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RESTRICTION FRAGMENT LENGTH POLYMORPHISM IN CALPAIN (CAPN2) GENE IN CROSSBRED CATTLE [1]

POLIMORFISMO DOS FRAGMENTOS DE RESTRIÇÃO NO GENE CALPAÍNA (CAPN2) EM BOVINOS MESTIÇOS

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With advances in molecular genetics have been possible to predict the genetic value of the animal, in particular its potential to transmit desired characters to their offspring, including characters difficult to evaluate or with low heritability, as is the case of the meat tenderization. It is known that *Bos taurus indicus* features differences in meat tenderization, being assigned this variability to their lowest proteolysis post-mortem, as result of high activity of calpastatin. This inhibitor decreases the activity of calpain, which are the enzymes responsible for the degradation of muscle fibers during the maturation of the meat. Moreover, there were previously observed differences in the frequencies of allele A of calpain among European breeds (Hereford, Aberdeen Angus and Holstein) and *Bos taurus indicus* (Gir, Guzerá and Nelore). This variability has been related to tenderness of meat, as cattle with *Bos taurus taurus* origin have more tender meat than *Bos taurus indicus*, showing small values of shear force. One explanation is that the $Capn2^{A}$ product could confer greater proteolytic activity than the encoded by the allele $Capn2^{B}$. If allele *A* is associated with tender meat, it will be possible the early identification of the animals that have the potential to produce meat with qualities that attend the needs of the consumer market, in order to add economic value to the final product of the animal production chain. For this reason, biochemical and genetic studies related to calpain and calpastatin systems have been considered promising for the clarification of the physiological changes that occur in muscle structure during the period post-mortem, whose results have contributed to the improvement of meat quality. The objectives of this study were to investigate the RFLP in calpain (*Capn2*) gene and its relation with meat tenderization in 252 crossbred (*Bos taurus taurus x Bos taurus indicus)*. The analyses were carried through by PCR-RFLP technique using the restriction enzyme *Hha*I. The meat tenderness analysis was evaluated in *Longissimus dorsi* by Warner-Bratzler Shear Forcer. The data of shear force (SF) were analyzed by model that included genotype effect (AA, AB, BB), genetic group and, as a covariate, the age at slaughter. The allele *A*, considered the most favorable for meat tenderization, was more frequent in Angus x Nelore (AxN) than Red Angus x Nelore (RxA), whose frequencies were 0,4697 and 0,3975, respectively. Significant effects were observed ($p<0.05$) of genetic group and genotype in FC. The average value of FC estimated for RxN was 32.24%, significantly ($p<0.05$) lesser that of AxN. All the averages of FC estimated for the genotypes AA, AB and BB, in two genetic groups differed ($p<0.05$) and were, respectively, 3.74, 5.43 and 7.43 in AxN and 2.64, 4.21 and 5.32 in RxN. The results obtained show that such polymorphism can assist the identification of animals for meat quality in crossbred *Bos taurus taurus x Bos taurus indicus*.

Key words: molecular marker, cattle, meat tenderization