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Single-Cell RNA Sequencing Identifies Stage-Specific Responses of Renal Endothelial Cells in Acute Kidney Injury

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Objectives : The inflammatory response to acute kidney injury (AKI) significantly influences subsequent renal health. Renal endothelial cells (ECs) are crucial for maintaining vascular homeostasis through their roles in regulating blood flow, vascular permeability, and immune cell trafficking. This study aims to elucidate the stage-specific transcriptional responses of human renal ECs following AKI.

Methods : We selected gene expression datasets from the Gene Expression Omnibus (GEO) database of the National Center for Biotechnology Information. Single-cell RNA sequencing data were analyzed to profile human renal EC subpopulations and examine their transcriptional changes at various AKI stages. The Seurat R package was utilized to process the UMI count matrix and to eliminate potential multiple captures.

Results : We observed unique gene expression changes corresponding to each AKI stage. Human renal ECs exhibited alterations in genes associated with endothelial apoptosis. In stage 1 AKI, there was a notable upregulation of Havcr-1, a recognized marker of kidney injury. Stage 2 AKI samples exhibited increased expression of Vcam1, indicating endothelial activation and inflammation. In stage 3 AKI, we observed elevated levels of Icam1 and E-selectin, markers of sustained endothelial activation and leukocyte adhesion. we identified key targets associated with AKI by cross-analyzing differentially expressed genes (DEGs) observed across different stages of AKI.

Conclusions : Our study elucidates the stage-specific gene expression profiles of human renal ECs during AKI. These findings suggest that distinct molecular responses in ECs at various AKI stages could serve as potential clinical indicators or therapeutic targets, enhancing the management and prognosis of kidney diseases.

Figure 1 KSN-2.jpg