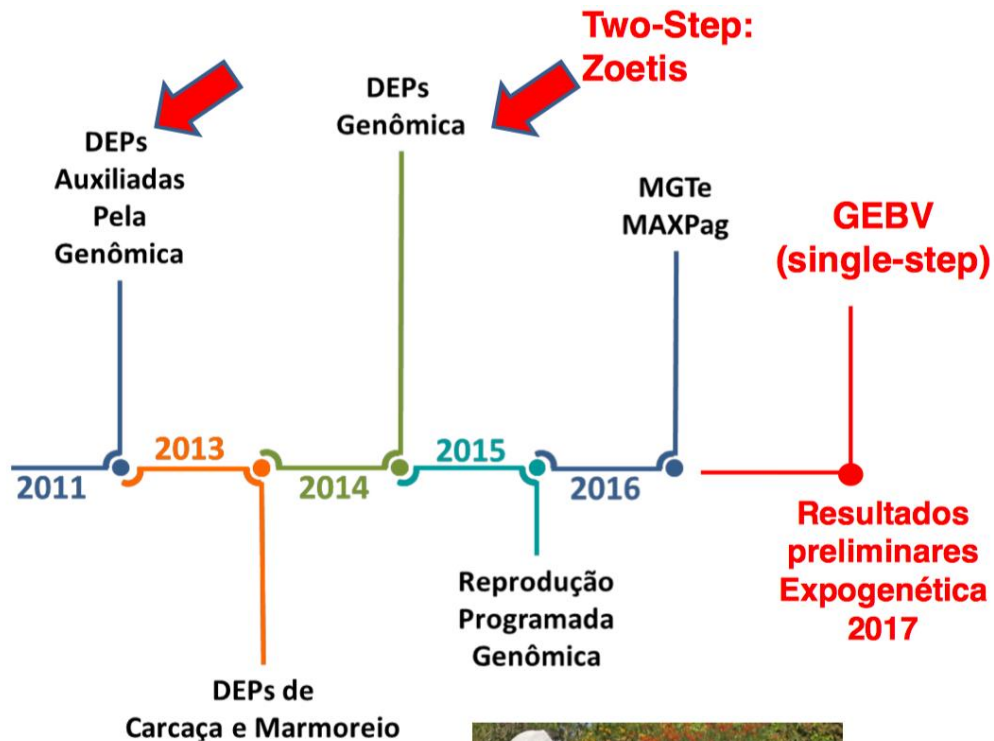


Impact of Genomics for Sustainable Intensification of Beef Production in the Tropics

Challenges for Sustainable Intensification of Beef Production in the Tropics (*from genetic perspective*)

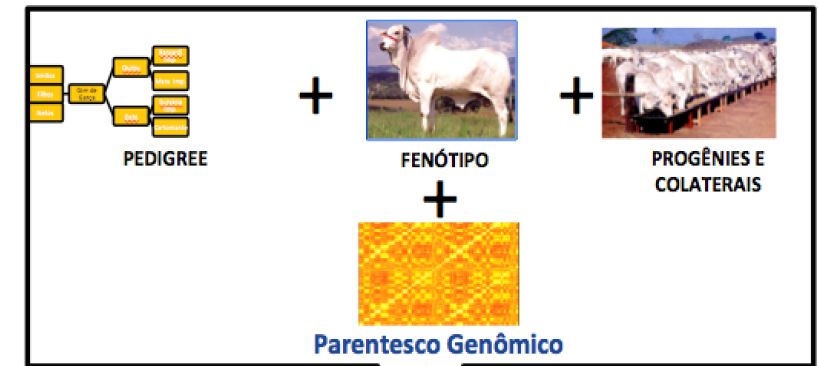
- Improve growth, sexual precocity and lifetime production
- Beef tenderness & others (*REA, BFT, MAR*)
- Feed efficiency (*enviromental concern*)
- Reduce inbreeding & mating decisions
- New novel phenotypes (livestock precision)
- Multi-breed evaluations with small reference populations
- Multi-omics approaches to increase the efficiency of meat production

Evolution of Genomic Evaluations at ANCP



$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A_{22}^{-1} \end{bmatrix}$$

Single step method (ssGBLUP):

