Dysregulation of MicroRNA Expression in Diabetes

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The purpose of this study was to determine the potential changes in the expression of microRNAs -155, -146a, -29a, and -21 in macrophages cultured under diabetic conditions. MicroRNA (miRNA) are gene regulators that bind to target messenger RNAs to inhibit the synthesis of protein. These specific miRNAs have been associated with the inflammatory response in other chronic inflammatory diseases. It was hypothesized that cells exposed to hyperglycemia exhibit altered expression levels of the target miRNAs at resting conditions. Further stimulation by a bacterial product, such as lippopolysaccharide (LPS), further induce the altered expression of these miRNAs, leading to an increase in the inflammatory response. The study was conducted by stimulating eight groups of THP-1 cells : control, LPS, high glucose, high glucose and LPS, S100B, S100B and LPS, high glucose and S100B, and high glucose, S100B and LPS. The expression of the target microRNAs was relatively quantified to the housekeeping gene RNU48 using a FirePlex miRSelect Assay and real-time PCR. The results show that LPS stimulation upregulates all the targeted microRNA's expression. Hyperglycemic stimulations cause an upregulated expression of microRNAs-155 and -21. The hyperglycemic stimulations in combination with LPS upregulate the expression of microRNAs -155 and -21 as well. These results shed light on the mechanisms of these targets and their possible therapeutic properties. The results suggest that the dysregulation of microRNAs -155 and -21 play a role in the inflammatory response in diabetes.

Awards Won:

Third Award of $1,000