INFLUENCE OF GENETIC MARKERS ON CARCASS AND MEAT QUALITY TRAITS IN NELLORE CATTLE

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Poster Session 1

Objectives

The objective of this study was to verify the association of genetic markers (Single Nucleotide Polymorphism or SNP) with carcass and meat quality traits and evaluate the use of those markers as auxiliary criteria for selection in Nellore cattle, the most important breed in the Brazilian beef herd.

Conclusions

Significant or suggestive allelic substitution effects of DNA polymorphisms on carcass, meat and lipid profile traits were detected and can be used as additional or auxiliary selection criteria on programs of improving carcass and meat quality traits in Nellore cattle, raised under tropical pasture conditions.

Introduction

The detection of genetic polymorphisms associated to genes that are involved with economically relevant traits is a very important auxiliary tool for selection in beef breeding programs, specially for traits difficult or expensive to measure, as carcass and meat quality.

One restrictive factor of the large use of those polymorphisms in beef breeding programs in Brazil is that they were discovered in *Bos taurus* animals or *Bos indicus* of Brahman breed, and, also in production systems that are very different for the Brazilian production systems. While the animals where those polymorphisms are normally fed in feedlots right after weaning, with high energy-high grain level diets, more than 80% of the Brazilian beef herd are composed by *Bos indicus* animals and are reared under extensive pasture conditions and only around 5% of them fed with high fiber, medium energy diets. Among the beef breeds raised in Brazil, the Nellore is a highlight and, in that breed, the influence of British *Bos taurus* is much lower and of Continental *Bos taurus* much higher than in the Brahman breed. That can indicate that genes can act differently in the metabolism and genetic markers can, also, have different effects on the Brazilian beef herd than in Angus, Hereford or Brahman, the breeds where those markers were studied.

A partnership between Merial Saúde Animal Ltda. and the Animal Breeding and Biotechnology Group of the College of Animal Science and Food Engineering of the University of Sao Paulo, Brazil, was established in 2005 to study the validation of genetic markers licensed by Merial Ltd. (Igenity) in Brazilian beef herd, including growth traits and carcass and meat quality in Nellore breed.

Methods

A. Data description
Data on 1,883 Nellore cattle, reared under pasture conditions in southwestern Brazil, and measured by ultra-sound for carcass traits and 674 bulls finished in a feedlot for 90 to 120 days and slaughtered at age from 21 to 29 months were analyzed.

B. Analyzed traits
Carcass traits measured by ultra-sound were rib eye area (REA_US), backfat (BF_US) and fat depth at rump (FD_P8) and, measured after slaughter, were hot carcass weight (HCW), rib eye area (REA), backfat (BF). Meat quality traits measured after 7, 14 and 21 days of ageing were weep loss (WL7, WL14 and WL21), cook loss (CL7, CL14 and CL21) and Warner-Braztler shear force (WBSF7, WBSF14 and WBSF21). Total lipids and cholesterol content in 100 g of samples aged for 7 days, were, also, measured and included on the analysis.
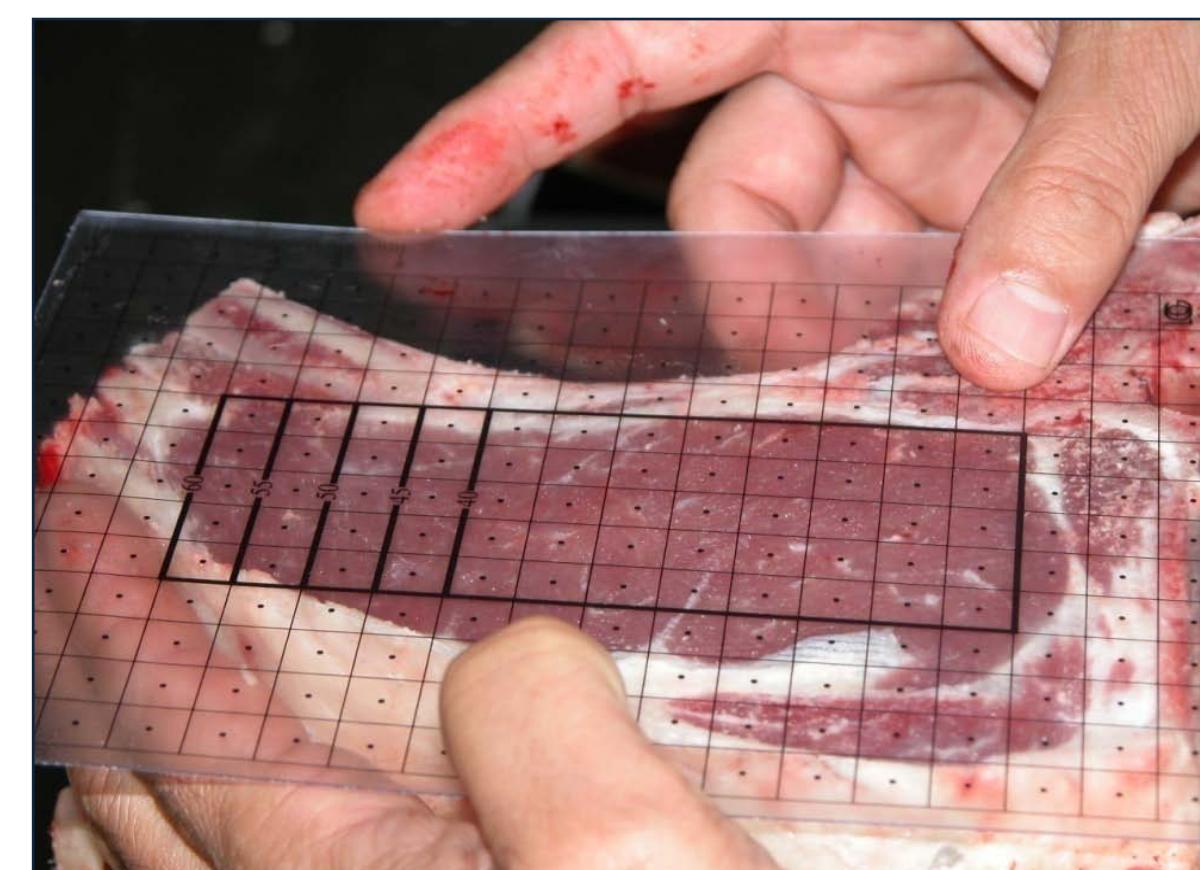

