Bovine beta-casein allele A1: the source of beta-casomorphin 7 peptide, prevalence in Holstein bulls and its association with breeding value

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Epidemiological studies suggest that beta-casein (CSN2) A1 protein variant might be one of the risk factors in the etiology of human diabetes and ischemic heart disease. It is hypothesized that during enzymatic digestion beta-casomorphin-7 (BTN7) peptide is released exclusively from CSN2 A1 variant and therefore it is thought to be harmful for human health. However, more research is needed to better understand the basis of this assumption: 1. to quantify BTN7 in digested milk, 2. to evaluate the frequency of the A1 allele in dairy cattle and, 3. to find out whether CSN2 is associated with milk production. In order to tackle these problems we determined the CSN2 genotype of 177 Holstein cows and 478 Holstein bulls by the use of the PCR-ACRS method. Eighteen cows in the same lactation period, but of different CSN2 genotypes were chosen to measure BTN7 content (by ELISA test) in the 30th, 100th and 200th day of the first lactation. Significant differences in BTN7 concentration between homozygotes and as well as between A1A2 and A2A2 cows were found. The frequency of the undesirable A1 allele was relatively high - 0.35. A linear regression model was used for testing the association between the polymorphism and breeding values for production traits. It was observed that the allele coding the A2 protein variant increases bulls' breeding values for milk protein yield and decreases breeding values for fat percentage. Although there are no clinical studies confirming the harmful effect of BTN7 on human health, it seems that selection for the A2 allele at CSN2 locus may be beneficial as it leads to increased protein yield, and at the same time, decreases the risk for human health.

Relative quantification of p53 and VEGF-C gene expression in canine mammary tumors

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Breast cancer is one of the most common cancers through the world that ranked second with respect to its mortality rate. If malignant cancer detected and cured in its initial stages, lifespan in more than 90 percent of patients can be increased. Because of scientific and ethical limitations of conducting researches on human diseases, it is necessary to establish suitable animal models for these purposes. The dog is an appropriate model for studying breast cancer. The main goal of current study was to optimize SYBR Green based quantitative Real-time PCR (qRT-PCR) approach to measure relative expression levels of p53 and VEGF-C genes in normal and cancerous specimens. Eight normal mammary glands and 11 mammary gland tumors (including 7 benign and 4 malignant mammary tumors) were used in this study. Total RNA was extracted and p53, VEGF-C and B-Actin genes fragments were reverse transcribed. Real-time PCR assay were used for quantification of mRNA expression levels. Results were statistically analyzed using Student t-test. Findings showed that all of these three genes were expressed in both normal and cancerous samples but VEGF-C expression in the malignant mammary tumors was much higher than in the benign mammary tumors or normal mammary tissue ($P<0.001$). In contrast to the normal samples, 9%, 18% and 73% of malignant samples had shown higher, equal and lower of p53 gene expression, respectively.