

GENETIC VARIATION ANALYSIS OF ATPASE GENE AND ITS ASSOCIATION WITH MILK COMPONENTS IN CATTLE

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ABSTRACT

There are huge number of cattle breeds or types are present all over the world and employed in different activities. The present study aimed to identify genetic variations and SNPs in mtDNA ATP6/8; among Holstein, Local Iraqi cattle and their crosses. The primer used in this study amplified 929-bp fragments from ATP6/8 gene. The results showed the presence of 8, 1 and 13 polymorphic sites leading to the construction of 5, 2 and 2 different haplotypes for Holstein, local and crosses respectively. Haplotype and nucleotide diversity were 0.576, 0.500 and 0.4786 and 0.00164, 0.00062 and 0.00763 respectively. Neighbor-joining trees were constructed using 34 samples showed that all studied cattle appeared into haplotype 1(H1), while Holstein also appeared in H4, H5, H6 and H7. Local breed included in H2 and the crosses in H3. AMOVA showed that variation within breed (between individuals was higher (85.83%) than between breeds (14.17%). Neutrality test both Tajim's D and Fu's Fs revealed that Holstein recorded highest negative values (-1.98343 and -1.18604 respectively). Whereas, the crosses cattle recorded positive values (0.91273 and 6.95086 respectively). The local breed showed positive and negative values near to zero (-0.61237 and 0.17185 respectively). Different haplotypes within Holstein breed associated significantly with fat%, lactose% and SNF%. Haplotypes 5 and 7 recorded highest percentages of fat, lactose and SNF when compared to other haplotypes. However, there were no such association within local or cross cattle. In conclusion, the identification of genetic variations and SNPs in cattle mitochondrial genes like ATP6/8 agene is of great interest because it has significant association with play important milk components and it can be recognized as a genetic marker for milk yield in cattle.

KEYWORDS: Cattle, Atpase, Mtdna, Milk Components

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