



Protein synthesis and degradation gene SNPs related to feed intake, feed efficiency, growth, and ultrasound carcass traits in Nelore cattle

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ABSTRACT. We looked for possible associations of SNPs in genes related to protein turnover, with growth, feed efficiency and carcass traits in feedlot Nelore cattle. Purebred Nelore bulls and steers (N = 290; 378 ± 42 kg body weight, 23 months ± 42 days old) were evaluated for daily feed intake, body weight gain (BWG), gross feed efficiency, feed conversion ratio, partial efficiency of growth, residual feed intake (RFI), ultrasound backfat, rump fat, and ribeye area. Genotypes were obtained for SNPs in the growth hormone receptor (GHR-1 and GHR-2); calpain (CAPN4751); calpastatin (UoGCAST); ubiquitin-conjugating enzyme 2I (UBE2I-1 and UBE2I-2); R3H domain containing 1 (R3HDM1-1, -2, -3, and -4), ring finger protein 19 (RNF19); proteasome 26S subunit, non-ATPase, 13 (PSMD13); ribosomal protein, large, P2 (RPLP2); and

isoleucine-tRNA synthetase 2, mitochondrial (IARS2) genes. Allelic substitution, additive and dominant effects were tested and molecular breeding values were computed. CAPN4751, GHR-1 and -2, IARS2, R3HDM1-4, and UoGCAST were found to be normally segregating polymorphisms. Additive and dominance effects were observed on BWG, feed efficiency and carcass traits, although dominant effects predominated. Significant allelic substitution effects were observed for CAPN4751, GHR-1 and -2, and UoGCAST on BWG, gross feed efficiency, RFI, and carcass traits, under single- or multiple-marker analyses. Correlations between molecular breeding values and phenotypes were low, excepted for RFI, based on allelic substitution estimates obtained by stepwise linear regression. We conclude that SNPs in genes related to protein turnover are related to economically important traits in Nellore cattle.

Key words: *Bos indicus*; Marker-assisted selection; Protein turnover; Molecular breeding value; Residual feed intake