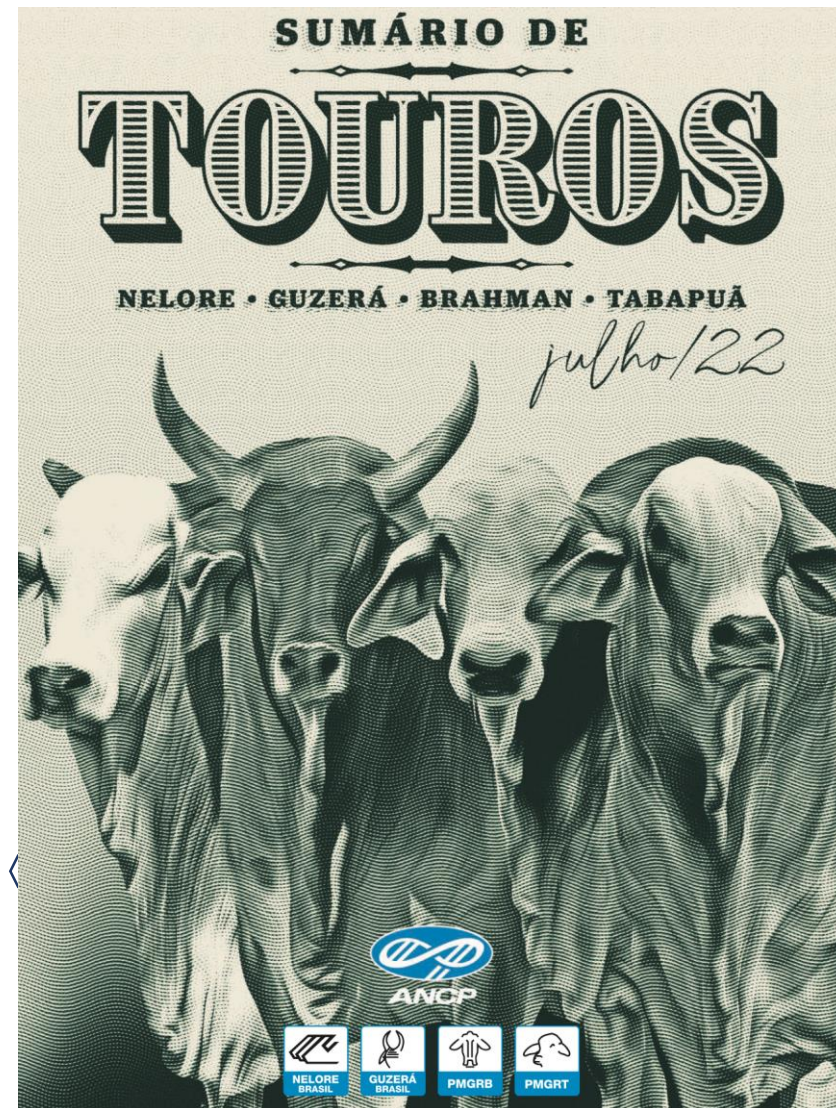
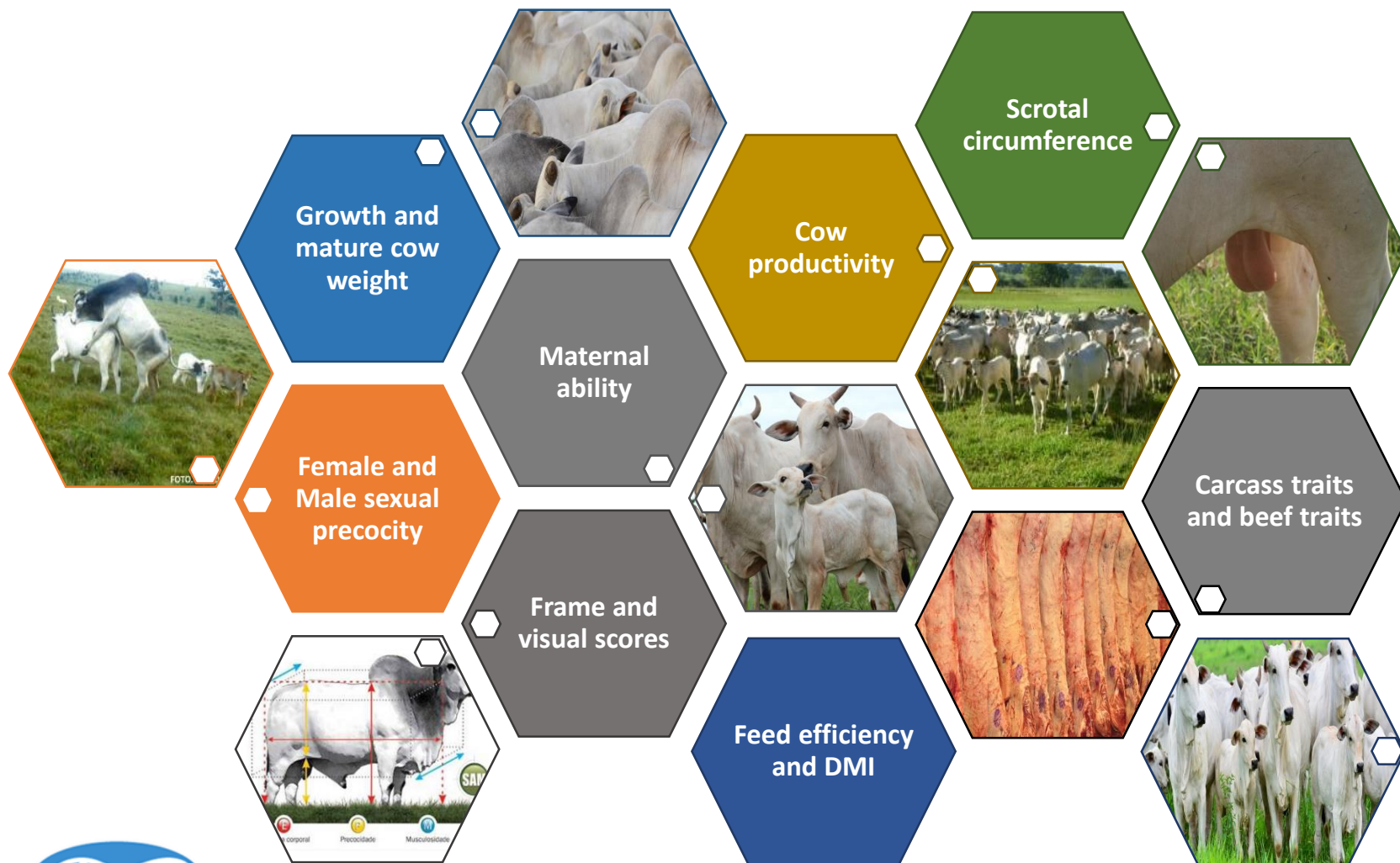


GEBV

Intensive use of young Sires

Most of the beef Zebu breeding programs have implemented genomic selection

Genomic breeding values available at ANCP



Estimated Progeny Equivalents (Nelore Clarified v3.1) for Validation Animals

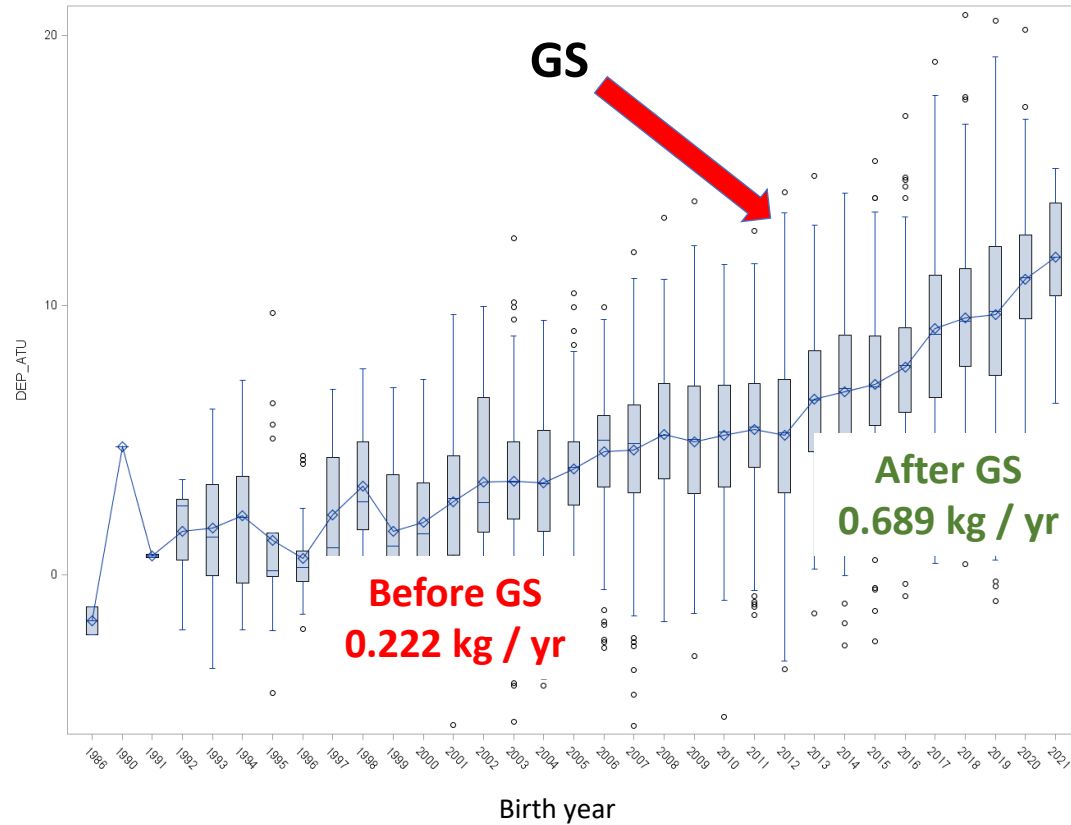
EBVs for cow-calf phase	BLUP Accuracy	Genomic Accuracy	Estimated Progeny Equivalents
Age first calving	0.16	0.23	10
Early heifer pregnancy	0.17	0.40	21
Stayability (longevidad)	0.11	0.28	22
Cow productivity	0.12	0.36	22
Maternal ability	0.14	0.41	45
Adjusted weight at 120 days	0.23	0.37	12
Adjusted weight at 210 days	0.23	0.38	11

EBVs for growth and fattening phase	BLUP Accuracy	Genomic Accuracy	Estimated Progeny Equivalents
Adjusted weight at 210 days	0.27	0.42	11
Marbling	0.20	0.36	6
Ribeye area	0.19	0.36	9
Fat thickness	0.19	0.32	6

