

Evaluation of *TFAM* and *FABP4* gene polymorphisms in three lines of Nellore cattle selected for growth

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ABSTRACT. We analyzed the polymorphisms *TFAM* *Hae*III, *TFAM* *Mbo*I and *FABP4* *Msp*A1I in three Nellore lines selected for growth in order to evaluate how selection affects the frequencies of these polymorphisms and evaluate their association with growth and carcass traits in Zebu cattle. Birth, weaning and yearling weights, rump height, longissimus muscle area, backfat thickness, and rump fat thickness were analyzed. The sample was constituted of animals from two lines selected for yearling weight (NeS and NeT), and a control line (NeC), established in 1980, at the São Paulo Instituto de Zootecnia. Two hundred and seventy-two heifers were genotyped for *TFAM* gene SNPs, and 325 heifers were genotyped for the *FABP4* SNP. High frequencies were observed for the alleles A (*TFAM* *Hae*III), C (*TFAM* *Mbo*I) and C (*FABP4* *Msp*A1I). Significant differences in allele frequencies between NeS and NeT were observed for the *TFAM* *Hae*III, and between the line NeT and lines NeC and NeS for the *FABP4* *Msp*A1I SNP. Five haplotypes were observed for the two polymorphisms in the *TFAM* gene, haplotype AACC being the most frequent. None of the markers

evaluated separately or according to haplotype was significantly associated with the growth and carcass traits. The low frequencies of alleles that are associated with high marbling scores and thick subcutaneous fat in taurine breeds might explain the low means for these traits in Nellore cattle.

Key words: Beef cattle; QTL; SNP; Marker assisted selection; Zebu