Evaluation of miR-146a, miR-155, NF-κB, TRAF6 and IRAK1 mRNA expression in the aorta of diabetic male rats

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Abstract

Introduction: Diabetic angiopathy mechanism is complicated. Many parts of this mechanism has remained unknowed. NF-kB presence as a factor involved in diabetic inflammation has been illustrated in majority of studies. In addition to, some of miRNAs including miR-146a and miR-155 as regulating elements are noted in NF-kB signaling pathway, recently. Therefore, the present study designed to evaluation miR-146a and miR-155 expression in aorta in probable signaling alters result from diabetes. Also this investigation evaluated IRAK1 and TRAF6 mRNA expression, ingredient of feedback loop between NF-kB, miR-146a and miR-155.

Methods and Meterials: Fourtheen male wistar rats were randomly divided into control and diabetic groups (n=7 in each). Diabetes was induced by a single injection of streptozotocin (55 mg/kg; i.p.). The gene expression of miR-146a, miR-155, NF-kB, IRAK1, and TRAF6 were determined by real time PCR.

Results: The expression of miR-146a was down-regulated in diabetic aorta when compared with the control group ($p < 0.05$). The mRNA expression levels of miR-155, NF-kB, TRAF6 and IRAK1 also increased in the diabetic rat aorta when compared with their control counterparts ($p < 0.01$ for all comparisons).

Conclusion: These results suggest that it is possible miR-146a down-regulation result from hyperglycemic products lead to IRAK1 and TRAF6 activity and flowing diabetic aorta inflammation, by miR-146a-NF-kB likely negative feedback loop. Furthermore miR-155 up-regulation can be inflammatory process provoker, because of miR-155-NF-kB probable positive feedback loop.

Key words: Diabetes, miR-146a, miR-155, NF-kB, Aorta