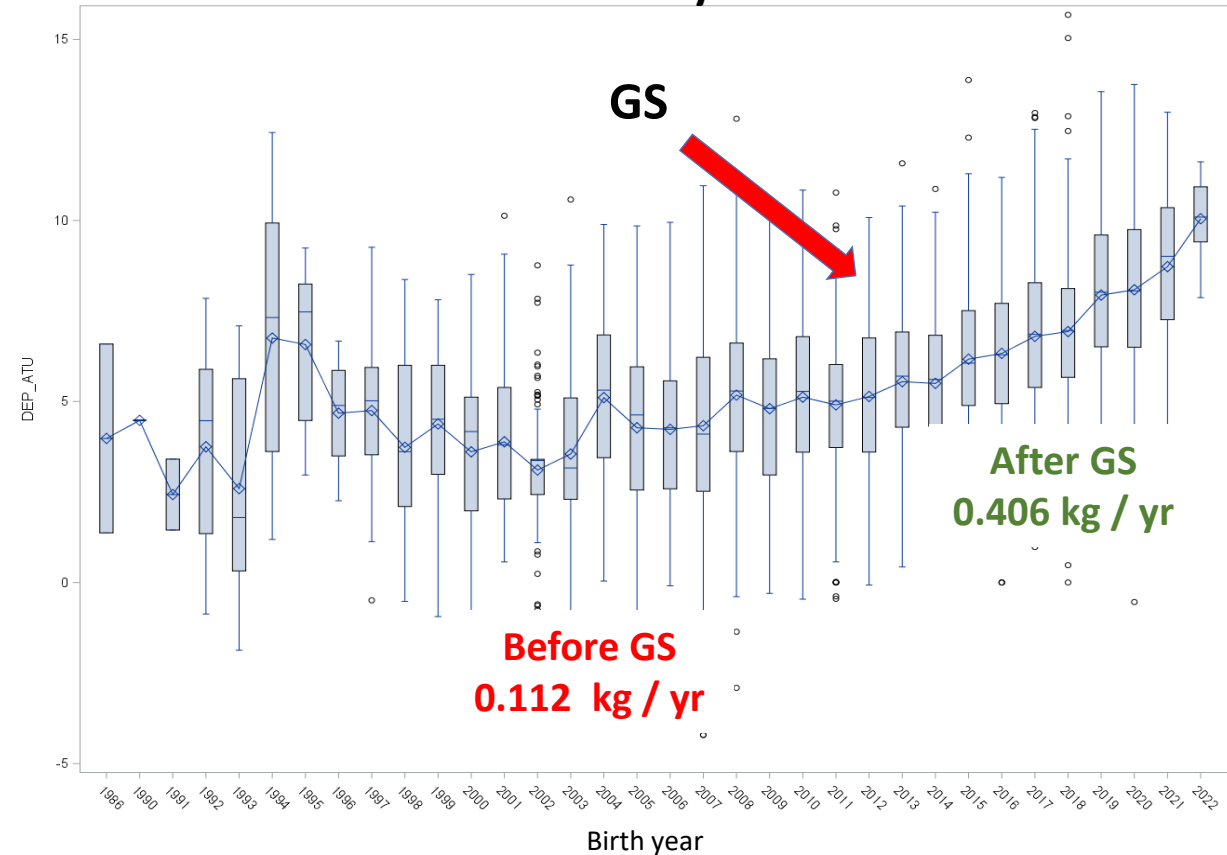
Higher impact on reproductive and maternal traits

GEV trends for growth and longevity: Impact of genomic selection

W210

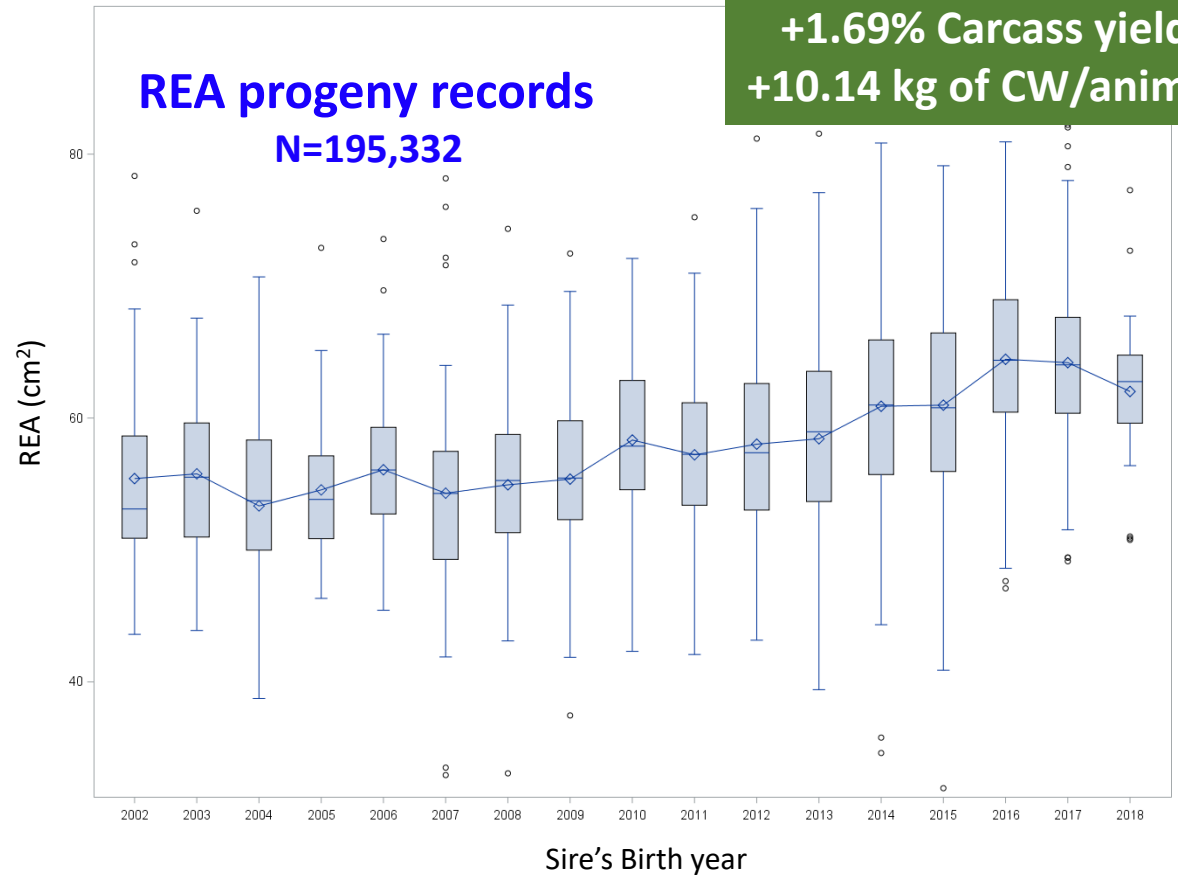
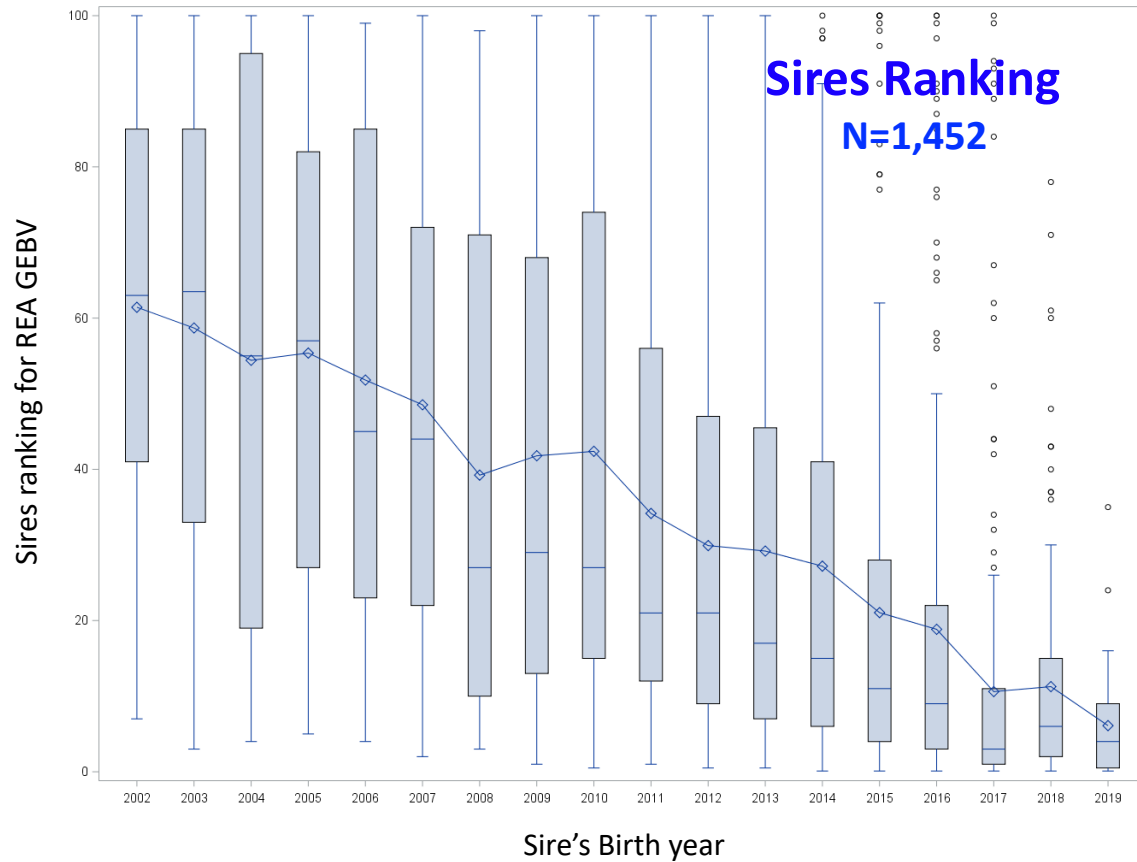


