

## **Abstract**

**In this study to determine the evolution effects on the variation of FASN gene nucleotide sequence, and its association with variety of economic traits including milk production, Calving interval and number of services per conception, 38 tail-vein blood samples were taken from Holstein cattle. Genomic DNA purification was performed by phenol-chloroform extraction, according to standard protocols. Polymerase chain reaction (PCR) for the amplification of a 750 bp- portion of the FASN gene was performed using specific primers targeting at the sequence between exon 37-39 of FASN gene. After amplification and purification, PCR product were sequenced. The nucleotide sequences of the target gene were aligned with genomic sequences of variety of eukaryotes in available databases. Evolutionary and phylogenetic tree analysis was performed by using MEGA6 software. Degree of substitution and substitution pattern were analyzed using maximum-likelihood (ML) and Phylogenetic trees were built using Neighbor-Joining method. Bioinformatics analysis results showed that the percentage substitution of purines was more than pyrimidine. The numerical value of  $d_N/d_S$  was 1/258, indicating positive selection during evolution of these genes. This selected type resulted in the development of new varieties, new proteins and also stabilizes their performance during the evolution and advance progress toward their performance has been purified, which caused the conversion of non-coding regions of a gene coding gene. Phylogenetic tree for the genes in different organisms show that in the mammals, buffalo and Bison bison, Cats and Cheetahs more closely (%98, %57). In FASN gene place of Holstein cows 58 polymorphism is identified. Of this number, SNPs of positions g.16593A>G, g.16670C>A and g.16776C>T with milk production traits, SNPs of positions g.16524G,C,T >A, g.16830G,C,T>A and 16833A,T>G with Calving interval traits and snps g.16594A,C>G and g.16811A,T>G with number of services per conception trait, showed a significant relationship ( $p>0.05$ ). Taken together these data suggest that the observed SNP within FASN gene could be used as molecular markers in addition to milk production traits for reproductive traits such as calving interval and number of services per conception used in Holstein Cattle.**

**Key words: FASN gene, sequencing, polymorphism, Phylogeny, Holstein cattle.**



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**Study of FASN gene polymorphism and  
it's association with milk production,  
calving interval and number of services  
per conception traits in Holstein cattle**

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