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The role of microRNA-370 in steroid-resistant focal segmental glomerulosclerosis

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***Abstract* — Dysregulated levels of microRNAs may be involved in the pathogenesis and response to steroid therapy in patients with focal segmental glomerulosclerosis (FSGS). An in-silico analysis indicated that miR-370 is contributed to biological adhesion, cation transport, regulation of ion transport, and metal ion transport in FSGS.**

Keywords* — *Nephrotic syndrome, FSGS, MicroRNAs, Steroid response

Motivation and Aim

Focal segmental glomerulosclerosis (FSGS) is the most common type of glomerular disease in adults [1]. Steroids are considered first-line therapeutic opportunities in these patients [2]. Patients with steroid-resistant FSGS without any improvement in their proteinuria are facing a gradual decline of kidney function and are destined to end-stage renal diseases (ESRD) [3]. Numerous lines of evidence suggested that microRNAs play a role in the modification of steroid responsiveness, consequently, they may act as potential molecular markers for steroid response.

An in-silico analysis was performed to understand the signaling pathways and biological procedures that may be regulated by miR-370 in steroid-resistant FSGS.

Methods

Gene expression data sets were downloaded from GEO datasets to find the significant differentially expressed mRNA. The GEO2R online tool was used for determining the differential expression of genes. miRwalk online tool was utilized for predicting target mRNAs of the miRNA. Twelve databases were selected for the predicting (miRWalk, Microt4, miRanda, mirbridge, miRDB, miRMap, miRNAMap, Pictar2, PITA, RNA22, RNAhybrid, and Targetscan). The target genes were chosen which exist in at least 3 aforementioned databases. The overlapping genes between the GEO datasets differentially expressed genes and predictive miRNA target genes were indicated by generating Venn diagram by R v3.5 programming. The shared gene sets were enriched by Gene Ontology (GO) (http://software.broadinstitute.org/gsea/msigdb/annotate.jsp). The GO data was visualized with R programming.

Results

Five newly updated datasets (GSE125779 (n=353), GSE129973 (n=176), GSE108113 (n=1531), GSE104948 (n=106), and GSE104066 (n=693) were downloaded for FSGS. Because of the similarity between the data, GSE108113 and GSE104066 were chosen for further investigations. GO annotation demonstrated that miR-370, mostly contributes to biological adhesion, cation transport, regulation of ion transport, cation transmembrane transport, and metal ion transport.

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