



In silico analysis of the effective miRNAs regulating the rheumatoid arthritis

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Abstract: MicroRNAs or miRNAs are small endogenous non-coding RNAs that play critical role in several processes of the cell including: cell death, survival, apoptosis, differentiation, and disease. MiRNAs control the expression of their target genes by RNA silencing and post transcriptional regulation mechanisms [1,2]. Rheumatoid arthritis is a chronic autoimmune joint disease that finally leads to joint destruction and bone resorption [3]. Rheumatoid arthritis is a complex disease, and microRNAs could regulate the genes involved in the disease. The goal of this study was to predict the miRNAs that target the effective genes in signaling pathways of joint destruction and bone resorption which are involved in the rheumatoid arthritis. Therefore, we have used KEGG pathway database to derive intended genes related to the rheumatoid arthritis. The genes were then uploaded to miRWalk database, and the miRNAs which target 3'UTR of these genes were predicted. After this, these predicted miRNAs were sorted based on the miRNAs which target common sequences. Here, we have concluded that hsa-miR-5692a and hsa-miR-548c-3p are the miRNAs that all together target 18 of 21 genes, reported in KEGG pathway, which are involved in the rheumatoid arthritis.

Keywords: Rheumatoid arthritis; MiRNA; Computational analysis

References

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