Abstract

The AMPK gene family in bovine has been seen to play a primary function in regulating cellular energy and metabolism. While their function has been identified, the difference between expression of those genes has not been accounted for. Changes in gene expression can determine any fluctuations in the function of cellular metabolism in the bovine AMPK gene family, such as high and low feed efficiency. DNA methylation is a method that is known to alter gene expression. The expectation is that less methylation will be found in high feed efficient cattle, because more genes will be expressed and therefore cellular function will be higher. Through the use of an online database, the identification of methylated regions in the bovine genome was determined. By the use of polymerase chain reaction the selected gene regions were amplified to be more readily studied. A simple PCR couldn't determine the methylated and unmethylated regions of the gene; therefore the DNA samples were treated to allow identification of methylation. A gel electrophoresis allowed for the separation and verification of methylation in each DNA sample. This was further studied by determining what specific regions of the DNA sequence are methylated throughout the use of restriction enzyme, also known as COBRA. Gel results will be analyzed to determine the presence of methylation between samples. Depending on the results, differences in methylation between high and low feed efficient cattle can be used to selectively breed these animals to be high feed efficient, thus lowering the costs of feed while increasing production.