2020

Sp. lss. 106

Identification of differentially expressed genes and signaling pathways in diabetic nephropathy tubule by bioinformatics analysis

Shumei Tang

Central South University, XiangYa Hospital, China



T he pathogenesis of diabetic nephropathy (DN) is not completely clear. As a wide range application of highthroughput omics technology, various public network database platforms have included extensive transcriptomics data. Integrating these data provides better understandings of molecular functions and biological processes. We performed integrated bioinformatics to recognize differentially expressed genes and discussed potential molecular mechanisms in DN. The four expression profiles about DN were downloaded from the GEO database. The four microarray datasets were centralized, integrated and performed a difference analysis. Differentially expressed genes (DEGs) were deeply analyzed by gene ontology annotation and enrichment analysis. STRING database was used to conducted a PPI network and MCODE software was used to identify central genes. We identified 18 target DEGs, C3, PROM1, LUM, CPA3, SERPINA3, ANXA1, CX3CR1, AGR2, CD48, REG1A, RARRES1, CYP24A1, C1R, CFB, CDH6, PVALB, GADD45B and KLK1. GO analysis indicated that biological processes of DEGs concentrate on proteolysis, inflammatory response, complement activation and regulation of complement activation. Main cellular components include extracellular exosome, extracellular region, extracellular space, blood microparticle, protein complex and plasma membrane. Molecular functions include calcium ion binding and serine-type endopeptidase activity. DEGs were found that maybe mainly involved in staphylococcus aureus infection, renin-angiotensin system, and complement and coagulation cascades by KEGG pathway analysis. PPI network of DEGs were established by STRING database and one significant modules were identified by MCODE software. In addition, 3 hub genes, C3, CX3CR1 and ANXA1, were discerned from the PPI network.



Biography:

Xiangcheng Xiao is the director of Department of Nephrology, Xiangya Hospital, Central South University and holds a number of academic positions in China. He has published 50 papers in reputed journals.

Speaker Publications:

1. "Identification of C3 as a therapeutic target for diabetic nephropathy by bioinformatics analysis"

2. "P0998identification Of Differentially Expressed Genes And Pathways Signaling In Diabetic Nephropathy By **Bioinformatics Analysis**"

3." Role of Artificial Intelligence in Kidney Disease"

"Complement C3 as therapeutic target in diabetic 4. nephropathy by bioinformatics analysis".

5. "Ferroptosis and kidney diseases"

5th World Kidney Congress; Webinar - June 22-23, 2020.

Abstract Citation:

Shumei Tang, Identification of differentially expressed genes and signaling pathways in diabetic nephropathy tubule by bioinformatics analysis, Kidney Meet 2020, 5th World Kidney Congress; Webinar- June 22-23, 2020.

https://kidneycongress.nephroconferences.com/2020

Journal of Interventional Nephrology