

INVESTIGATING THE ADDITIVE AND DOMINANCE EFFECTS OF STAT5A GENE ON PRODUCTION TRAITS AND MILK COMPOSITION OF DAIRY CATTLE IN HOLSTEIN CATTLE

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STAT5A gene has an important role in intracellular signal transduction, in epithelial cells including breast and uterine (3). *STAT5A* protein has been studied as one of the regulators of milk proteins gene expression in mammary tissue (2). The SNP12195 in exon eight of the *STAT5A* gene has showed to be related to the percentage of milk fat and proteins (1). In this study we have investigated the incremental effects of *STAT5A* genes on production traits and milk composition of industrial Holstein herds in Isfahan. 355 animals from five different herds were randomly selected and the genomic DNA was extracted from blood using Miller salting method. RFLP-PCR performed on SNP12195 in order to obtain all the polymorphisms in this locus. The PCR products then digested with *BstEII* enzyme resulted in three different genotype including, TT, TC, CC. Linear regression analysis revealed significant increased in milk production with TT genotype, however the percentage of milk fat and protein significantly decreased ($P < 0.05$). In this study the dominance effect for all the studied traits was not significant ($P > 0.05$) however, the additive effects were showed to be present at genomic levels of the traits. The results indicate that the TT genotype has improving effects on quantitative traits of milk. In addition, the TC genotype has increasing impact on both milk production traits and the percentage of milk fat and proteins but it is not the dominant genotype in our cattle. According to this research we recommend that Using CC genotype could have increasing effects on milk fat and protein percentage in Holstein dairy cows.

Keywords: Additive Effects- Dominance- *STAT5A*

References

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