

## Identification of microRNA bind to multiple gene associated with intramuscular fat deposition

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The factor that regulates gene expression has a direct effect on the protein or phenotype variation. Only about 2% of the genome codes for proteins, and the majority of the genome consists of non-coding RNAs that play essential roles in a variety of biological processes. miRNAs are a class of small ncRNAs, 22nt in length, that play a role in post-transcriptional regulation by targeting the 3'UTR of mRNA leading to mRNA degradation and translational repression. A given miRNA can bind to multiple non-coding regions and a given target can be regulated by multiple miRNAs. The seed region is located 2-7nt from the miRNA 5'-end, the miRNA target sites are more conserved than other regions of the 3'UTR, which can be attributed to many factors such as mutation, structural variation, gene conversion. Bovine intramuscular fat(IMF) is the most important determining the quality of meat, so approaches to improve IMF deposition are significant. Several studies have reported that by increasing the deposition of IMF in bovine, the expression level of mRNAs related to glycerolipid synthesis was up-regulated. Furthermore, the mRNA abundance of GPAM gene showed the strongest correlation with IMF content. In a previous study, we reported that 4 miRNAs target the 3' UTR of GPAM and also identified bta-miR-375 and bta-miR-2479 as multiple miRNAs targeting the same region. Therefore, the aim of this study is to verify the binding ability of four miRNAs to the 3' UTR of the GPAM gene and to identify their multifunctional role in adipocytes. As a result, we identified four miRNAs that bind to the GPAM 3'UTR, and the seed region of miR-375 is highly conserved. Furthermore, we demonstrated that miR-375 not only upregulates the GPAM gene and genes related to lipid metabolism, but also promotes the accumulation of lipid droplets in 3T3-L1 cells. In conclusion, our results suggest that miR-375 is a multifunctional regulator that regulates multiple genes involved in lipid metabolism, which may contribute to obesity research as a biomarker.