Investigation of genes related to lipid metabolism as candidate for sexual precocity in Nellore cattle

M.M. Dias[1,3], H.N. Oliveira[1] , F.R.P. Souza[2] , L.G. Albuquerque[1], L. Takada[1], I.D.P.S. Diaz[1]

[1] Faculdade de Ciências Agrárias e Veterinária, Jaboticabal – SP, 14884-980, Brazil.
[2] Universidade Federal de Pelotas, Pelotas – RS, 96001-970, Brazil.
[3] Student of the Graduate Program in Animal Breending – PhD - UNESP - Jaboticabal. e-mail: marina.mortati@gmail.com

INTRODUCTION

The Nelore is important for the production of Brazilian beef because it is well adapted to the tropical climate. But one of the problems of Brazilian beef cattle refers to low sexual precocity of the flock. The pregnant probability of heifers is a characteristic of high economic value to Nellore. The influence of fat on early pregnancy is possibly related to the endocrine function of this tissue, being responsible for releasing hormones that are precursors of sex hormones which act directly on the sexual precocity (Siiteri ,1987). The aim of this study was to evaluate possible associations between known polymorphisms in genes related to adipose tissue and sexual precocity in Nellore cattle.

METHODS

- 1,085 precocious and non-precocious heifers Nellore belonging to Delta G Connection (Conexão Delta G) breeding program were analyzed.
- The DNA extraction method performed by phenol-chloroform-isoamyl alcohol from the bulb of hair at the tail of the heifers.
- It were analyzed 54 candidate genes that were related to lipid metabolism.
- The location of genes was found in NCBI (http://www.ncbi.nlm.nih.gov/gene/)
- A subset of SNPs from the panel of High Density Bovine SNP BeadChip of 777,000 SNPs was evaluated. This subset of SNPs is located within a region of candidate genes with a distance up to 5 Kb, since it is considered that in this distance there is linkage disequilibrium (LD).
- Only 445 precocious and non-precocious heifers were genotyped, for the remained 640, the average number of copies of each allele from the genotyped population, was used.
- The statistical evaluation was made by linear models.
- To analyze the reconstruction of haplotypes and LD presence, the fastPHASE and GenomeStudio softwares were used, using r^2 procedure.

RESULTS

In total, 54 candidate genes and 443 SNPs were analyzed. Among these SNPs, 370 formed 83 haplotypes while the remained SNPs were studied separately. The statistical analyses revealed that only two sets of haplotypes, formed by two and four SNPs located on FABP4 and PPP3CA, and one isolated SNP on PPP3CA gene, had significant effect (p<0.05) for the sexual precocity trait.

Table 1. Frequencies and the average effect of the allele and its standard error of the alleles of the haplotype located in the gene FABP4:

Allele	*SNPs base*	*Frequency*	*Average effect*	*Standard error*
Alelo1	AA	0,547	0,0088	0,0616
Alelo2*	CA	0,343	0,3081	0,0662
Alelo3*	CG	0,110	- 0,3170	0,0902

*average effect significantly different from zero (P <0.05).

Table 2. Frequencies and the average effect of the allele and its standard error of the alleles of the haplotype located in the gene PPP3CA

Allele	*SNPs base*	*Frequency*	*Average effect*	*Standard error*
Alelo1	AAAA	0,094	0,035	0,146
Alelo2*	GGGG	0,539	0,263	0,092
Alelo3*	GAGA	0,284	0,428	0,106
Alelo4*	GGGA	0,084	-0,727	0,152
SNP isolated				
Alelo1*	A	0,176	-0,164	0,037
Alelo2*	G	0,824	0,164	0,037

*average effect significantly different from zero (P <0.05).

CONCLUSIONS

These results indicate that FABP4 and PPP3CA genes have an influence on sexual precocity of the animals and should be considered in selection breeding programs in Nellore cattle to evaluate this trait.

REFERENCES

SIITERI, P. K. Adipose tissue as a source of hormones. **The American Journal of Clinical Nutricion**, v.45, p. 277-282, 1987.