Cow Accumulated Productivity



Impact of using genotyped young sires on carcass traits

GEV sires ranking evolution for rib eye area (REA) and the REA records of their progeny

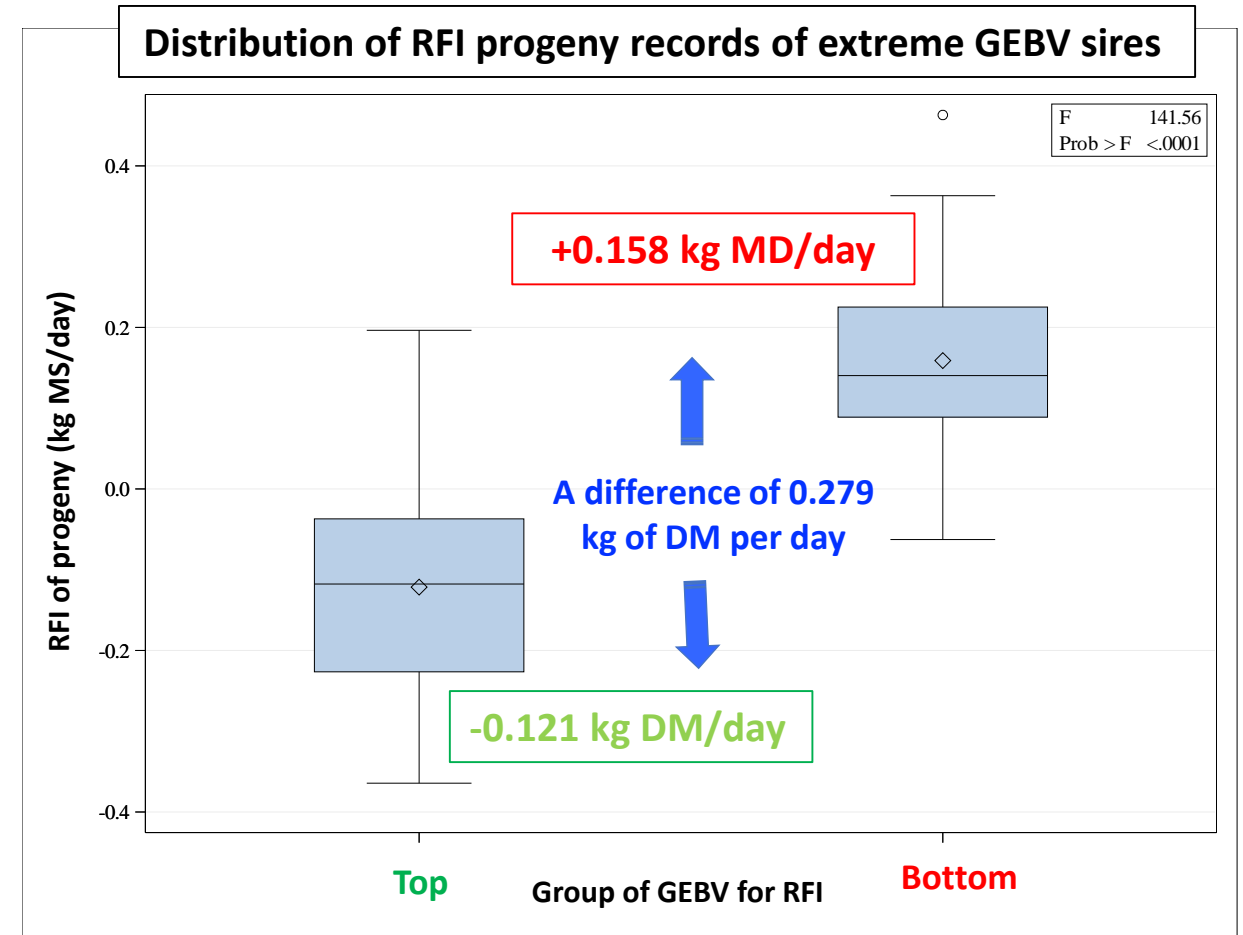


REA increased 12.1 cm²
+1.69% Carcass yield
+10.14 kg of CW/animal

6.5 million of head in feedlots in Brazil: Potential to increase approx. 66,000 tons the CW

Impact of selection for residual feed intake (RFI): Extreme Sires

- Top ranked GEBV sires for RFI
 - ✓ 74 genotyped sires with at least 10 progeny records for RFI (5,269 records)
- Bottom ranked GEBV sires for RFI
 - ✓ 40 genotyped sires with at least 10 progeny records for RFI (3,891 records)

