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Single-cell RNA sequencing reveals immune landscape and cellular dynamics in peritoneal dialysis effluent

Siao Muk Cheng[1], Chih-Chuan Yu[1], An-Fu Lee[1], Chi-Yen Chang[1], Yi-Wen Chiu[2], Daw-Yang Hwang[1]
[1]Department of National Institute of Cancer Research, National Health Research Institutes, Taiwan
[2]Department of Division of Nephrology, Medical University Hospital, Taiwan

Objectives : Peritoneal dialysis (PD) is a widely used renal replacement therapy for patients with end-stage renal disease (ESRD). However, the roles of various cell populations in peritoneal fibrosis associated with dialysis remain poorly characterized.
Methods : Single-cell transcriptomic analysis was conducted on effluent samples from patients undergoing Early PD (1–2 years, n=5), Intermediate PD (3–6 years, n=5), and Late PD (7–12 years, n=3). Single-cell RNA sequencing was performed using the Chromium Single Cell 3' Reagent Kits v3.1 (10X Genomics) following the manufacturer's protocol. Sequencing data were processed with the Cell Ranger pipeline and further analyzed using the Seurat package (version 4.0.3) in R.
Results : A total of 102,698 high-quality cells were included in the analysis. Using UMAP visualization, we identified 28 distinct clusters. Based on differential gene expression (DEG) profiles, these clusters were classified into seven cell types: NKT cells, myeloid cells, mesothelial cells, B cells, plasmacytoid dendritic cells (pDCs), conventional dendritic cells type 1 (cDC1s), and neutrophils. Among these, NKT cells and myeloid cells were predominant across all PD stages. Compared with the early PD group, the proportion of myeloid cells significantly decreased, whereas NKT cells increased in the intermediate and late PD groups. Progressive enrichment of inflammatory response pathways was observed from short-term to long-term dialysis. Additionally, intercellular crosstalk analyses based on ligand-receptor interactions highlighted potential communication networks among different cell types during PD progression.
Conclusions : By investigating cellular functions at single-cell resolution, this study revealed distinct immune cell dynamics and their roles in PD. These findings contribute to a deeper understanding of PD biology and may inform future diagnostic and therapeutic strategies.