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Letter to Editor

The MiR-29 Family as Novel Therapeutic Option for Retroviral Infection

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Dear Editor;

MicroRNA is a small non-coding RNA (about 18-22 nucleotides) molecules which regulate post-translation process in eukaryotic cells by interfering with messenger RNAs (mRNAs); There are 1900 different microRNAs which can cause silencing different gene expression in humans [1]. According to the review of literatures, expression levels of microRNAs are alternated during infection which can be used as diagnosis biomarker for monitoring of treatment [1-2].

The miR-29 families in human include hsa-miR-29a, hsamiR-29b-1, hsa-miR-29b-2, and hsa-miR-29c which are coded by MIRN29 in chr 7q32.3 (position 6651878-6651943) in human [3]. The miR-29 family is regulated by extracellular matrix, cell proliferation, differentiation, apoptosis and inflammatory process of human [3-4]. In recent years, it is suggested that the role of the microRNA 29 family in retroviral pathogenesis particularly HIV-1, HTLV-1 and HCV infections is significant. There are serious limited information about the potential roles of the miR-29 family in retroviral pathogenesis. The aim of this study was to report the potential role of the miR-29 members on retroviral pathogenesis in present short letter.

The PI3K-Akt signaling pathway is known as an important signaling pathway during retroviral infection because of its role in cell death and survival.

Initially, the microRNAs influenced the PI3K-Akt signaling pathway which were obtained by searching in micro-RNA databases including DIANAmT, miRanda, miRDB, miRWalk, RNA hybrid, PITA, mirtarget, RNA22, PICTAR5 and Targetscan. The microRNAs influenced seve-ral genes of PI3K-Akt signaling pathway and were selected for subject study. On the other hand, we performed a systematic search of original papers to provide microRNAs reported based on practical study and to compare with our results.

This investigation showed that, there are miR-155, miR-125a and miR29 which are common between our bioinformatics and previous published papers. Then, the expression levels of the microRNAs (miR-155, miR-125a and miR29) are evaluated in differentially expressed genes (DEGs) analysis using Gene Expression Omnibus (GEO) databases. We noted that expression levels of the miR-29 are down-regulated in retroviral infection compared to healthy individuals (Accession numbers: GDS4231, GDS4227, GDS4390).

Subsequently, we determined targets of the miR-29 members on the PI3K-Akt (KEGG pathway: hsa04151) for next evaluation (Figure 1).

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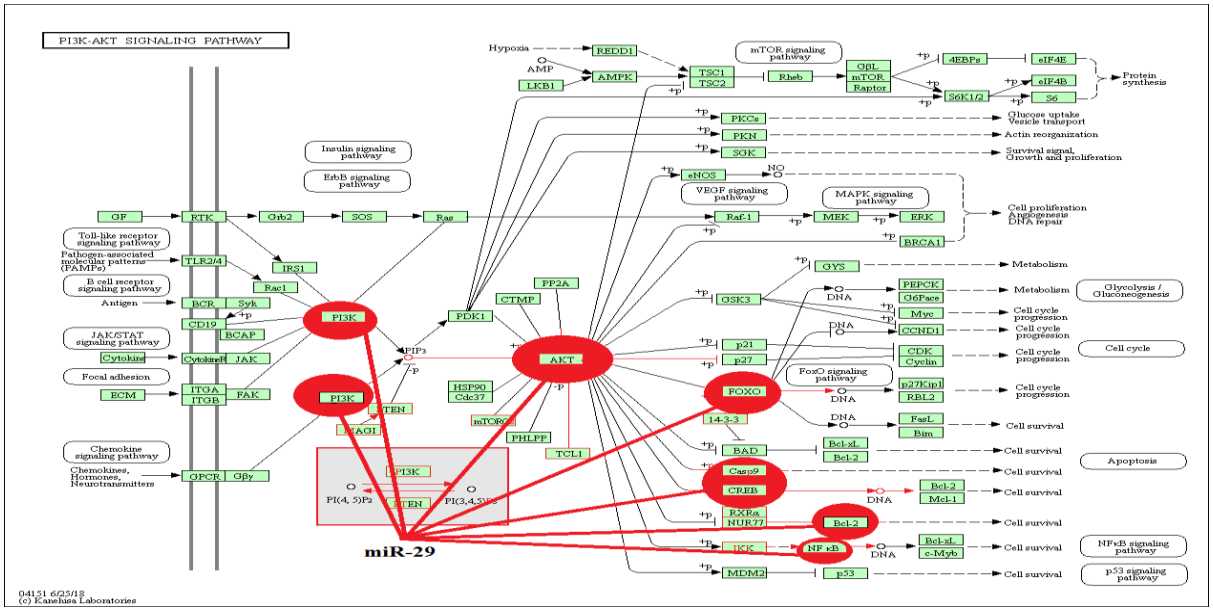


Fig. 1. The miR-29 targeting option in PI3K-Akt signaling pathway.

Finally, the miR29 family role in PI3K-Akt was constructed by Cytoscape software (Figure 2). We concluded that the miR-29 members influenced numerous genes in the PI3K-Akt particularly AKT3 which activated cascade for proliferation, death and pro-inflammatory process.

According to Adoro et al. microRNA-29 has antiviral effects which are induced by IL-21 throughout STAT3 signaling cascade. They found that HIV viremia declined due to up-regulation of MIR29 gene in mice [5]. McCaffrey et al have shown that the miR29 expression levels are reduced following administration of TGF-β during HCV infection. In addition, they reported that miR-29 can cause reduction of fibrosis and inhibition of HCV replication [6]. Saito et al. suggested that the expression levels of PI3K-Akt signaling pathway are upregulating in HTLV-1 infection caused by Tax oncoprotein which leads to cell proliferation and HTLV-1 replication; in which miR29 is down-regulate during HTLV-1 infection [7]. The miR-29 has critical role in regulation of apoptosis, cell proliferation and induction of pro-inflammatory response in response to intra-cellular pathogeneses; therefore, targeting of the miR29 expression by retroviral plays key role in cell proliferation and evading from immune-response [8].

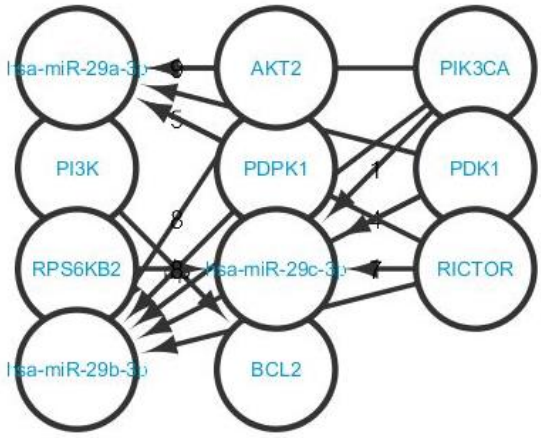


Fig. 2. The network interaction of the miR29 members and their outcomes.

In summary, we accomplished the in silico survive for determination of the miR-29 role in the PI3K-Akt signaling pathway using various microRNA online databases. In addition, the expression level of miR-29 during retroviral infection by GEO database information provide several documents which can imply potential role of the miR-29 family as novel therapeutic option against retroviral infection particularly HIV, HTLV-1 and HCV infection cases.

Conflict of Interests

None to declared.

Ethcal Considerations

The Ethics Committee of Mashhad University of Medical Sciences was approved the study.

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