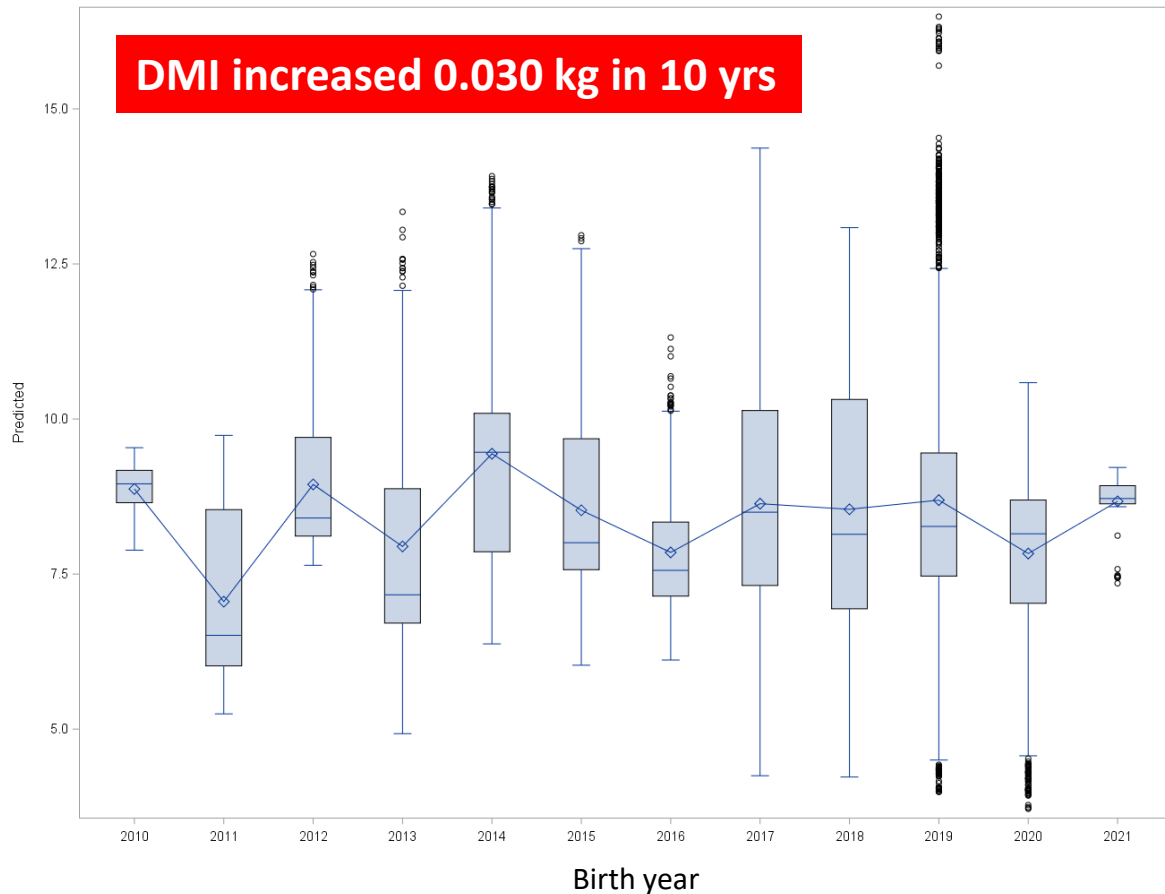


✓ We need approx. 470 tons less of corn grain (90% DM) to feed 10,000 animals during 150 days of feedlot during the finishing phase

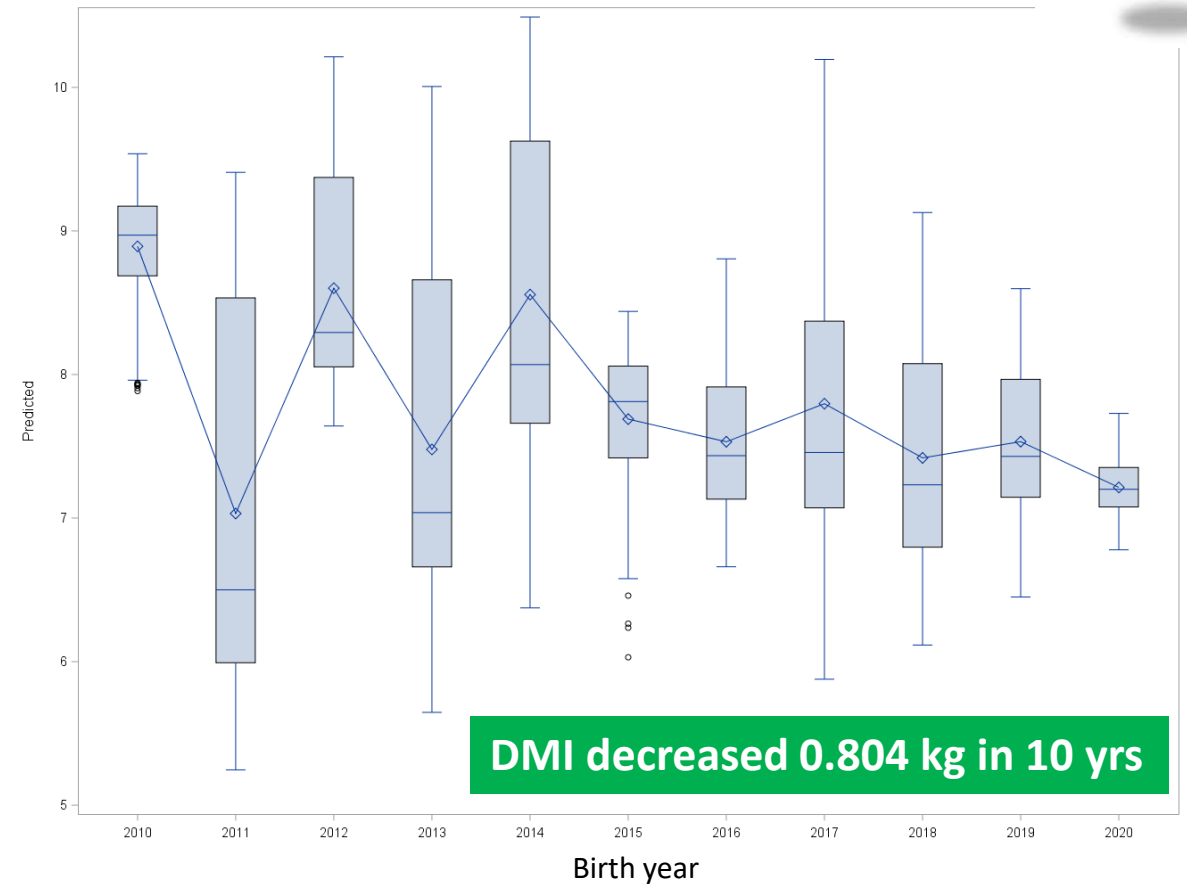
Decreased feed intake after 10 years of selection for increased feed efficiency (RFI) in Nelore cattle



DMI Records from Nelore Breeding Program (N=14,771)
RFI is not considered as selection criterion



DMI Records from Rancho da Matinha (N=4,112)
Including RFI as one selection criterion



