CKM GENE VARIANTS IN THE RACING AND CUTTING LINES OF QUARTER HORSES

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As a result of different selection objectives, different segments of the Quarter Horse breed currently exist, including the cutting line and racing line. Animals of the racing line show a better performance in short-distance races than any other line or breed. The cutting line is destined for functional tests, exploring skills such as agility and obedience, traits that are important for cattle management in the field. The *CKM* gene encodes a muscle isoenzyme of creatine kinase found exclusively in striated muscle, which is involved in important energy processes in the cell, especially the generation of adenosine triphosphate (ATP) during the first seconds of intense exercise. Using a sample of 296 Quarter Horses of the racing line and 68 animals of the cutting line, the objective of this study was to compare the allele and genotype frequencies of the *CKM* SNP g.15884567A>G between a random subsample of animals of the cutting line (n = 20) and animals with extreme phenotypes for racing performance (n = 20 per extreme phenotype). The genotyping of *CKM* SNP was performed by direct sequencing of PCR products. The g.15884567A>G SNP of the *CKM* gene was found to be polymorphic in Quarter Horses. However, analysis of the probability of occurrence of the alternative allele of this polymorphism based on odds ratio (OR), 95% confidence interval and *p*-value calculated by the test, indicated that this variant is not associated with the different lines (OR = 0.7235, 95%CI = 0.1123 – 3.3761, *p*-value = 0.7434) or with the contrasting groups of the racing line (OR = 1.1149, 95%CI = 0.2197 – 5.7905, *p*-value = 0.8764). On the basis of their importance for muscle energy metabolism during intense and short exercises, it was expected that *CKM* gene variations would play a major role in the racing performance of Quarter Horses, or even that they were associated with different lines of the breed. However, the involvement of the *CKM* gene in aerobic metabolism through its interaction with IRF-1 may explain the lack of a significant association of this SNP with racing performance in the breed studied here.

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