Association of single nucleotide polymorphisms with carcass traits in Nellore cattle

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ABSTRACT. The association between two single nucleotide polymorphisms (SNPs), *T945M* and *UCP1SNP1*, with hot carcass weight (HCW, kg, N = 618), longissimus dorsi muscle area (REA, cm^2, N = 633), and backfat thickness (BF, mm, N = 625), measured in Nellore cattle in Brazil, was evaluated. Likelihood ratio tests were used to evaluate reduced (fixed effects of general mean, contemporary group, yearling weight, age at slaughter, and random effect of infinitesimal genetic value) and full model (reduced model effects plus quantitative trait locus effects). Additive and dominance effects were tested for each SNP. Genotypic and gene frequencies were also obtained for the SNPs and a descriptive phenotype analysis was made. Mean values for HCW, REA and BF were equal to 288.13 ± 0.55 kg, 73.14 ± 0.27 cm^2, and 4.28 ± 0.07 mm, respectively; the coefficients of variation were 4.74, 9.24, and 42.43%, respectively. Gene frequencies for *T945M* and *UCP1SNP1* were f(C) = 0.89, f(T) = 0.11, f(C) = 0.81, and f(G) = 0.19. The SNP *T945M* had a genotypic frequency of only three animals for

TT genotype. Additive effects were observed for *T945M* on REA and BF, while *UCP1SNP1* affected HCW and BF. Based on the significant additive effects of the SNPs and the gene frequencies that we found, we can expect genetic gains with marker assisted selection.

Key words: *Bos indicus*; Leptin; Linkage disequilibrium; Markers; UCP1