



The data point to interesting crosstalk between the cell types



GENE EXPRESSION

Single-cell RNA sequencing of collecting duct cells

Gene expression analyses of microdissected tubules have described the genes that are expressed by epithelial cells in all segments of the renal tubule. Most segments contain only one cell type in contrast to the collecting duct, which comprises at least three cell types: type A intercalated cells (A-ICs), type B intercalated cells (B-ICs) and principal cells (PCs). Consequently, gene expression analyses of microdissected collecting ducts provide only composite gene profiles. Researchers have now used single-cell RNA sequencing (RNA-seq) to assess the genes expressed by each of the cell types in the collecting duct, completing transcriptome coverage of every major epithelial cell type in the kidney.

To enrich for each of the three collecting duct cell types, Mark Knepper and colleagues first used FACs, employing known lectin cell-surface markers for PCs and B-ICs. Use of RNA-seq to quantify mRNA levels in the different populations identified two transcripts — *Hepacam2* and *c-Kit* — that encode additional cell-surface markers for ICs.

Single-cell RNA-seq of enriched cells defined transcriptomes for the three cell types. “The data point to interesting crosstalk between the cell types,” says Knepper. “For example, *Notch2* is expressed mainly in principal cells whereas its ligand *Jag1* is expressed predominantly in ICs. There were also some interesting findings regarding the expression of different G protein-coupled receptors. However, one of the key outcomes was the generation of a publicly accessible database of all mRNAs present in the three collecting duct cell types.” The researchers hope this database will provide useful information for investigators looking at development, physiology and pathophysiology of the collecting duct.

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DATABASES <https://hpcwebapps.cit.nih.gov/ESBL/Database/scRNA-Seq/>