10.4% of DMI reduction in 10 yrs of selection for feed efficiency

Multibreed genomic evaluation (metafounders) in indicine beef cattle



	W210			
	¹ SLB Guzera	² MTB Guzera	SLB Brahman	MTB Brahman
Accuracy	0.52	0.80	0.71	0.80
Bias	-1.70	-1.07	-1.60	-1.71
Dispersion	1.03	1.06	0.99	1.01
	W450			
	SLB Guzera	MTB Guzera	SLB Brahman	MTB Brahman
Accuracy	0.23	0.64	0.33	0.74
Bias	-15.7	-6.8	-7.98	-6.05
Dispersion	0.32	0.76	0.33	0.74
	SC450			
	SLB Guzera	MTB Guzera	SLB Brahman	MTB Brahman
Accuracy	0.25	0.69	0.32	0.72
Bias	-0.82	-0.49	-0.62	-0.48
Dispersion	0.46	0.86	0.59	1.01

¹SLB: Single breed genomic evaluation of Nelore, Guzera and Brahman; ²MTB: Multibreed genomic evaluation of Nelore, Guzera and Brahman

Higher impact on breeds with small reference populations

Genomic prediction for healthy beef production in the tropics



CSIRO PUBLISHING

Animal Production Science
<http://dx.doi.org/10.1071/AN16107>

Genetic parameters for fatty acids in intramuscular fat from feedlot-finished Nelore carcasses

Carolyn Aboujaoude^A, Angélica Simone Cravo Pereira^B, Fabieli Louise Braga Fei
Marcos Vinicius Antunes de Lemos^A, Hermenegildo Lucas Justino Chiaia^A,
Mariana Piatto Berton^{A,E}, Elisa Peripolli^A, Rafael Medeiros de Oliveira Silva^A,
Adrielle Mathias Ferrinho^B, Lenise Freitas Mueller^C, Bianca Ferreira Olivieri^A,
Lucia Galvão de Albuquerque^{A,D}, Henrique Nunes de Oliveira^{A,D}, Humberto To
Rafael Espigolan^A, Rafael Tonussi^A, Daniel Mansan Gordo^A, Ana Fabricia Braga Ma
and Fernando Baldi^{A,D}

DOI: 10.1071/AN16107

ANIMAL GENETICS • ORIGINAL PAPER

Genetic correlation estimates between beef fatty acid profile with meat and carcass traits in Nelore cattle

Fabieli Louise Braga Feitosa¹ • Bianca Ferreira Olivieri¹ • Carolyn Aboujao
Angélica Simone Cravo Pereira² • Marcos Vinicius Antunes de Lemos¹ •
Hermenegildo Lucas Justino Chiaia¹ • Mariana Piatto Berton¹ • Elisa Peri
Adrielle Matias Ferrinho² • Lenise Freitas Mueller³ • Mônica Roberta Maz
Lucia Galvão de Albuquerque^{1,5} • Henrique Nunes de Oliveira^{1,5} • Humbert
Rafael Espigolan¹ • Rafael Lara Tonussi¹ • Rafael Medeiros de Oliveira Sil
Daniel Gustavo Mansan Gordo¹ • Ana Fabricia Braga Magalhães¹ • Ignaci
Fernando Baldi^{1,5}

RESEARCH ARTICLE

Gene expression profile of intramuscular muscle in Nelore cattle with extreme values of fatty acid

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Luiz L. Coutinho^{3,5}, Marcos Vinicius A. de Lemos¹, Carolyn Aboujaoude¹, Angélica S. C. Pereira²,
Rafael M. de O Silva¹, Nedenia B. Stafuzza¹, Fabieli L. B. Feitosa¹, Hermenegildo L. J. Chiaia¹, Bianca F. Olivieri¹,
Elisa Peripolli¹, Rafael L. Tonussi¹, Daniel M. Gordo¹, Rafael Espigolan¹, Adrielle M. Ferrinho², Lenise F. Mueller⁴,
Lucia G. de Albuquerque^{1,5}, Henrique N. de Oliveira^{1,5}, Susan Duckett⁶ and Fernando Baldi^{1,5*}



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Meat Science

journal homepage: www.elsevier.com/locate/meatsci



Genomic prediction for beef fatty acid profile in Nelore cattle



Hermenegildo Lucas Justino Chiaia^{a,*}, Elisa Peripoli^a, Rafael Medeiros de Oliveira Silva^a, Carolyn Aboujaoude^a,
Fabieli Loise Braga Feitosa^a, Marcos Vinicius Antunes de Lemos^a, Mariana Piatto Berton^a,
Bianca Ferreira Olivieri^a, Rafael Espigolan^a, Rafael Lara Tonussi^a, Daniel Gustavo Mansan Gordo^a,
Tiago Bresolin^a, Ana Fabrícia Braga Magalhães^a, Gerardo Alves Fernandes Júnior^a,
Lúcia Galvão de Albuquerque^a, Henrique Nunes de Oliveira^a, Joyce de Jesus Mangini Furlan^b,
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BMC GENOMICS

Open Access



alheiro¹, Daniel M. Gordo¹, Rafael Ton
e Oliveira¹, Susan Duckett³,



Genomic prediction for beef tenderness in Nelore cattle



Accuracy of genomic breeding values for meat tenderness in Polled Nelore cattle¹

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E. C. Eifert,* B. D. Valente,† G. J. M. Rosa,† and R. D. Sainz‡

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The international journal of animal biosciences



ABSTRACT: Zebu (*Bos indicus*) cattle, m Nelore breed, comprise more than 80% of cattle in Brazil, given their tolerance of the climate and high resistance to ectoparasites. Disadvantages for production in tropical environments zebu cattle tend to produce tougher meat than other breeds. Traditional genetic selection for meat tenderness is constrained by the difficulty of phenotypic evaluation for meat quality. Genomic selection may be the best strategy to improve meat quality traits. This study was performed to compare the accuracies of different Bayesian models in predicting molecular breeding values for meat tenderness in Polled Nelore cattle. It was composed of Warner–Brazler shear force of longissimus muscle from 205, 141, and 141 animals, which were selected and mated so as to create segregation for WBSF. The animals were genotyped with either the Illumina BovineHD (HI) from 90 samples) chip or the GeneSeek Profiler (GGP Indicus HD; 77,000 from 33 samples). The quality control of SNP were Hardy–Weinberg P -value $\geq 0.1\%$, minor allele frequency $\geq 1\%$, and call rate $> 90\%$. The FImpute program was used for imputation from the GGP Indicus

Key words: Bayesian regression

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Genome-enabled prediction of meat tenderness using Bayesian regression, single-step genomic selection, and blending methods in Nelore cattle

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Warner–Brazler shear force

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ORIGINAL ARTICLE

Improving genomic prediction accuracy for meat tenderness in Nelore cattle using artificial neural networks

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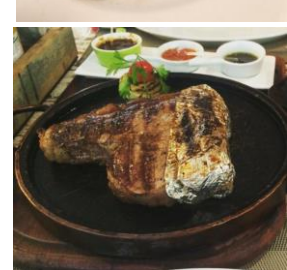
Funding information

Fundação de Amparo à Pesquisa do Estado de São Paulo, Grant/Award Number: 2017/03221-9

Abstract

The goal of this study was to compare the predictive performance of artificial neural networks (ANNs) with Bayesian ridge regression, Bayesian Lasso, Bayes A, Bayes B and Bayes C π in estimating genomic breeding values for meat tenderness in Nelore cattle. The animals were genotyped with the Illumina Bovine HD Bead Chip (HD, 777K from 90 samples) and the GeneSeek Genomic Profiler (GGP Indicus HD, 77K from 485 samples). The quality control for the genotypes was applied on each Chip and comprised removal of SNPs located on non-autosomal chromosomes, with minor allele frequency $< 5\%$, deviation from HWE ($p < 10^{-6}$), and with linkage disequilibrium > 0.8 . The FImpute program was used for genotype imputation. Pedigree-based analyses indicated that meat tenderness is moderately heritable (0.35), indicating that it can be improved by direct selection. Prediction accuracies were very similar across the Bayesian regression models, ranging from 0.20 (Bayes A) to 0.22 (Bayes B) and 0.14 (Bayes C π) to 0.19 (Bayes A) for the additive and dominance effects, respectively. ANN achieved the highest accuracy (0.33) of genomic prediction of genetic merit. Even though deep neural networks are recognized to deliver more accurate predictions, in our study ANN with one single hidden layer, 105 neurons and rectified linear unit (ReLU) activation function was sufficient to increase the prediction of genetic merit for meat tenderness. These results indicate that an ANN with relatively simple architecture can provide superior genomic predictions for meat tenderness in Nelore cattle.

