



Candidate genes for carcass traits in a tropical-adapted Brazilian composite beef breed

G. Veneroni-Gouveia¹, P.C. Tizioto², S.L.C. Meirelles³, A.C. Santiago²,
M.M. Alencar⁴ and L.C.A. Regitano⁴

¹Colegiado Acadêmico de Zootecnia, Universidade Federal do Vale do São Francisco, Campus Ciências Agrárias, Projeto de Irrigação Nilo Coelho, Petrolina, PE, Brasil

²Departamento de Genética e Evolução, Universidade Federal de São Carlos, São Carlos, SP, Brasil

³Departamento de Zootecnia, Universidade Federal de Lavras, Campus Universitário, Lavras, MG, Brasil

⁴Embrapa Pecuária Sudeste, São Carlos, SP, Brasil

Corresponding author: G. Veneroni-Gouveia
E-mail: gisele.veneroni@univasf.edu.br

Genet. Mol. Res. 14 (4): 16667-16674 (2015)

Received August 15, 2015

Accepted October 4, 2015

Published December 11, 2015

DOI <http://dx.doi.org/10.4238/2015.December.11.14>

ABSTRACT. Backfat thickness (BFT) and ribeye area (REA) are important production traits but, because they are measured late in the animal's life, they have not been efficiently included in breeding programs. The aim of this study was to evaluate whether single nucleotide polymorphisms (SNPs) mapped to the leptin, *PPARGC1A*, *PSMC1*, *CRH*, and *FABP4* genes, which influence BFT and REA in Canchim cattle, a composite beef breed (5/8 Charolais + 3/8 Zebu). BFT and REA phenotypic records were obtained by ultrasound measurements from 18-month-old animals. All SNP markers were genotyped by restriction fragment length polymorphism-polymerase chain reaction. Restricted maximum likelihood analysis revealed that the non-synonymous SNP located in exon 2 of the *FABP4* gene has an additive effect on BFT ($P \leq 0.05$). Significant allele substitution

effects showed that the substitution of G by A may lead to a decrease of 0.1055 mm in mean BFT. This information can be used for inclusion of this trait-associated marker in commercial SNP panels.

Key words: Backfat thickness; Ribeye area; Canchim cattle ;
Single nucleotide polymorphism