

## عنوان مقاله:

In silico analysis of the miR-200 family target genes as diagnostic biomarkers in prostate cancer

## محل انتشار:

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## خلاصه مقاله:

Prostate cancer is one of the common cancers in men worldwide [1]. Because of the diagnostic limitations of serum prostate-specific antigen (PSA) for the screening of prostate cancer, the use of alternative biomarkers with higher specificity and sensitivity is desired [2]. Recent molecular biology advances have revealed the signaling pathways involved in the initiation and progression of prostate cancer [3]. The epithelial-to-mesenchymal transition (EMT) is a key process in transformation of local tumors into metastatic cancer [4]. microRNAs are non-coding small RNAs that play regulatory role in the post-transcriptional level. They affect several biological processes via simultaneous regulation of multiple target genes [5]. The miR-200 family, including miR-200a, miR-200b, miR-200c, miR-141, and miR-429 regulates the EMT process [6]. Hence, the miR-200 family and their target genes can be candidates for diagnostic biomarkers in prostate cancer. On the other hand, bioinformatics computational tools with the ability to predict microRNAs target genes in silico have been widely developed [7-9]. Aim and Methods: The aim of this study was to predict miR-200 family target genes in prostate cancer. This study was based on binding affinity of miRNAs to the 3' UTR of target gene and overall scores determined by various online prediction tools. To predict the most relevant gene as potential targets for miR-200 family in silico, we investigated the has-miR-141-3p, has-miR-200a, has-miR-200b, has-miR-200c, has-miR-429 target genes by online prediction tools, including the miRWalk2.0, miRanda, TargetScan and RNA22[9,10]. Result: Among the genes that were suggested by the prediction tools, prostate cancer relevant genes with higher affinity scores were selected. Then, the genes which were targets of more than two miRNAs of the miR-200 family were picked up. The study of interaction between the selected genes and the signaling pathways involved in prostate cancer revealed E2F3, DLC1, CTBP2 and EP300 genes for further in vitro analysis. Conclusions: According to bioinformatics studies, miR-200 family members and their specific target genes can be potential diagnostic biomarkers in prostate cancer. However, more experimental investigation is needed to validate their specificity and sensitivity for clinical applications.

## کلمات کلیدی:

Bioinformatics, miR-200 Family; Target Prediction; Prostate Cancer