NOME	GEN	PAI	MAC		
			DEP	AC	TOP
RECOMENDADO OB		OBG 5883	-0.135	29	0.1%
MOGNO OB		OBG 5883	-0.095	42	0.1%
TALCO OB		OBG 7751	-0.093	29	0.1%
SONOLENTO OB	G	HA6204	-0.090	47	0.1%
AUSTIN DE CV	G	MANA C2569	-0.071	46	0.1%
VETERANO FIV DE CV	G	CVCV 2014	-0.068	56	0.1%
APOGEU DE NAVIRAI		CSCM 1484	-0.067	46	0.1%
METEORO OB		OBG 5883	-0.064	39	0.1%
TANADO FIV DE CV	G	CSCM 3315	-0.063	46	0.1%
SETUBAL FIV DE CV	G	ESL 1513	-0.060	45	0.1%
QUADRADA DE CV	G	CSCM 1635	-0.057	58	0.1%
HELIX CERRADOS	G	OBG 7751	-0.051	41	0.1%
LIMINHA DE CV		CSCM 1484	-0.050	28	0.1%
XE 40 DA BACURI		MGL 1202	-0.047	42	0.1%
QUARAÇA 34 DA BACURI		MGL 532	-0.040	56	0.5%
STALONE FIV DE CV	G	I1111	-0.036	47	0.5%
AVESSO DA BELA	G	I1111	-0.035	50	0.5%
SANSAO DE CV	G	CVCV 2014	-0.035	46	0.5%
XE 11 DA BACURI		MGL 1157	-0.034	41	0.5%
XINGU DE CV	G	CVCV 7989	-0.033	48	0.5%
MINUANO AGMN 0906	G	MGL 962	-0.032	42	0.5%
MONARCA FIV DA BELA	G	C6881	-0.032	37	0.5%
JUBILOSO DE CV		F9902	-0.031	45	0.5%
MACUNI DO SALTO	G	G5191	-0.030	48	0.5%
BRONZEADO OB		OBG 3845	-0.030	27	0.5%
SUMO FIV DE CV	G	CVCV 2235	-0.029	50	0.5%
URUBATÁ 7 DA BACURI		MGL 1202	-0.029	42	0.5%
CROMO JR TAR		CSCM 3315	-0.028	21	0.5%
XYSTO FIV DE CV	G	CVCV 7989	-0.028	21	0.5%



Fapesp funding 2017/03221-9



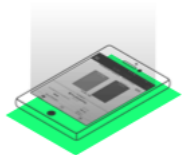
Feedlot Profitability : Optimal Slaughter Point



Heritability - h^2d

Feedlot Profitability **0.34**

- 1
- 2
- 3



Algoritmos, mercado e IA calculam o Ponto de Negociação Ótimo (OTP) usando a análise de Pesquisa Operacional



O software captura dados de IoTs (sensores inteligentes)



BeefTrader mostra lucro diário e previsto de confinamentos e animais individualmente

- 1
- 2
- 3

Sincronização de dados fenotípicos observados com BeefTrader na Fase 1

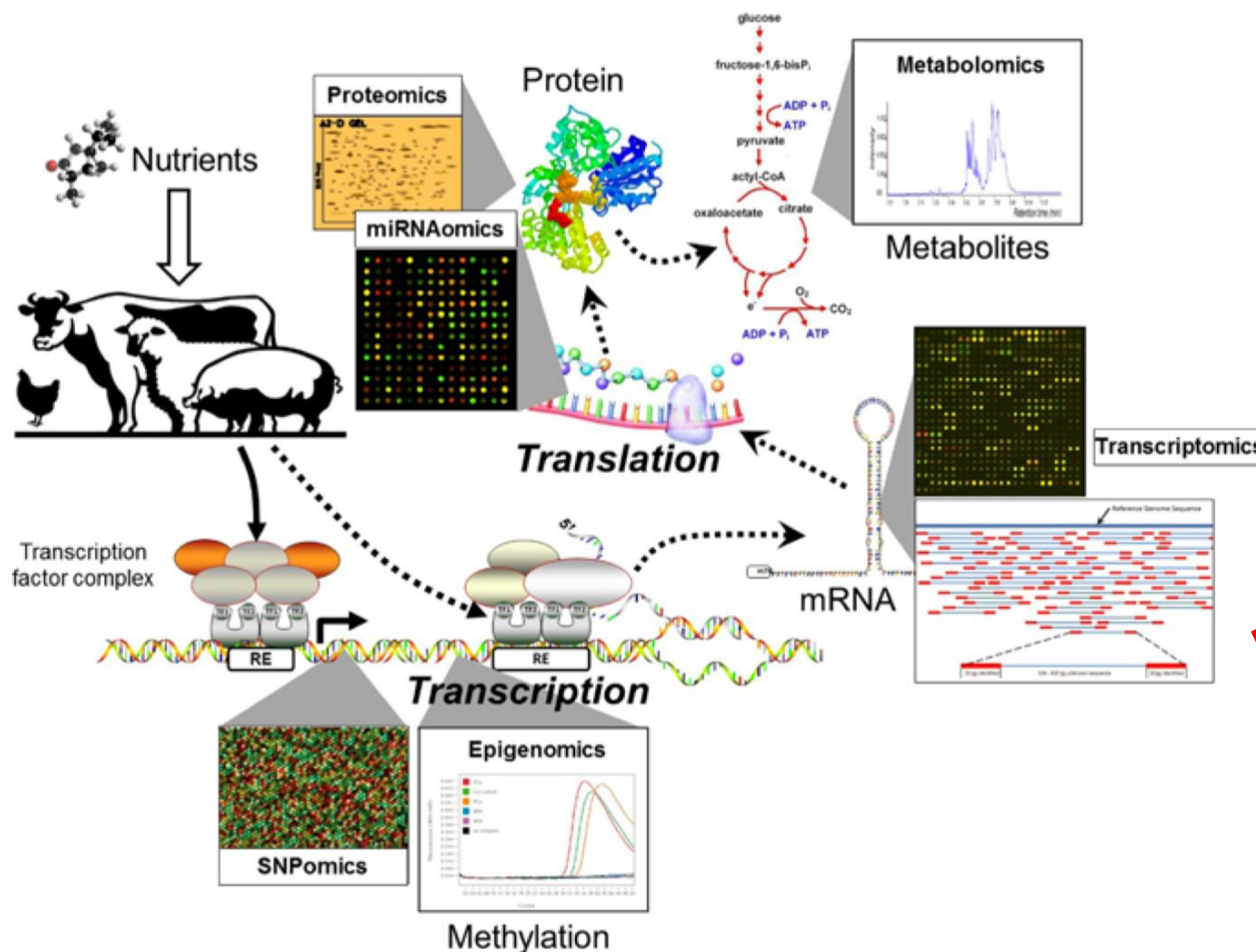
Padronização de base de dados e ajustes de parâmetros zootécnicos, econômicos e genéticos

