

Analysis reveals how kidney cancer develops and responds to treatment

June 7 2021



Arul Chinnaiyan, M.D., Ph.D. Credit: University of Michigan Rogel Cancer Center

Not all kidney cancers behave the same, with wildly different responses to immunotherapy or other treatments—and wildly different outcomes

for patients as a result.

By sequencing the RNA of individual cells within multiple benign and cancerous kidney tumors, researchers from the University of Michigan Rogel Cancer Center have identified the cells from which different subtypes originate, the pathways involved and how the [tumor microenvironment](#) impacts cancer development and response to treatment.

The findings, published in *PNAS*, could help researchers better understand what forces are influencing [renal cell carcinoma](#) and guide oncologists in selecting the [best treatment](#) for each patient.

"Single cell RNA sequencing was key to allowing us to monitor [gene expression patterns](#) in each individual cell, revealing the mechanisms at play within the tumor microenvironment that can predict overall survival," says study author Arul Chinnaiyan, M.D., Ph.D., director of the Michigan Center for Translational Pathology and S.P. Hicks Professor of Pathology at Michigan Medicine.

Researchers generated gene expression atlases of both normal kidney and renal cell carcinoma samples. They predicted the putative cell of origin for more than 10 subtypes of renal cell cancer. The analysis also revealed pathways and interactions within the tumor microenvironment that predicted whether the tumor would respond to immunotherapy. This could lead to biomarkers to help guide [kidney cancer](#) treatment.

"By understanding the cell type where a cancer originates, it may allow us to target more precise treatments for that cancer type as well as better understand response to therapy," Chinnaiyan says.

More information: Yuping Zhang et al., "Single-cell analyses of renal cell cancers reveal insights into tumor microenvironment, cell of origin,

and therapy response," *PNAS* (2021).

www.pnas.org/cgi/doi/10.1073/pnas.2103240118

Provided by University of Michigan

Citation: Analysis reveals how kidney cancer develops and responds to treatment (2021, June 7)
retrieved 23 April 2024 from

<https://medicalxpress.com/news/2021-06-analysis-reveals-kidney-cancer-treatment.html>

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