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Promoting Sustainable Kidney Health: The Asia-Pacific and Beyond

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Identification of Hub Genes and Biomarkers Associated with Oxidative Stress of Acute Kidney Injury Via Machine Learning Algorithm

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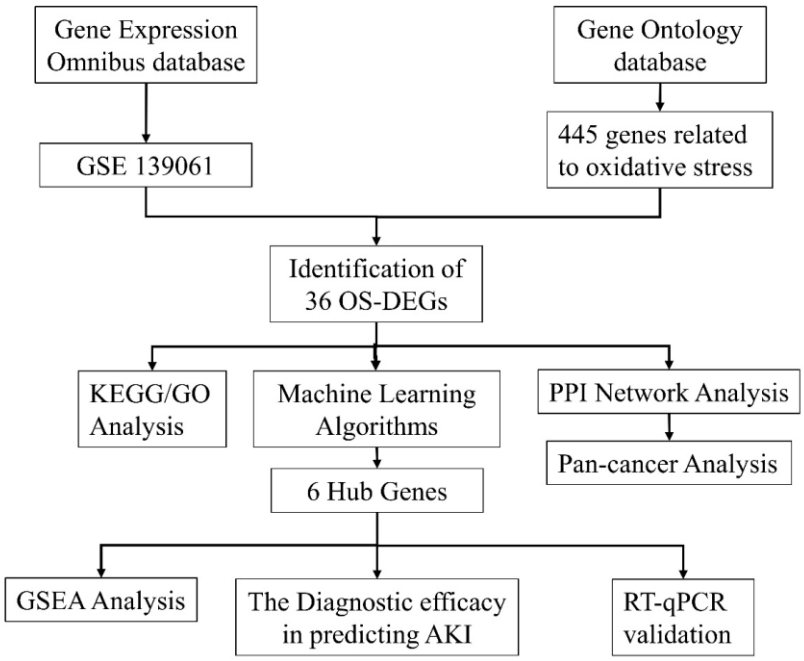
Objectives : Acute kidney injury (AKI) is a clinical complication that occurred in short term with deterioration of renal function. Numerous mechanisms contributed to the pathophysiology of AKI, where oxidative stress (OS) exerts an indispensable role. Enhanced OS from reactive oxygen species (ROS) and insufficient antioxidant systems aggravated AKI. Until now, effective early biomarkers and therapies for AKI have been lacking, however, broad application of bioinformatic analysis has the potential to ameliorate this situation.
Methods : In this study, we analyzed Gene Expression Omnibus (GEO) database of AKI and genes relevant to oxidative stress (OS) from Gene Ontology (GO) database with three kinds of machine learning algorithms to identify co-expressed different expressed genes. The associated pathway analysis was performed via DAVID (The Database for Annotation, Visualization and Integrated Discovery) and GSEA (Gene set enrichment analysis). Protein-protein interaction (PPI) network was constructed using the String database, and in vitro hypoxia-reoxygenation (H/R) model was established in HK-2 cells. Besides, the pan-cancer analysis of the intersection gene (HGF) in PPI and machine learning were used to further confirm its clinical value.
Results : In this study, we analyzed Gene Expression Omnibus (GEO) database of AKI and genes relevant to oxidative stress (OS) from Gene Ontology (GO) database with three kinds of machine learning algorithms to identify co-expressed different expressed genes. The associated pathway analysis was performed via DAVID (The Database for Annotation, Visualization and Integrated Discovery) and GSEA (Gene set enrichment analysis). Protein-protein interaction (PPI) network was constructed using the String database, and in vitro hypoxia-reoxygenation (H/R) model was established in HK-2 cells. Besides, the pan-cancer analysis of the intersection gene (HGF) in PPI and machine learning were used to further confirm its clinical value.
Conclusions : These data deepened current understanding of molecular mechanism of OS in AKI and provide novel biomarkers for clinical diagnosis and treatment.

Figure.png


Gene Expression Omnibus database
GSE 139061
Gene Ontology database
445 genes related to oxidative stress
Identification of 36 OS-DEGs
KEGG/GO Analysis
Machine Learning Algorithms
PPI Network Analysis
Pan-cancer Analysis
6 Hub Genes
GSEA Analysis
The Diagnostic efficacy in predicting AKI
RT-qPCR validation