Processamento das informações individuais de touros e/ou intra-rebanho com os algoritmos LPT

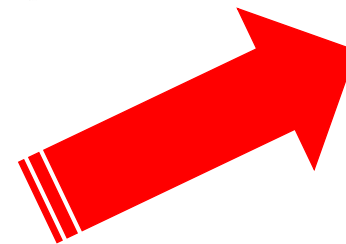
Sire's GEBV for feedlot profiability and feedlot profit of their progeny



Future: the challenge of multi-omics science integration



**Understand and Predict
Better (“BigData”):
Use of biomarkers in genetic
evaluation and management
decisions**



Prediction ability for early heifer pregnancy including quantitative trait nucleotides in single-step GBLUP



	BLUP	BLUP + phenotype	ssGBLUP	ssGBLUP + QTN
Accuracy	0.36	0.39	0.49	0.57
Bias	0.155	0.164	0.018	0.007
Inflation	0.90	0.87	0.99	0.65

Peripolli et al. unpublished

Prediction ability for residual feed intake including potential functional variants using multi-tissue RNA-Seq data



Validation for functional mutations	Adrenal		Pituitary		Hypothalamus		Muscle		Liver	
	Acc	b (SE)	Acc	b (SE)	Acc	b (SE)	Acc	b (SE)	Acc	b (SE)
ssGBLUP_QTN:1-fold	0.16	0.74 (0.03)	0.16	0.723 (0.03)	0.15	0.73 (0.03)	0.15	0.85 (0.03)	0.15	0.82 (0.03)
ssGBLUP_wG_QTN:2-fold	0.18	0.67 (0.03)	0.18	0.65 (0.03)	0.18	0.66 (0.03)	0.18	0.75 (0.03)	0.18	0.79 (0.03)
ssGBLUP_wG_QTN:3-fold	0.20	0.62 (0.03)	0.19	0.60 (0.03)	0.19	0.61 (0.03)	0.20	0.71 (0.03)	0.20	0.77 (0.03)
ssGBLUPrecords_wG_QTN:1-fold	0.31	1.02 (0.02)	0.31	1.00 (0.02)	0.31	1.02 (0.02)	0.29	1.11 (0.2)	0.30	1.08 (0.02)

Ribeiro et al., unpublished

Genomic information to improve mating decisions and decrease inbreeding in Nelore cattle

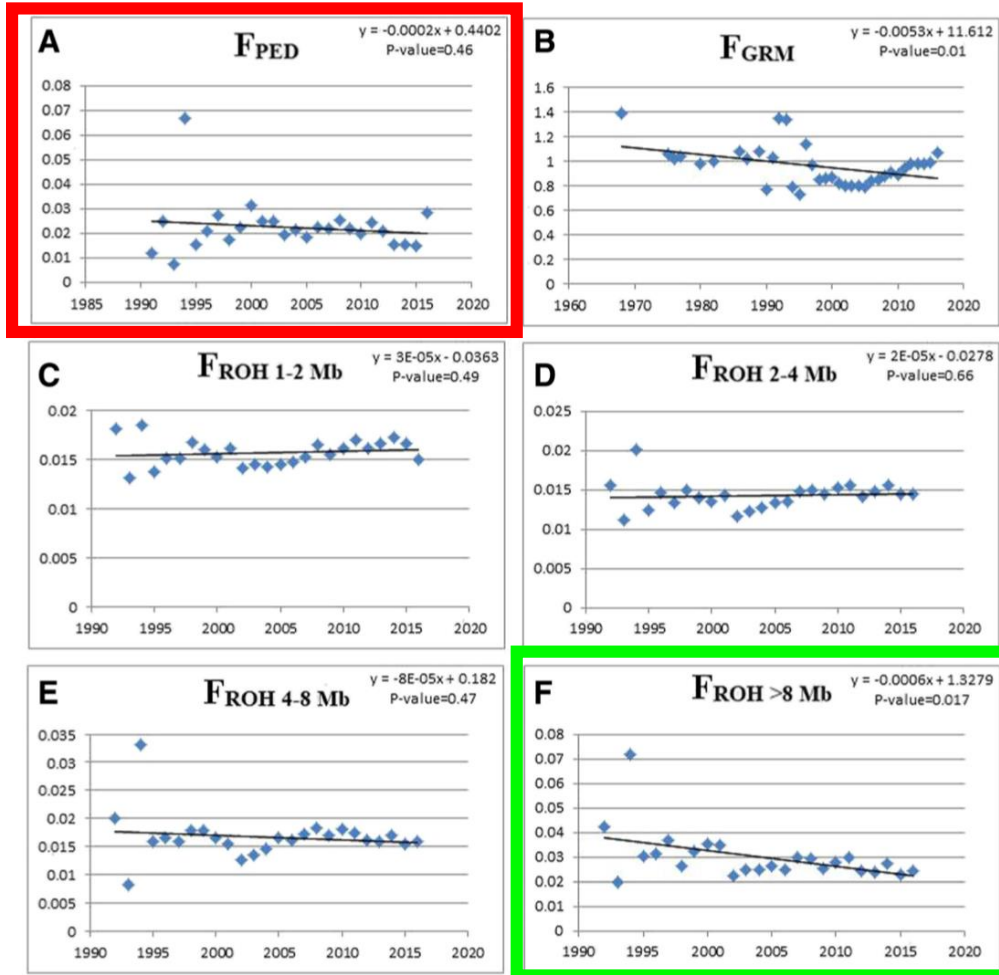


Fig. 3 Inbreeding evolution over the past 30 years for pedigree-based inbreeding (F_{PED}), genomic relationship matrix approach (F_{GRM}), and F_{ROH} ($F_{ROH1-2\ Mb}$, $F_{ROH2-4\ Mb}$, $F_{ROH4-8\ Mb}$, and $F_{ROH > 8\ Mb}$) coefficients and their respective regression equations and p -values. The X-axis represents the years and the Y-axis shows the inbreeding coefficients. Each blue dot represents the inbreeding average per year

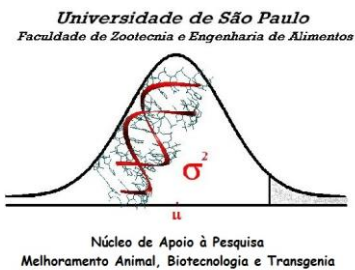
Future Perspectives for Sustainable Intensification of Beef Production in the Tropics

- **Genomic selection for crossbreeding decisions**
 - Combination ability in terminal crossbreeding system to improve beef quality and efficiency
- **New traits need to be recorded with more emphasis on environmental impact**
 - High-dimensional phenomics
- **Genotype x environment interaction**
 - Selection for specific objectives and environment
 - Epigenetic markers and environmental records
- **Next Generation Sequencing**
 - New genetic variations associated with adaptive traits
- **Holistic multi-omics approaches to improve mating and management decisions**
 - System genetic approach

Acknowledgment



Thank you!



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