

COUNTRY: BRAZIL**SESSION:** ANIMAL GROWTH AND DEVELOPMENTAssociation of microsatellite CSFM50 with weaning weight in Hereford beef cattle¹R.M.C.Bressel⁴; L.C.A.Regitano², F.L.B. Toral³; H.L.M. Moreira²¹Part of doctoral Thesis of 1st author – UFPel. Supported by ANC-Herd Book Collares/CAPEs – Brazil.²Embrapa Pecuária Sudeste – São Carlos/SP³Programa de Pós Graduação em Zootecnia, UNESP – Jaboticabal/SP;⁴ Programa de Pós Graduação em Biotecnologia Agrícola, Cenbiot, UFPel, Caixa Postal 354, Pelotas/ RS, CEP 96010-900, Brazil**ABSTRACT**

Molecular markers for production traits have been intensively investigated in cattle for application in marker-assisted selection program (MAS). In beef cattle, the microsatellite CSFM50 (located in the chromosome 2) had been correlated with weight gain from weaning to maturity. The objective of this study was to determinate the influence of microsatellite CFM50 polymorphism on birth weight (BW), weaning weight (WW) and yearling weight (YW) in a Hereford beef cattle herd. There were no influence of CSFM50 on BW and YW ($P>0.1$), but significant effects were observed on WW ($P=0.03$), with positive effects associated to 180/184 genotype. The analysis of the results suggest that 180bp allele can be associated with highest WW and 176bp can be associated with lower WW at this Hereford herd.

KEYWORDS

Molecular Markers, CSFM50, Hereford cattle, weaning weight

INTRODUCTION

The Hereford herd in Rio Grande do Sul comprises 4% of total beef cattle breed. These animals are recognized to produce quality meat in pasture. They are rustic and docile, with high fertility index. This breed is spread worldwide, for example, South Africa, Argentina, Brazil, Canada, Chile, Denmark, Sweden, USA and many others.

Meat production traits have a phenotype variation, with many genes in control, reducing genetic selection efficiency, mainly with sires. Selection for meat production traits is currently done through EPDs, progenie test or other tests that measure the progenies value (Kepler, 1997).

Molecular markers are defined as every molecular phenotype originated from genic expression, as isoenzymes or DNA specific fragments (Ferreira & Grattapaglia, 1998). Markers are located near the desired gene, but not necessarily define it (McMillan, 2001). Hypothesis used to locate quantitative trait loci (QTLs) for production traits is that some polymorphism markers are located near and linked to a QTL. So, in a heterozigote parental, it is possible to associate the variation in a quantitative trait with marker genotype in its majority progenie.

Potential to improve the selection intensity and reduce generation intervals are the major expected benefits from marker assisted selection (MAS). DNA genotyping

could be done in early animal development and independent of gender (Georges, 2001).

Stone et al., 1999 have done a primary screen in bovine genome and found 238 microsatellites associated with carcass quantitative traits. Casas et al., 1998 refined bovine chromosomal around double muscle locus and analyzed its effects in birth and carcass traits. These researches suggested that it is located 3 cM to centromeric region on chromosome 2 (BTA2).

In beef cattle, the microsatellite CSFM50, located in the BTA2 at 10,9 cM (Moore et al., 1994) had been correlated with weight gain from weaning to maturity in a Angus and Brahman reference family (Davis & Taylor, 1995) and with maturity weight in Canchim animals, a Charolais and Nelore crossbreed (Gasparin, 2002).

MATERIALS AND METHODS

This experiment was conducted with 270 animals, born in 2001, from a commercial herd in the south region of Rio Grande do Sul. The DNA was extracted from white blood cells according to procedures describe by Regitano & Coutinho (2001).

Animals were scored for a microsatellite locus CSFM50. Its sequence are CSFM50 (1) 5' AGT TCT CCT CTT GAT TTC AGT AAC 3' and CSFM50 (2) 5'CCT ACT TCC TGC CTT TGT AGC ATA 3'. Genotype identification was done by PCR in 50mM KCl, 1.5mM MgCl₂, 20mM Tris-HCl, pH 8.4, 0,4mM forward primer labelled with fluorescein, 0,4mM reverse primer, 0.2mM dNTP and 0,5units Taq DNA polymerase and followed by resolution in A.L.F. DNA SequencerTM. Genotype effects for birth weight (BW), weaning weight (WW) and yearling weight (YW) were studied by a model with fixed effects of genotypes, sire, month of birth, sex, nutrition treatment by least squares method. Linear and quadratic effects of age of dam were included as covariable only for BW and WW.

RESULTS AND DISCUSSION

The microsatellite CSFM50 was associated with weight gain from weaning weight to yearling weight in a reference family (Davis & Taylor, 1995). The objective of the present study was to correlate CSFM50 genotypes with weight at different ages in Hereford herd. The F-statistic indicated no influence of CSFM50 on BW and YW ($P>0.1$). These results do not agree with Gasparin (2002), that find CSFM50 polymorphism associated with yearling weight in Canchim animals. In this work significant effects were observed on WW ($P=0.03$), with positive effects associated to the 180/184 genotype. Table 1 show statistic test. Animals with this genotype were heavier, but do not differ from others genotypes with allele 180 bp (Table 2). The analysis of the results suggests that 180 bp allele can be associated with highest WW, because these animals are heavier than animals without this allele. The allele 176 bp can be associated with lower WW at this Hereford herd. These results suggest a QTL for WW near this microsatellite. Production traits and molecular markers association studies are important to implement MAS. These associations allow measuring animal genetic value earlier, reducing time needed to introduce a sire in genetic improvement program, allowing to reduce the time between generations. For the implementation of MAS in our herds more knowledge of these associations is necessary, and in this sence, more studies in this area should be done.

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