



GENETIC MARKERS INFLUENCE ON GROWTH TRAITS IN NELLORE CATTLE

***Ferraz, J.B.S.; Rezende, F.M.; Meirelles, F.V.;
Balieiro, J.C.C.; Eler, J.P.; Mattos, E.C.***

Animal Breeding and Biotechnology Group, Department of Basic Sciences, College of Animal
Science and Food Engineering, University of Sao Paulo, Brazil (✉ jbferraz@usp.br)



Poster Session 1

Objectives

This study was conducted with the objective of detecting association of genetic markers (Single Nucleotide Polymorphism or SNP) with economically relevant growth traits and verify the possible use of those markers as auxiliary tools for selection in Nellore breed.

Conclusions

DNA polymorphisms that had significant or suggestive allelic substitution effects were detected and can be used as additional or auxiliary selection criteria for growth traits in Nellore cattle, raised under tropical pasture conditions in Brazil.

Introduction

An important partnership between Merial Saúde Animal Ltda. and the Animal Breeding and Biotechnology Group (GMAB) 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.

That work included researches in traits related to growth, reproduction, carcass and meat quality, among others.

Brazil is a major player in the international beef market, exporting around 30% of the total beef trade in the planet. Nellore, a *Bos indicus* breed, is the largest breed in the Brazilian beef industry, influencing more than 80% of the 190 million head bovine population of that country.

The majority of breeding programs in Nellore breed considers as selection criteria growth traits, like the weights at birth (BW), weaning (WW, measured at 7 months of age), yearling (YW, measured at 18 months of age) and weight gains, mainly post weaning gain (WG345), not only because they are easy and have low cost of measurement, but, also, because they have clear and direct impact on the ranchers revenues. The results of those programs were an important increase in the weights of animals.

The identification of genetic polymorphisms that are associated to growth traits in the Nellore population and the use of those markers as auxiliary tools in selection will have important impact in accuracy of the process, besides allowing the recognition of parents in multi-sire pasture, that, also, will increase the accuracy of genetic merit prediction and the results of selection.

The results presented in this poster are part of a broad work that studied the association of genetic markers, originally discovered in *Bos taurus* or in Brahman cattle, with growth traits of Nellore animals, reared under pasture conditions.

Methods

A. Data description

Data on growth traits of 3,844 Nellore cattle reared under pasture conditions in two different farms in southwestern Brazil were analyzed.

B. Analyzed traits

Traits considered were birth weight (BW), weaning weight (WW), yearling weight, measured at 18 mo (YW), post weaning weight gain (WG345) and visual scores for carcass conformation (CONF), finishing (PREC) and muscle score (MUSC).

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 using micro-array panels in laboratories licensed by Merial Limited, a private company that holds the rights of exploration of SNPs analyzed.

Results

Descriptive statistics of analyzed traits are described on Table 1.

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

TRAITS	N	MEAN	SD	CV	MIN	MAX
BW, kg	3358	31,76	3,50	11,01	19,00	50,00
WW, kg	3396	192,87	25,77	13,36	89,00	289,00
WEAN_AGE, days	3396	207,81	19,26	9,27	120,00	318,00
YW, kg	3371	312,62	43,22	13,83	176,00	473,00
YEAR_AGE, days	3371	546,17	35,39	6,48	389,00	659,00
WG345, kg	3351	121,50	31,88	26,24	19,63	245,77
CONF	2845	3,17	0,91	28,69	1,00	6,00
PREC	2238	3,17	0,94	29,56	1,00	6,00
MUSC	2237	3,06	0,90	29,32	1,00	6,00

In Table 2 the number of polymorphism for which was detected statistically suggestive ($0,05 < P \leq 0,20$) or significant ($P \leq 0,05$) allele substitution effect for each analyzed trait are described.

Table 2. Number of polymorphism with suggestive or significant allele substitution effect for growth traits measured on Nellore beef cattle.

TRAITS	SUGGESTIVE EFFECT	SIGNIFICANT EFFECT
BIRTH WEIGHT	13	1
WEANING WEIGHT	11	4
YEARLING WEIGHT	12	1
POST WEANING GAIN	10	3
CONFORMATION	4	4
FINISHING	4	1
MUSCLE SCORE	1	1

In a set of almost two hundred polymorphism, many DNA polymorphisms showed to be fixed or the frequencies for one of the alleles were too high on analyzed population. In those cases, association analysis could not be performed or results were not conclusive. However, for many others polymorphisms, which were observed variability on allele frequencies, it was possible to carry out the association analysis. All analyzed traits were influenced by, at least, four polymorphisms with significant or suggestive effects.