

Title: Integrated Bioinformatics and Machine Learning Analysis Uncovers Key Pathways and Therapeutic Targets for Hypertension and Chronic Kidney Disease

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Abstract: Hypertension is a serious cardiovascular disease that substantially raises morbidity and mortality rates worldwide. People who have high blood pressure have been found to have an increased risk of developing chronic kidney disease (CKD) in recent years. The goal of this research is to use modern bioinformatics approaches to find potential treatment candidates and clarify the underlying biological pathways linked to both hypertension and CKD. Sample from individuals with CKD and hypertension were taken from two publicly available microarray datasets, GSE33463 and GSE66494. Consistent differentially expressed genes (DEGs) were found following thorough pre-processing and Python analysis. A Venn diagram was used to show where these DEGs' regulatory crossings were. The most functionally important genes were then identified via topological analysis after protein-protein interaction (PPI) networks were built. UBC, ARRIB1, FADD and EIF3D have been identified as important hub genes. These concordant DEGs are tightly linked to the Toll-like receptor signaling pathway, which is a crucial mechanism in the control of the immunological response, according to pathway enrichment analysis performed using the Kyoto Encyclopedia of Genes and Genomes (KEGG). In order to better understand gene relationships, future research will examine modular network studies, transcription factor (TF), microRNA (miRNA) network regulation, and gene ontology (GO) analysis. Concordant DEGs have been used to select a number of possible medicinal molecules, providing a promising path forward for therapeutic research..

Keywords: Hypertension, Chronic kidney disease (CKD), Differentially expressed genes, Protein-protein interactions, Hub gene, Drug molecule.

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