عنوان مقاله:

In silico analysis of the miR-۲۰۰ 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 [۱]. 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 [۲]. Recent molecular biology advances have revealed the signaling pathways involved in the initiation and progression of prostate cancer [۳]. The epithelial-to-mesenchymal transition (EMT) is a key process in transformation of local tumors into metastatic cancer [۴]. 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 [۵]. The miR-۲۰۰ family, including miR-۲۰۰a, miR-۲۰۰b, miR-۲۰۰c, miR-۱۴۱, and miR-۴۲۹ regulates the EMT process [۶]. Hence, the miR-۲۰۰ 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 [۷-۹]. Aim and Methods: The aim of this study was to predict miR-۲۰۰ family target genes in prostate cancer. This study was based on binding affinity of miRNAs to the ۳ UTR of target gene and overall scores determined by various online prediction tools. To predict the most relevant gene as potential targets for miR-۲۰۰ family in silico, we investigated the has-miR-۱۴۱-۳p, has-miR-۲۰۰a, has-miR-۲۰۰b, has-miR-۲۰۰c, has-miR-۴۲۹ target genes by online prediction tools, including the miRWalk۲.۰, miRanda, TargetScan and RNA۲۲[۹,۱۰]. 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-۲۰۰ family were picked up. The study of interaction between the selected genes and the signaling pathways involved in prostate cancer revealed E۲F۳, DLC۱, CTBP۲ and EP۳۰۰ genes for further in vitro analysis.Conclusions: According to bioinformatics studies, miR-۲۰۰ 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-۲۰۰ Family; Target Prediction; Prostate Cancer

لینک ثابت مقاله در پایگاه سیویلیکا: