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Integrative medical informatics approach for analyzing metabolic syndrome

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Dyslipidemia is one of the major forms of lipid disorder, which is characterized by increased triglyceride (TG), increased low-density lipoprotein-cholesterol (LDL-C) and decrease high-density lipoprotein-cholesterol (HDL-C) levels in blood. Recently, microRNAs (miRNAs) have been reported to involve in various biological processes, their potential usage as a biomarker as well as therapeutic marker in various diseases. Although searching disease related miRNAs is multifaceted due to expensive and time-consuming technologies with variable sensitivity and specificity. We used text-mining co-occurrence based approach for analyzing huge PubMed data to explore microRNA-lipid disease association. After retrieving and extracting information, construction of network was done by Cytoscape using edge-weighted tool to visualized significant associations. For miRNAs target predictions; existing network further extended with regulatory interaction network (RIN) by using CyTargetLinker Plug-in tool on Cytoscape. For biological process, associations of targeted genes were confirmed by gene ontology by using Biological Networks Gene Ontology BiNGO (GO) Plug-in tool on Cytoscape. We were text-mined 227 miRNA-disease associations including 148 miRNAs and four lipid diseases and five identifiers. The top 20 miRNA-disease was associated by Fisher's exact p-value 0.000034 to 0.033 and by TP score 0.0164 to 0.048. Significant GO terms were found on targeted genes for lipid, cholesterol, apolipoprotein and fatty acids. Present study could help future experimental studies, could walk around the biological functions and primary molecular mechanism of miRNAs in the development, progression, diagnosis and prognosis of lipid, cholesterol, and fatty acid disorders. However, additional computational tools and databases could provide broad perspective on relationships between miRNAs and disease.

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Effects of TRPC6 on invasibility of low-differentiated prostate cancer cells

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Objective: To study the expression of transient receptor potential cation channel (TRPC6) among prostate cancer (PCA) cells, establish high expression cell lines of TRPC6 and to provide potential cell mode for PCA oncogenesis and development.

Methods: Occurrence and development of PCA cells, PC3, PC-3M, DU145, 22 rv1, LNCaP and normal prostate epithelial cells in the PrEC TRPC6 expression level were detected by QPCR. Calcium phosphate transfection was used to package retrovirus pLEGFP-N1-TRPC6 and pLEGFP-N1-vector and infect the PCA cells, a stable high expression of TRPC6 PCA cells. Sable cell lines of TRPC6, MMP-2, MMP-9 expression was detected by QPCR and Western blot. Change of cell invasion ability was detected by Transwell.

Results: The expression level of PCA cells TRPC6 were higher than control group PrEC cells. Among TPRC6, the expression of cell line PC3 transfer potential were the lowest, and high transfer cell line PC-3M expression was the highest. RT-PCR and Western blot results showed that after filter, the seventh generation of cell TRPC6 protein and mRNA expression levels were higher than the control group. Transwell experimental results showed that the overexpression of TRPC6 could promote the invasion ability of PC3 PCA cells.

Conclusions: TRPC6 expressed in PCA cells is in disorder, and its action may be associated with the invasion and metastasis of PCA cells; successful establishment of stable high expression of TRPC6 PCA cells primarily confirm the invasion-trigger ability of TRPC6 on PCA, and lay down the foundation for exploring the TRPC6's role in the occurrence and development of PCA mechanism.

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