Figure 1. Details of data collection for rib eye area and backfat in carcasses

C. Statistic model
Allele substitution effects were estimated in single and multi-polymorphism analysis. Additive and dominance effects were also estimated. Both analysis were performed by PROC MIXED, SAS, considering sire as a random effect.

D. Genetic analysis
The genotypes of DNA markers were carried out in laboratories licensed by sponsoring company using their micro-array panels.

Results

Descriptive statistics of analyzed traits are described on Table 1.

Table 1. Number of observations and descriptive statistics for carcass and meat quality traits measured on Nellore beef cattle

Traits	N	MEAN	SD	CV	MIN	MAX
YEARLING_AGE. days	3,371	546.17	35.39	6.48	389.00	659.00
REA_US. cm²	1,883	65.35	7.38	11.29	40.20	93.80
BF_US. mm	1,671	2.50	1.09	43.49	0.50	7.70
FD_P8. mm	1,824	3.97	1.78	44.80	0.50	11.90
SLAUGHTER_AGE. days	640	739.38	54.85	7.42	631.00	1,021.00
HCW. kg	674	290.51	17.68	6.08	255.50	393.00
PH24	667	5.96	0.25	4.23	5.20	6.99
REA. cm2	668	73.35	7.03	9.59	56.00	101.00
BF. mm	666	4.39	2.00	45.65	1.00	15.00
WL7. %	617	2.85	1.34	47.02	0.06	12.74
CL7. %	663	12.50	5.05	40.40	0.75	49.00
WL14. %	630	3.79	1.67	43.99	0.05	12.28
CL14. %	669	10.68	3.15	29.50	1.98	34.43
WL21. %	618	4.63	2.10	45.45	0.74	33.62
CL21. %	662	10.91	3.85	35.26	1.13	49.37
WBSF7_TEMP. ºC	656	18.24	1.45	7.94	13.40	23.00
WBSF7. kg	671	5.93	1.45	24.37	1.82	9.99
WBSF14_TEMP. ºC	666	18.14	1.62	8.95	3.85	23.00
WBSF14. kg	671	4.95	1.27	25.65	1.38	9.34
WBSF21_TEMP. ºC	667	17.75	1.49	8.40	13.60	20.90
WBSF21. kg	671	4.41	1.12	25.32	1.61	8.53
LIPIDS. g/100g	589	2.19	0.65	29.59	0.96	4.60
CHOLESTEROL. mg/100g	627	56.42	8.26	14.64	28.76	83.95

Many DNA polymorphisms, initially discovered in *Bos taurus*, and that were analyzed in Nellore breed showed to be fixed or the frequencies for one of the alleles were too high, more than 99 %. In those cases, association analysis could not be performed or their results were not conclusive. However, for many others polymorphisms there were observed variability on allele frequencies, what made possible to carry out the association analysis.

All traits analyzed were influenced by, at least, four polymorphisms with statistically significant (P≤0.05) or suggestive (0.05<P≤0.20) effects.