KSN SEOUL, KOREA 2023
April 27(Thu) - 30(Sun), 2023
Coex, Seoul, Korea

Abstract Type : Poster
Abstract Submission No. : 1729

Transcriptome analysis in healing stage of ischemic reperfusion injury (IRI) mice model

Min Jee Jo[1], Jeong-An Gim[2], Ji Eun Kim[1], So Yon Bae[1], Shin-Young Ahn[1], Joo Kyung Lee[1], Eunjung Cho[1], Young-Joo Kwon[1], Gang-Jee Ko[1]
[1]Department of Internal Medicine-Nephrology, Korea University Guro Hospital, Korea, Republic of
[2]Department of Medical Science Research Center, Korea University College of Medicine, Korea, Republic of

Objectives: Vulnerability and incomplete recovery from acute kidney injury is considered as one of the main reasons for high prevalence of kidney dysfunction in aging kidney. This study aimed to identify novel diagnostic and prognostic targets for aging kidney through genome-based investigation.

Methods: Analysis of RNA sequencing (RNA-seq) data of kidneys were performed with Illumina's HiSeq 2000 at four weeks after unilateral reperfusion injury (IRI) for 45 minutes in 2 and 18-month-old C57BL/6 mald mice. Comparison with baseline genomic expression were examined by utilizing public RNA-seq data (GSE121330). Differentially expressed genes (DEGs) between old and young downregulated in old mice. GO enrichment network analysis based on 1,587 DEGs ischemic with cutoff of $p<0.001$ meaning significant difference between young and old mice kidneys in recovery phase after IRI revealed that biologic processes such as spliceosome and viral carcinogenesis, which were closely young groups were retrieved through t-test. P-value and fold change of DEGs were obtained, and visualized with volcano plot and heatmap. We performed 'PathfindR' R package for enrichment analysis.

Results: Sixty DEGs of kidneys changed after IRI significantly with distinct characteristics between old and young mice (satisfied with p-value<0.001 and |fold change|>2.5) were identified, and 51 of them were manifested in old mice. Fifty one genes including Car15, Fxyd2 and Slc17a1 significantly upregulated, whereas nine genes including Mmp12, Dcn and Arntl were associated with cell proliferation, were demonstrated to be downregulated significantly at four weeks after IRI in old mice.

Conclusions: Our study demonstrated a resource of gene profiles in the recovery phase of aging kidneys after IRI, which may be utilized as potential therapeutic targets.