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Title
Bioinformatic analysis of FEZL gene sequence in Sistani cattle population and its crossbreds

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Abstract:

FEZL is one of the candidate genes associated with mastitis disease resistance in dairy cows. In the studies that were conducted in order to investigate the genetic variation in the FEZL gene locus and their relationship with milk somatic cell count (SCC). It is one of the common diseases in the population of dairy cows, which imposes a lot of economic losses on the farmer. The purpose of this research is to investigate the amount of different deletion and addition polymorphisms in the FEZL locus, to identify important variants related to milk composition, and to investigate the difference between pure and mixed breeds of Sistani and Holstein cows. In this research, 27 purebred Sistani and Holstein cows (10 from each group) and mixed Sistani with Holstein (7) from the Sistani Cattle Research Center and native herds of the Sistan region were randomly selected and blood was taken from the jugular vein. . During blood sampling, a milk sample of 30 ml was taken from each animal to analyze the characteristics of milk. Extraction of total DNA from blood samples was done by optimized saline method. Then the extracted DNA was electrophoresed on a 0.5% agarose gel and the samples that were of good quality were used for the PCR amplification reaction. To amplify the 229 bp fragment of the FEZL gene locus, a specific primer pair was used with temperature cycling in a thermocycler. Sequencing was done with Chromas software in fasta format and low-quality sequences were removed. The next step after removing the areas is the production of a single thread from the back-and-forth sequence, canting production was done using cap3 software. Alignment of 27 samples was done with MEGA software in pairs and multiples. 4 samples were removed due to unfavorable alignment and 23 samples were saved for further analysis. In the transitional and crossover substitution matrix of Holstein FEZL gene sequence, the highest percentage of cytosine to thymine conversion was in Cystani, Adenine to Cytosine conversion and Cytosine to Thymine conversion in all cases, and in all cases, Adenine to Thymine and Guanine to Thymine conversion were the lowest. The highest divergence within breeds was related to Holstein and Sistani mixes (0.15), the lowest divergence was for Sistani breed (0.044) and in different breeds, the highest between mixes with Holstein (0.126) and the lowest between Sistani was with mixed people (0.012). The effects of marker polymorphisms on milk fat percentage, lactose percentage, milk protein percentage and fat-free dry matter percentage traits had a significant effect on the marker at the position of 97 base pairs of the first exon of the FEZL gene. Therefore, despite different polymorphisms and the amount of genetic distance that exists between and within breeds, the breeding value of livestock will improve if marker information is used.

Keywords: FEZL gene, Gaussian, mastitis, polymorphism, SNP