

【ISN-TSN Joint Symposium 1-5】

Multi-omics application in nephrology

Yi-Chun Tsai

Kaohsiung Medical University Chong-Ho Memorial Hospital, Kaohsiung Medical University

Multi-omics is an approach in biological and biomedical research that integrates data from multiple "omics" technologies, such as genomics, transcriptomics, proteomics, metabolomics, and epigenomics, to provide a more comprehensive understanding of biological systems. This approach helps researchers explore complex biological processes and diseases at different molecular levels, offering a holistic view of the interactions and pathways of kidney disease.

Single cell RNA sequencing (scRNA-seq), one tool of transcriptomics, is a cutting-edge technology that enables the study of gene expression at the level of individual cells. Unlike traditional RNA sequencing, which analyzes pooled RNA from a bulk tissue sample, scRNA-seq profiles gene expression in single cells, revealing cellular heterogeneity within a tissue. This high-resolution approach provides unique insights into the complex and dynamic processes that underlie kidney diseases. Our study group used scRNA-seq to explore early stage of diabetic kidney disease (DKD) and provided insights into the potential molecular mechanisms and therapeutic targets of early DKD.

In summary, multi-omics approaches including scRNA-seq represent a transformative strategy in biological research, offering more detailed insights into the molecular mechanisms of health and disease, and ultimately paving the way for more personalized and effective treatments.

